

Data Analysis

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```
knitr::opts_chunk$set(message=FALSE, warning=FALSE, fig.height=3, fig.width=5, fig.align="center")
library(tidyverse)
library(broom)
library(plyr)
library(survival)
library(survminer)
aids <- read.csv( "http://pages.pomona.edu/~jsh04747/courses/math150/AIDSdata.csv")
dim(aids)
```

```
## [1] 851 16
```

```
summary(aids)
```

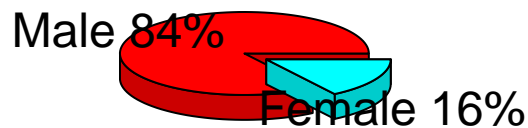
```
##      id      time      censor      time_d
## Min.   : 1.0   Min.   : 1.0   Min.   :0.00000   Min.   : 1.0
## 1st Qu.:287.5  1st Qu.:179.5  1st Qu.:0.00000   1st Qu.:199.5
## Median :581.0  Median :257.0  Median :0.00000   Median :266.0
## Mean   :579.5  Mean   :231.8  Mean   :0.08108   Mean   :243.4
## 3rd Qu.:873.0  3rd Qu.:300.0  3rd Qu.:0.00000   3rd Qu.:306.0
## Max.   :1156.0 Max.   :362.0  Max.   :1.00000   Max.   :362.0
##      censor_d      tx      txgrp      strat2
## Min.   :0.0000   Min.   :0.0000   Min.   :1.000   Min.   :0.0000
## 1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:1.000   1st Qu.:0.0000
## Median :0.0000   Median :1.0000   Median :2.000   Median :1.0000
## Mean   :0.0235   Mean   :0.5041   Mean   :1.504   Mean   :0.6157
## 3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:2.000   3rd Qu.:1.0000
## Max.   :1.0000   Max.   :1.0000   Max.   :2.000   Max.   :1.0000
##      sex      raceth      ivdrug      hemophil
## Min.   :1.000   Min.   :1.000   Min.   :1.000   Min.   :0.00000
## 1st Qu.:1.000   1st Qu.:1.000   1st Qu.:1.000   1st Qu.:0.00000
## Median :1.000   Median :1.000   Median :1.000   Median :0.00000
## Mean   :1.157   Mean   :1.706   Mean   :1.317   Mean   :0.03408
## 3rd Qu.:1.000   3rd Qu.:2.000   3rd Qu.:1.000   3rd Qu.:0.00000
## Max.   :2.000   Max.   :5.000   Max.   :3.000   Max.   :1.00000
```

```
##      karnof      cd4      priorzdv      age
## Min.   : 70.00   Min.   : 0.00   Min.   : 3.00   Min.   :15.00
## 1st Qu.: 90.00   1st Qu.: 22.25   1st Qu.: 11.00   1st Qu.:33.00
## Median : 90.00   Median : 75.00   Median : 21.00   Median :38.00
## Mean   : 91.34   Mean    : 86.45   Mean    : 30.63   Mean    :38.81
## 3rd Qu.:100.00   3rd Qu.:135.75   3rd Qu.: 44.00   3rd Qu.:44.00
## Max.   :100.00   Max.    :348.00   Max.    :288.00   Max.    :73.00
```

The data set contains a sample size equal to 851 participants and 16 different variables.

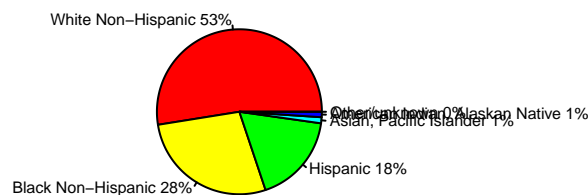
```
library(plotrix)
male<-sum(aids$sex==1)
female<-sum(aids$sex==2)
slices <- c(male, female)
lbls <- c("Male", "Female")
pct <- round(slices/sum(slices)*100)
lbls <- paste(lbls, pct)
lbls <- paste(lbls, "%", sep="")
pie3D(slices,labels=lbls,explode=0.1,
      main="Gender Distribution ", cex.lab=0.1)
```

Gender Distribution



The Pie Chart represents the gender distribution in the sample, with 84% male and 16% female. This shows the potential for the data to not be able to correctly represent the difference of the data variance by gender, if there were to be one. Therefore, gender is something to look into in future data analysis.

```
wnh<-sum(aids$raceth==1)
bnh<-sum(aids$raceth==2)
h<-sum(aids$raceth==3)
api<-sum(aids$raceth==4)
aian<-sum(aids$raceth==5)
oth<-sum(aids$raceth==6)
slices <- c(wnh,bnh,h,api,aian,oth)
lbls <- c("White Non-Hispanic", "Black Non-Hispanic", "Hispanic", "Asian, Pacific Islander", "American Indian or Alaska Native", "Other")
pct <- round(slices/sum(slices)*100)
lbls <- paste(lbls, pct)
lbls <- paste(lbls, "%", sep="")
pie(slices, lbls, col = rainbow(length(lbls)), cex=0.5 )
```

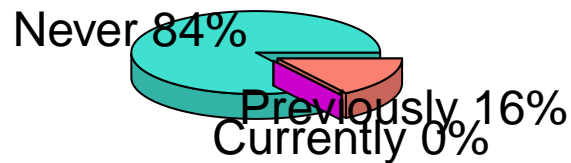


The distribution of race/ethnicity shows that the greatest number of participants consists of white non-hispanic identifying individuals, with black non-hispanic following and hispanic as the 3rd largest represented

group.

```
never<-sum(aids$ivdrug==1)
cur<-sum(aids$ivdrug==2)
prev<-sum(aids$ivdrug==3)
slices <- c(never,cur,prev)
lbls <- c("Never", "Currently", "Previously")
pct <- round(slices/sum(slices)*100)
lbls <- paste(lbls, pct)
lbls <- paste(lbls,"%",sep="")
pie3D(slices,labels=lbls,explode=0.1,col=c("turquoise","magenta","salmon"),cex.sub=0.5,
      main="IV Drug Use History ")
```

IV Drug Use History



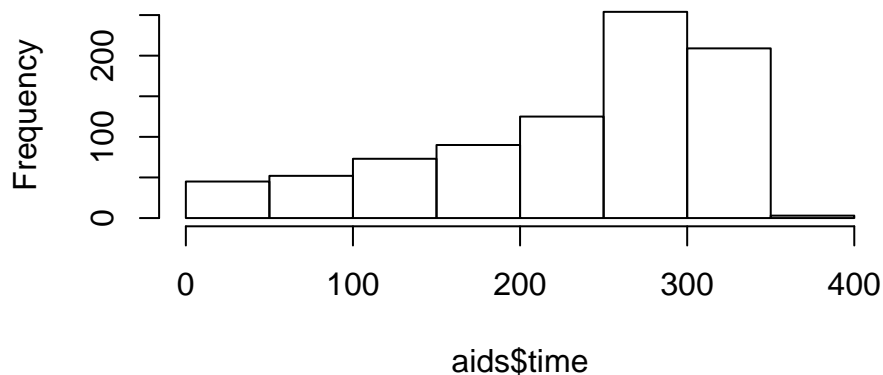
From this chart we see that most of the participants (84%) have never used IV drugs, whereas 16% of participants have some type of history of usage and none of the participants reported to be currently using the drugs.

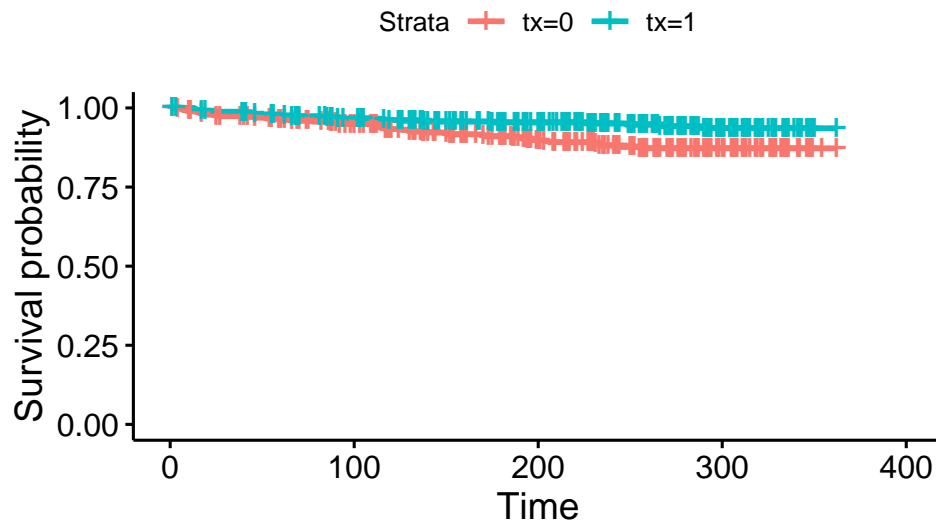
```
hist(aids$time)

###Data Plots

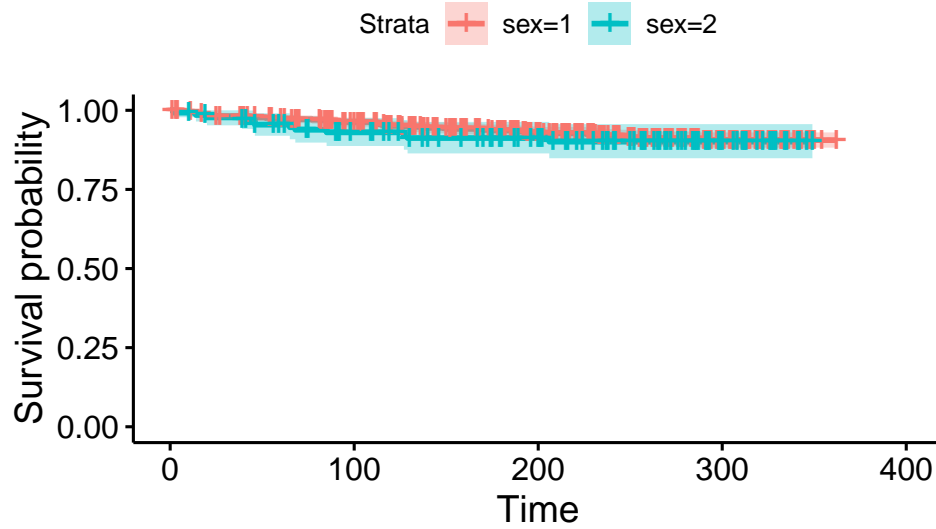
fit <- survfit(Surv(time,censor)~tx, data = aids)
ggsurvplot(fit,data = aids,conf.int = FALSE)
```

Histogram of aids\$time

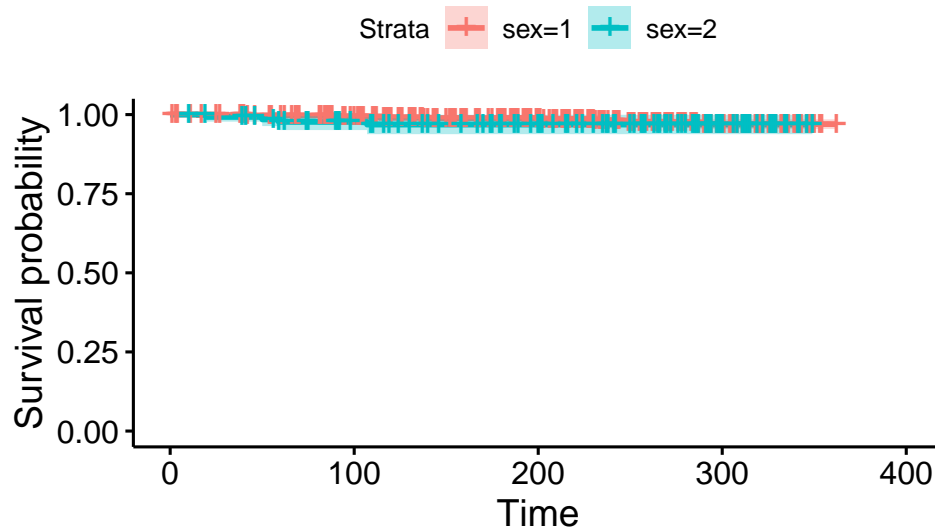




```
aids_fit_time <- survfit(Surv(time, censor) ~ sex, data=aids)
ggsurvplot(aids_fit_time, data=aids, conf.int = TRUE)
```



```
aids_fit_time.d <- survfit(Surv(time_d, censor_d) ~ sex, data=aids)
ggsurvplot(aids_fit_time.d, data=aids, conf.int = TRUE)
```



Survival Analysis

```
#mutation of age
aids <- read.csv( "http://pages.pomona.edu/~jsh04747/courses/math150/AIDSdata.csv")
aids <- aids %>%
  mutate(age = ifelse(age <= 20, "under20",
                      ifelse(age <=30, "20-30",
                              ifelse(age <= 40, "30-40",
                                      ifelse(age <=50, "40-50",
                                              ifelse(age <=60, "50-60",
                                                      ifelse(age <=70, "60-70", "over70")))))))) %>%
  mutate(age = factor(age,
                      levels = c("under20", "20-30", "30-40","40-50", "50-60","60-70","over70")), sex
```

```
library(survival)
library(survminer)
library(ggplot2)
library(broom)

coxph(Surv(time_d,censor_d) ~ sex , data=aids) %>% tidy()
```

```
## # A tibble: 1 x 7
##   term      estimate std.error statistic p.value conf.low conf.high
##   <chr>      <dbl>    <dbl>    <dbl>   <dbl>   <dbl>    <dbl>
## 1 sexmale    0.390    0.559     0.697   0.486   -0.706    1.49
```

```
coxph(Surv(time,censor) ~ sex, data=aids) %>% tidy()
```

```
## # A tibble: 1 x 7
##   term      estimate std.error statistic p.value conf.low conf.high
##   <chr>      <dbl>    <dbl>    <dbl>   <dbl>   <dbl>    <dbl>
## 1 sexmale    0.199    0.318     0.625   0.532   -0.424    0.821
```

```
coxph(Surv(time,censor) ~ age+ txgrp+ karnof, data=aids) %>% tidy()
```

```
## # A tibble: 8 x 7
```

```
##      term      estimate std.error statistic      p.value conf.low conf.high
##      <chr>         <dbl>    <dbl>    <dbl>      <dbl>    <dbl>    <dbl>
## 1 age20-30    -0.438      1.07    -0.409    0.682        -2.53     1.66
## 2 age30-40    -0.442      1.02    -0.434    0.665        -2.44     1.55
## 3 age40-50    -0.361      1.03    -0.352    0.725        -2.37     1.65
## 4 age50-60     0.460      1.04     0.442    0.659        -1.58     2.50
## 5 age60-70    -0.780      1.42    -0.551    0.582        -3.55     2.00
## 6 ageover70  -14.1      2688.    -0.00525  0.996        -Inf      Inf
## 7 txgrp       -0.844      0.257    -3.28    0.00103       -1.35    -0.340
## 8 karnof      -0.0814     0.0138   -5.89    0.00000000385 -0.109   -0.0543
```

```
cox.zph(coxph(Surv(time,censor) ~ age + txgrp+karnof, data=aids))
```

```
##           rho    chisq    p
## age20-30  0.09054 5.70e-01 0.450
## age30-40  0.19294 2.53e+00 0.112
## age40-50  0.14871 1.50e+00 0.220
## age50-60  0.19861 2.69e+00 0.101
## age60-70  0.16251 1.81e+00 0.179
## ageover70 0.16355 2.57e-07 1.000
## txgrp     -0.10779 8.34e-01 0.361
## karnof     0.00121 1.03e-04 0.992
## GLOBAL      NA 7.98e+00 0.435
```

```
coxph(Surv(time,censor) ~ age *txgrp*karnof, data=aids) %>% tidy()
```

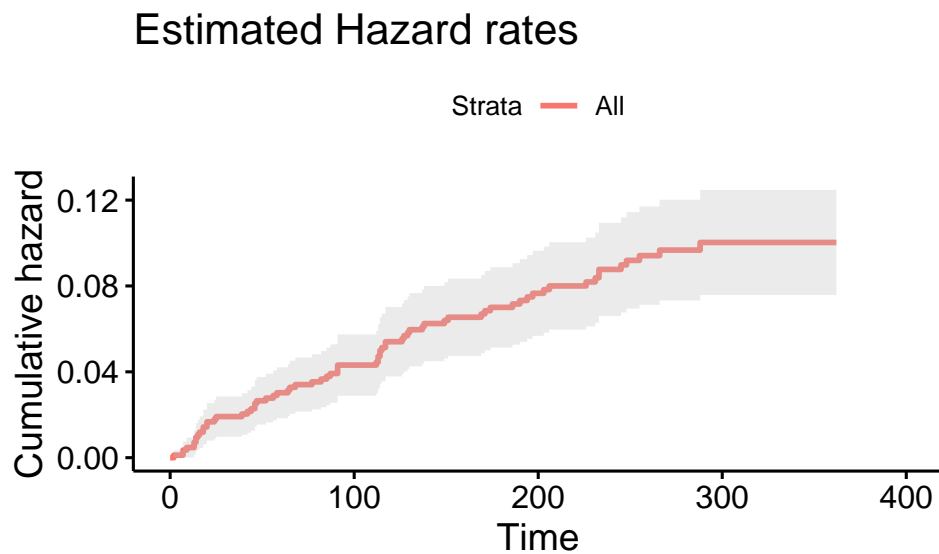
```
## # A tibble: 27 x 7
##      term      estimate std.error statistic p.value conf.low conf.high
##      <chr>         <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1 age20-30      307.    138277.  0.00222    0.998        -Inf      Inf
## 2 age30-40      319.    138277.  0.00231    0.998        -Inf      Inf
## 3 age40-50      327.    138277.  0.00237    0.998        -Inf      Inf
## 4 age50-60      343.    138277.  0.00248    0.998        -Inf      Inf
## 5 age60-70      287.    176491.  0.00163    0.999        -Inf      Inf
## 6 ageover70    -1.66    29414. -0.0000565 1.000        -Inf      Inf
## 7 txgrp         150.    92392.  0.00163    0.999        -Inf      Inf
## 8 karnof         3.36     1424.  0.00236    0.998        -Inf      Inf
## 9 age20-30:txgrp -144.    92392. -0.00156    0.999        -Inf      Inf
## 10 age30-40:txgrp -146.    92392. -0.00158    0.999        -Inf      Inf
## # ... with 17 more rows
```

```
cox.zph(coxph(Surv(time,censor) ~ age *txgrp*karnof, data=aids))
```

```
##           rho    chisq    p
## age20-30    -0.1008 4.31e-08 1.000
## age30-40    -0.1583 3.15e-08 1.000
## age40-50    -0.0965 1.25e-08 1.000
## age50-60    -0.2071 6.53e-08 1.000
## age60-70    -0.2062 3.04e-08 1.000
## ageover70   -0.2493 7.81e-11 1.000
## txgrp       -0.2032 2.68e-08 1.000
## karnof      -0.1974 5.24e-08 1.000
## age20-30:txgrp 0.0921 2.14e-08 1.000
## age30-40:txgrp 0.1142 1.08e-08 1.000
## age40-50:txgrp 0.0826 5.64e-09 1.000
## age50-60:txgrp 0.1851 3.47e-08 1.000
```

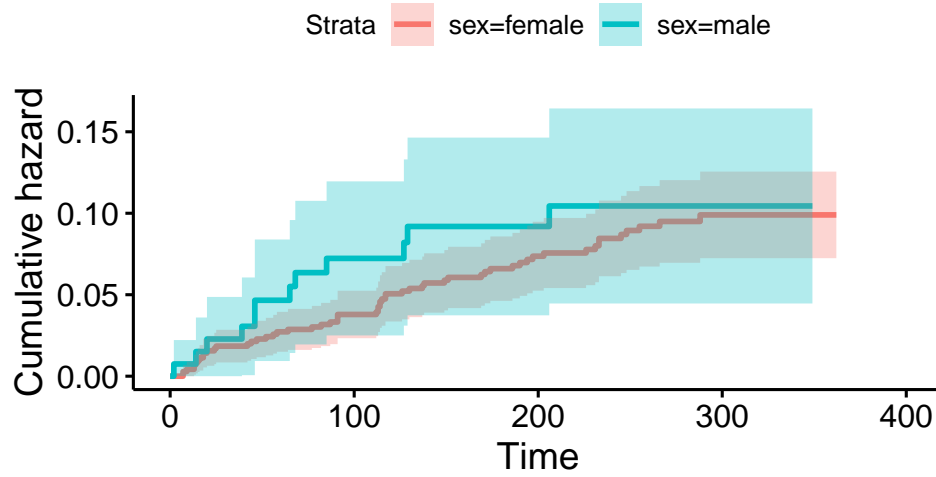
```
## age60-70:txgrp      0.2102 2.15e-08 1.000
## ageover70:txgrp     0.1967 3.96e-11 1.000
## age20-30:karnof     0.0984 4.53e-08 1.000
## age30-40:karnof     0.1524 3.44e-08 1.000
## age40-50:karnof     0.0938 1.40e-08 1.000
## age50-60:karnof     0.2053 7.78e-08 1.000
## age60-70:karnof     0.1978 3.00e-08 1.000
## ageover70:karnof      NA      NaN   NaN
## txgrp:karnof         0.1996 2.81e-08 1.000
## age20-30:txgrp:karnof -0.0910 2.15e-08 1.000
## age30-40:txgrp:karnof -0.1020 9.71e-09 1.000
## age40-50:txgrp:karnof -0.0823 6.23e-09 1.000
## age50-60:txgrp:karnof -0.1796 3.72e-08 1.000
## age60-70:txgrp:karnof -0.1981 1.98e-08 1.000
## ageover70:txgrp:karnof  NA      NaN   NaN
## GLOBAL              NA 1.84e+01 0.891
```

```
ggsurvplot(survfit(Surv(time,censor) ~ 1, data=aids),
  censor=F, conf.int=T, fun="cumhaz") + ggtitle("Estimated Hazard rates")
```



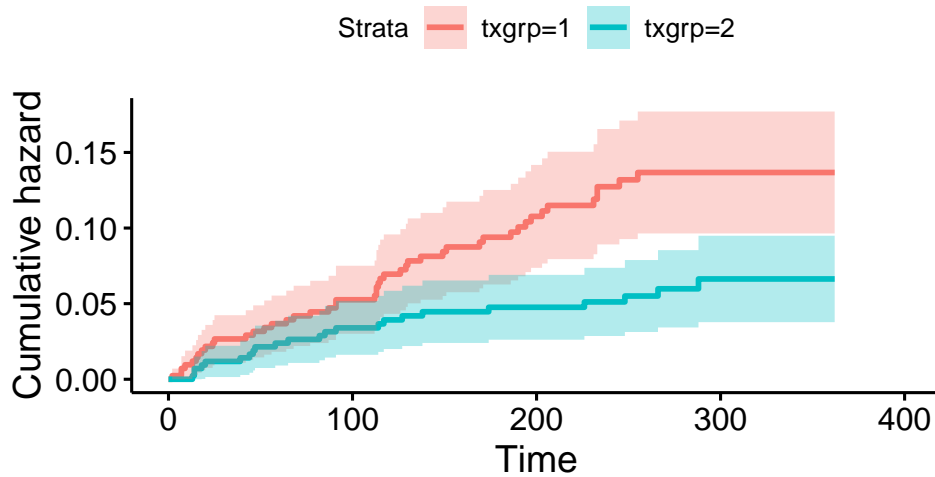
```
ggsurvplot(survfit(Surv(time,censor) ~ sex, data=aids),
  censor=F, conf.int=T, fun="cumhaz") + ggtitle("Estimated Hazard rates based on sex")
```

Estimated Hazard rates based on sex



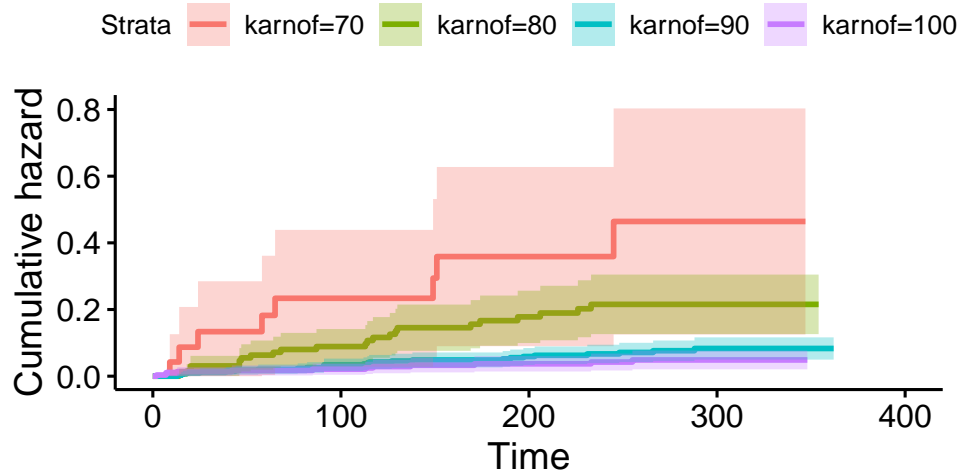
```
ggsurvplot(survfit(Surv(time,censor) ~ txgrp, data=aids),
  censor=F, conf.int=T, fun="cumhaz") + ggtitle("Estimated Hazard rates based on treatment group")
```

Estimated Hazard rates based on treatment



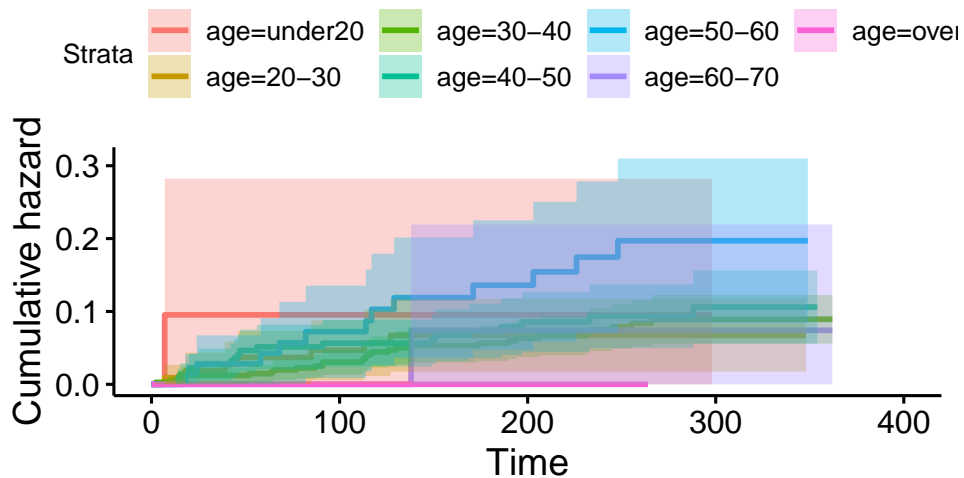
```
ggsurvplot(survfit(Surv(time,censor) ~ karnof, data=aids),
  censor=F, conf.int=T, fun="cumhaz") + ggtitle("Estimated Hazard rates based on karnofsky")
```


Estimated Hazard rates based on karnofsky



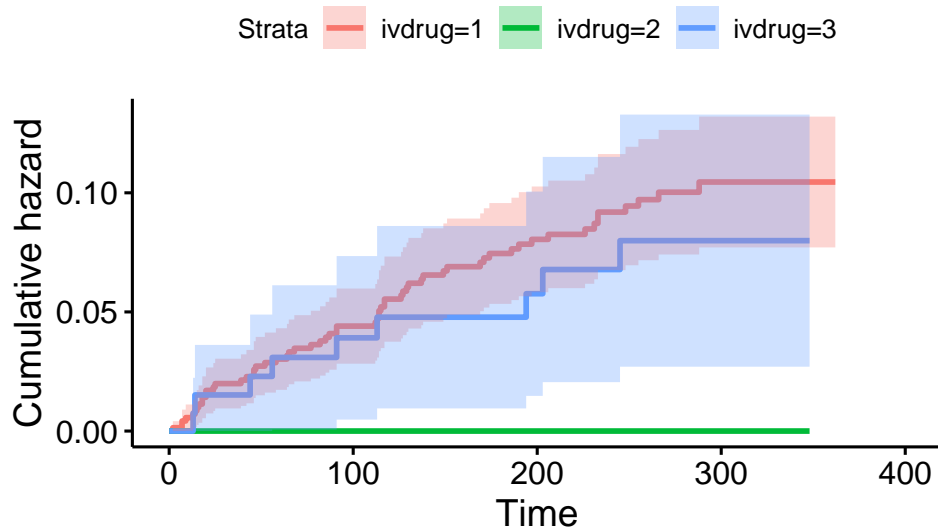
```
ggsurvplot(survfit(Surv(time, censor) ~ age, data=aids),
  censor=F, conf.int=T, fun="cumhaz") + ggtitle("Estimated Hazard rates based on age")
```

Estimated Hazard rates based on age



```
#ggsurvplot(survfit(Surv(time, censor)~hemophil, data = aids),
  #censor=F, conf.int = T, fun = "cumhaz")

ggsurvplot(survfit(Surv(time, censor)~ivdrug, data = aids),
  censor=F, conf.int = T, fun = "cumhaz")
```



```
coxph(Surv(time,censor) ~ ivdrug, data=aids) %>% tidy()
```

```
## # A tibble: 1 x 7
##   term      estimate std.error statistic p.value conf.low conf.high
##   <chr>      <dbl>    <dbl>    <dbl>  <dbl>   <dbl>   <dbl>
## 1 ivdrug    -0.130     0.179    -0.723  0.470   -0.481   0.222
```

```
coxph(Surv(time,censor) ~ ivdrug*karnof, data=aids) %>% tidy()
```

```
## # A tibble: 3 x 7
##   term      estimate std.error statistic p.value conf.low conf.high
##   <chr>      <dbl>    <dbl>    <dbl>  <dbl>   <dbl>   <dbl>
## 1 ivdrug    -0.711     1.71    -0.416  0.678   -4.07    2.64
## 2 karnof    -0.0903    0.0294   -3.07  0.00214 -0.148   -0.0326
## 3 ivdrug:karnof 0.00573    0.0201    0.285  0.775   -0.0336  0.0451
```

```
#how to modify so that sex is labeled as male and female
```

```
coxph(Surv(time,censor)~sex+tx+age+txgrp, data = aids) %>% tidy()
```

```
## # A tibble: 9 x 7
##   term      estimate std.error statistic p.value conf.low conf.high
##   <chr>      <dbl>    <dbl>    <dbl>  <dbl>   <dbl>   <dbl>
## 1 sexmale    0.302     0.324    0.931  0.352   -0.333    0.937
## 2 tx        -0.790     0.256   -3.08  0.00205 -1.29    -0.288
## 3 age20-30  -0.424     1.07    -0.396  0.692   -2.52    1.67
## 4 age30-40  -0.214     1.02    -0.209  0.834   -2.21    1.79
## 5 age40-50  -0.0490    1.03    -0.0475  0.962   -2.07    1.97
## 6 age50-60   0.639     1.05     0.611  0.541   -1.41    2.69
## 7 age60-70  -0.328     1.42    -0.231  0.817   -3.11    2.46
## 8 ageover70 -14.1    2672.    -0.00528  0.996   -Inf     Inf
## 9 txgrp      NA         0      NA      NA      NA      NA
```

Patricia's "Something New"

I will be doing a power analysis by simulating survival analysis curves

1. What is the topic?

The topic is using `sim.survdata` in R to simulate survival data. Using that simulated data, we will make that the alternative and control for the coefficient beta by setting it equal to some value. Then using power analysis, we will see how many times we reject H_0 .

2. How it is relevant? How it relates to survival analysis/analysis at hand?

Power analysis relates to survival analysis because if power is large after comparing our data to the simulated survival data, this tells us that there is a high chance that we would reject the null in favor of the alternative (control versus treatment?)

3. Resources to learn about the topic.

Below are some of the resources I have begun to use to learn about creating simulations of survival curves and performing power analysis:

a). https://cran.r-project.org/web/packages/coxed/vignettes/simulating_survival_data.html b). http://www.icssc.org/documents/advbiosgoa/tab%2026.00_survss.pdf

4. What will be challenging about learning something new?

Learning something new will be challenging because in this case, the concept of power analysis is something I just recently learned in Intro to Statistics. So learning to apply this concept in the context of survival analysis curves will be a challenge for me to learn. Learning how to simulate survival curves will also be challenging because I will have to learn how to use and interpret new functions in R.

Juste's "Something New"

I will be analyzing the Schoenfeld residuals for the Cox PH model.

1. What is going on? What is the topic? 2. How it is relevant? How it relates to survival analysis/analysis at hand?

Cox proportional hazards (PH) model is considered a great way to identify combined effects of several covariates on the relative risk (hazard). This model assumes that the hazards of the different strata formed by the levels of the covariates are proportional. This proportional hazards assumption is particularly important and can be tested via three different classes of tests. The first class is focused on the piecewise estimation of models for subsets of data defined by stratification of time. The second one considers the interactions between covariates and some function of time. Final, third one is based on examinations of regression residuals. The Schoenfeld Residuals are a part of the third class of proportional hazard assumption testing and I will be exploring it in order to be able to eradicate a method for testing for the PH assumption in the current and future data set analyses. This topic is particularly important in relation to survival analysis since it provides an idea of whether the model is appropriate for the data set at hand and whether some covariates should be considered as variants of time in order to supply the best model for prediction of proportional hazards.

3. Resources to learn about the topic.

I have been researching articles and scientific journals that provide insights into this model and comparisons between the Cox PH and the parametric model. Sources include: a) <https://krex.k-state.edu/dspace/bitstream/handle/2097/8787/AngelaCrumer2011.pdf> b) http://nematilab.info/bmijc/assets/weibull_cox.pdf c) <https://www.jstatsoft.org/article/view/v070i08>

4. What will be challenging about learning something new?

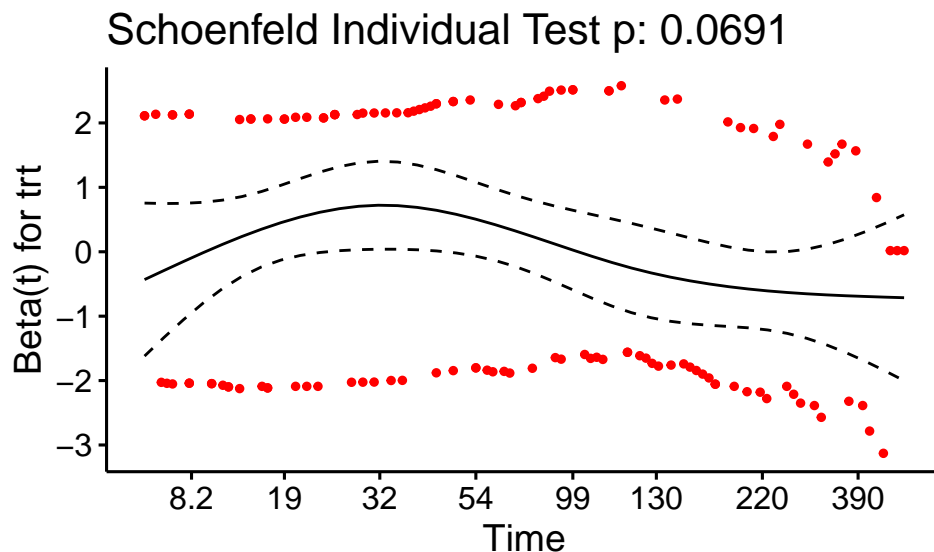
Taking a completely new model of analyzing survival data is particularly difficult since the mathematical derivations and notations are also very varied from what we have seen in class. Although, I do remember some of the ideas behind parametric functions, their applications to statistical models are much more challenging than I have expected. Therefore, it will require me a lot of time and extensive research to be able to understand and learn how to apply this model to our data and other instances of survival analysis.

SHoenfeld:

```
veteran.ph <- coxph(Surv(time,status) ~ trt, data=veteran)
cox.veteran <- cox.zph(veteran.ph)
cox.veteran
```

```
##      rho chisq      p
## trt -0.16   3.3 0.0691
```

```
ggcoxzph(cox.veteran)
```



```
ggcoxdiagnostics(veteran.ph, type="schoenfeld")
```

