

Math 150 - Methods in Biostatistics - Homework 7

your name here

Due: Friday, April 2, 2021

Assignment Summary (Goals)

- understanding of what a KM curve measures
- using R to plot KM curves and CIs
- considering KM curves separately for a categorical explanatory variable
- testing the null hypothesis of equality of $S(t)$ across an explanatory variable

Note that if you don't know the R code either check my notes or ask me!!! Happy to scaffold, debug, send resources, etc. Don't go down a rabbit hole trying to figure out an R function or syntax.

Important

The data are in the files tab on Canvas (in a folder called "data").

Make sure you have the **survival** (for the survival estimates) and the **survminer** (for the plots) packages installed.

Q1. PodQ Describe one thing you learned from someone in your pod this week (it could be: content, logistical help, background material, R information, etc.) 1-3 sentences.

Q2. Chp 9, A26 Provide a brief explanation of why the estimated variance of $\hat{S}_{KM}(0)$, and hence the standard error of $\hat{S}_{KM}(0)$, is equal to 0.

Q3. Chp 9, E4 Immediately after a heart transplant, patients are randomly assigned to two treatment therapies to improve recovery from the transplant, therapy 1 and therapy 2. The patients are then followed for up to 5 years after their surgery. Define the time-to-event random variable T as the time (in months) until recovery (the event) after a heart transplant. For each of the following study descriptions that involve T , sketch the graph of the survival curve (or curves) with as much detail as necessary. Please note that parts (a) through (d) are completely independent of each other.

- Therapy 1 is not very effective shortly after surgery, but everybody recovers before the study period is over.
- Therapy 2 is very effective shortly after surgery, but becomes less effective after 3 years. Not every patient fully recovers by the end of the study period.
- Two curves on the same plot: Therapy 1 is consistently more effective than Therapy 2 over time.
- Two curves on the same plot: Therapy 1 is more effective than Therapy 2 for the first 2.5 years, and then Therapy 2 is more effective than Therapy 1 for the remaining duration of the study.

Q4. Chp 9, E6 The Kaplan-Meier curve in Figure 9.17 (see the text, on Sakai) displays hypothetical estimated survival probabilities of death due to brain cancer, where time (from diagnosis) until death is measured in months.

- Is the largest event time censored or complete? How do you know?

(b) Use the curve to estimate the mean time until death due to brain cancer. [Read page 295 in the text.]

Q5. Chp 9, E11 Male Fruit Fly Longevity (Lots to read in the text about the dataset.)

- (a) Construct the Kaplan-Meier curve with a confidence interval for the **Fruitfly** data and describe the survival pattern for the fruitflies over time. Use **Longevity** as the time-to-event variable.

Look at the online notes example (<http://st47s.com/Math150/Notes/survival-analysis.html#Rsurv>) for how to implement the R code, but the basics of what you need are below. Look up `?ggsurvplot` (in the **survival** package) to see the different confidence interval types.

Notice that the “response variable” is now **two** variables!!! And we put them together with the **Surv()** function. The **Surv()** function takes two arguments. The first argument is the time variable. The second argument is the censoring information. You shouldn’t have to transform any of the variables in the dataset which is provided.

```
# look at the fruitfly data after you read it in!
fruitfly <- read_csv("https://pomona.box.com/shared/static/qnsl0sp0twdutz6azidxb5yt37boee7v",
  na="*")

fly_surv <- survfit(Surv(____, ____ ) ~ 1, data=____ )

ggsurvplot(____, conf.type = "____") +
  ggtitle("____")
```

- (b) Construct the Kaplan-Meier curve for the lifetimes of the fruitflies by number of partners, using **Partners** as the grouping variable. Briefly comment on the observed relationship between survival and number of female partners.

The R code will be very similar to part (a), but model the survival response variable as a function of the explanatory variable **Partners**.

```
fly_surv_part <- survfit(Surv(____, ____ ) ~ Partners, data=____ )
```

- (c) Perform the log-rank and Wilcoxon tests. Report the test statistics and p-values for both tests. State the conclusions for both tests. If the tests yield different conclusions, briefly explain why. [We will cover these tests on Monday in class.]

The R function which runs the two tests is called **survdifff()**. It acts on the **Surv()** response variable broken down by the explanatory variable, **Partners**.

The argument “rho = ____” controls which test you’d like to run. “rho = 0” gives the log-rank test. “rho = 1” gives the Wilcoxon test. Try typing `?survdifff` to see the help file.

```
survdifff(Surv(____,____) ~ ____ , data= ____ , rho=____)
survdifff(Surv(____,____) ~ ____ , data=____ , rho=____)

praise()
```

```
## [1] "You are stupendous!"
```