Kaplan-Meier plots

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```
bcdf<-readRDS("breastcancerdf.rds")
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(survival)
library(survminer)
```

```
## Loading required package: ggplot2

## Loading required package: ggpubr
```

###Pre-select Select 8 variables that are used to draw the Kaplan Meier Plots: race(DEMO_RACE),age(DEMO_AGE_AT_D
ER(PATH_ER), PR(PATH_PR), HER2(PATH_HER2), grade(PATH_SURGERYOVERALLGRADE),
stage, menopause(HORMO_HORMO_MENOPAUSESTATUS)
and 5 death and relapse status variables (response) Then, we change the variable names for convenience.

```
kmpdf<-bcdf[,c(1:3,6:8,13,20,4,15:16,19,18,17)]
names(kmpdf)<-c("id","race","age","ER","PR","HER2","grade","stage","menopause",
                "metastatic","survival","survival_month","relapse","relapse_month")
```

```
head(kmpdf)
```

```
## # A tibble: 6 x 14
##      id race    age    ER    PR  HER2 grade stage menopause metastatic survival
##   <dbl> <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>     <dbl> <chr>         <dbl>
## 1   835 White    91     1     1     0    NA     0         0 No                1
## 2   838 White    87     1     0     1     0     0         0 No                1
## 3   837 White    43     0     1     1    NA     0         1 No                0
## 4   841 White    59     1     1     0     0     0         0 No                0
## 5   865 White    69     1     1     0     0     0         0 No                0
## 6   881 White    42     1     1     1     1     0         1 No                0
## # ... with 3 more variables: survival_month <dbl>, relapse <dbl>,
## #   relapse_month <dbl>
```

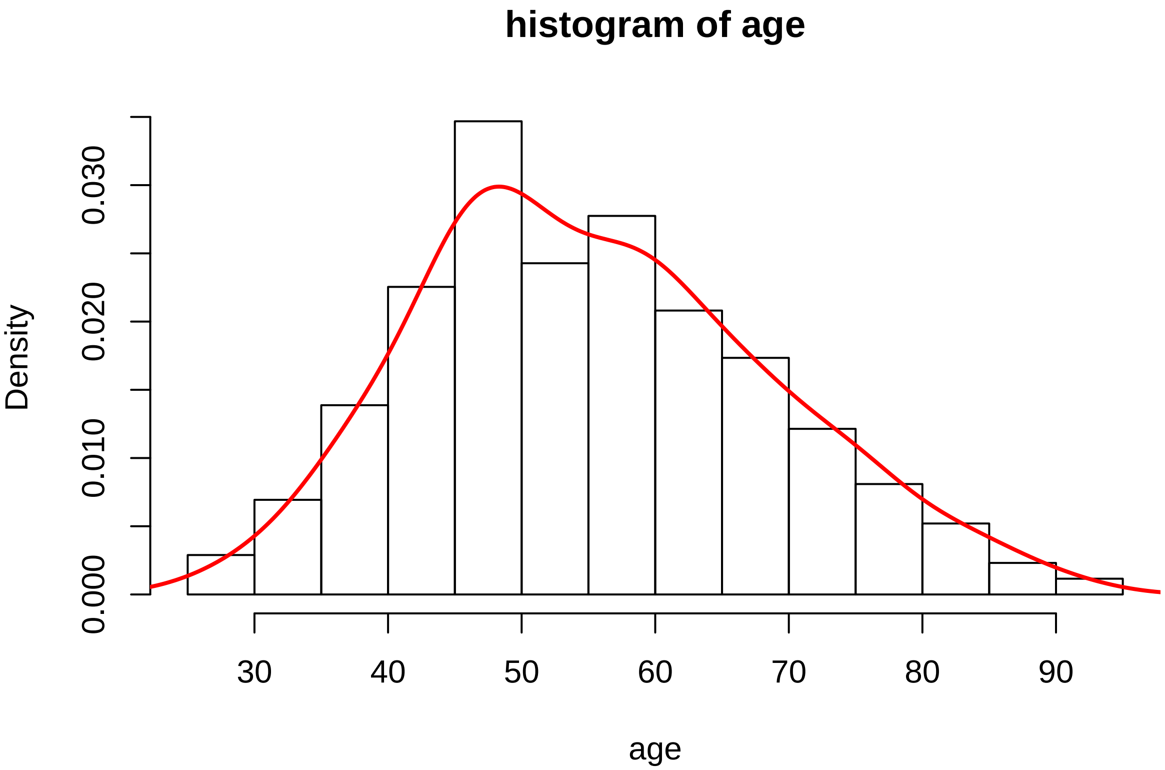
```
median(kmpdf$age)
```

```
## [1] 54
```

```
mean(kmpdf$age)
```

```
## [1] 55.58671
```

```
hist(kmpdf$age,freq=FALSE,main="histogram of age", xlab="age" )
lines(density(kmpdf$age),lwd=2, col=2) #kernel density plot
```



The density plot shows that the age variable is approximately normal distributed. Since mean(55.58671) is slightly greater than median(54), the variable is slightly right skewed. Divide age into two groups by the median of age. If age is below the 54, we note it as “young”; otherwise “old”.

```
kmpdf$age<-ifelse(kmpdf$age<median(kmpdf$age),"young","old")
head(kmpdf)
```

```
## # A tibble: 6 x 14
##      id race  age      ER    PR  HER2 grade stage menopause metastatic survival
##   <dbl> <chr> <chr> <dbl> <dbl> <dbl> <dbl> <dbl>     <dbl> <chr>         <dbl>
## 1   835 White old       1     1     0    NA     0         0 No                1
## 2   838 White old       1     0     1     0     0         0 No                1
## 3   837 White young     0     1     1    NA     0         1 No                0
## 4   841 White old       1     1     0     0     0         0 No                0
## 5   865 White old       1     1     0     0     0         0 No                0
## 6   881 White young     1     1     1     1     0         1 No                0
## # ... with 3 more variables: survival_month <dbl>, relapse <dbl>,
## #   relapse_month <dbl>
```

Delete observations that race are specified as “other”. We only focus on “Black” and “White” in race.

```
kmpdf<-kmpdf[kmpdf$race!="Other",]
summary(kmpdf[,-1])
```

```
##      race               age                  ER               PR        
##  Length:341         Length:341         Min.   :0.0000   Min.   :0.0000  
##  Class :character   Class :character   1st Qu.:0.0000   1st Qu.:0.0000  
##  Mode  :character   Mode  :character   Median :1.0000   Median :1.0000  
##                                        Mean   :0.7214   Mean   :0.6334  
##                                        3rd Qu.:1.0000   3rd Qu.:1.0000  
##                                        Max.   :1.0000   Max.   :1.0000  
##                                                                         
##       HER2            grade            stage          menopause     
##  Min.   :0.0000   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000  
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000  
##  Median :0.0000   Median :0.0000   Median :0.0000   Median :0.0000  
##  Mean   :0.2053   Mean   :0.4768   Mean   :0.1877   Mean   :0.4194  
##  3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.:1.0000  
##  Max.   :1.0000   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000  
##                   NA's   :18                                        
##   metastatic           survival      survival_month     relapse      
##  Length:341         Min.   :0.0000   Min.   :  1.0   Min.   :0.0000  
##  Class :character   1st Qu.:0.0000   1st Qu.: 69.0   1st Qu.:0.0000  
##  Mode  :character   Median :0.0000   Median :118.0   Median :0.0000  
##                     Mean   :0.2845   Mean   :112.1   Mean   :0.1906  
##                     3rd Qu.:1.0000   3rd Qu.:148.0   3rd Qu.:0.0000  
##                     Max.   :1.0000   Max.   :225.0   Max.   :1.0000  
##                                                                      
##  relapse_month   
##  Min.   :  0.00  
##  1st Qu.: 13.00  
##  Median : 37.00  
##  Mean   : 49.82  
##  3rd Qu.: 82.00  
##  Max.   :166.00  
##  NA's   :276     
```

Convert most variables to factors except id and the response(survial, survival months, relapse, and relapse month). Not convert survival and relapse because survival analyses require them to be numeric events.

```
kmpdf[,-c(1,11:14)]<-lapply(kmpdf[,-c(1,11:14)],as.factor)
summary(kmpdf)
```

```
##       id             race        age      ER      PR      HER2     grade    
##  Min.   :     92   Black: 87   old  :177   0: 95   0:125   0:271   0    :169  
##  1st Qu.:    907   White:254   young:164   1:246   1:216   1: 70   1    :154  
##  Median :    998                                                   NA's: 18  
##  Mean   :   6885                                                             
##  3rd Qu.:   1092                                                             
##  Max.   :2000978                                                             
##                                                                              
##  stage   menopause metastatic    survival      survival_month     relapse      
##  0:277   0:198     No :290    Min.   :0.0000   Min.   :  1.0   Min.   :0.0000  
##  1: 64   1:143     Yes: 51    1st Qu.:0.0000   1st Qu.: 69.0   1st Qu.:0.0000  
##                               Median :0.0000   Median :118.0   Median :0.0000  
##                               Mean   :0.2845   Mean   :112.1   Mean   :0.1906  
##                               3rd Qu.:1.0000   3rd Qu.:148.0   3rd Qu.:0.0000  
##                               Max.   :1.0000   Max.   :225.0   Max.   :1.0000  
##                                                                                
```

```
##  relapse_month
##  Min.   :  0.00
##  1st Qu.: 13.00
##  Median : 37.00
##  Mean   : 49.82
##  3rd Qu.: 82.00
##  Max.   :166.00
##  NA's   :276
```

```
sapply(c(11,13),function(x){table(kmpdf[,x])})
```

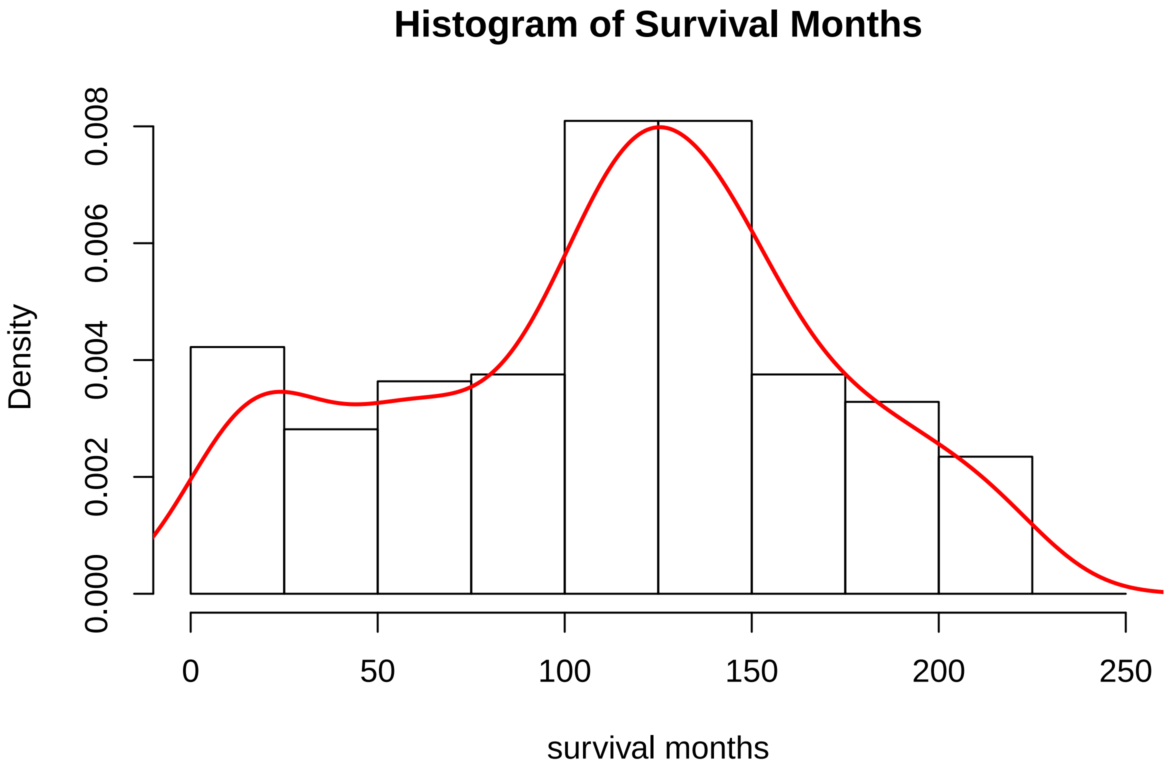
```
##   [,1] [,2]
## 0  244  276
## 1   97   65
```

survival: 0: alive 1:dead relapse: 0: no relapse 1: local and/or distant cancer recurrence or died of disease

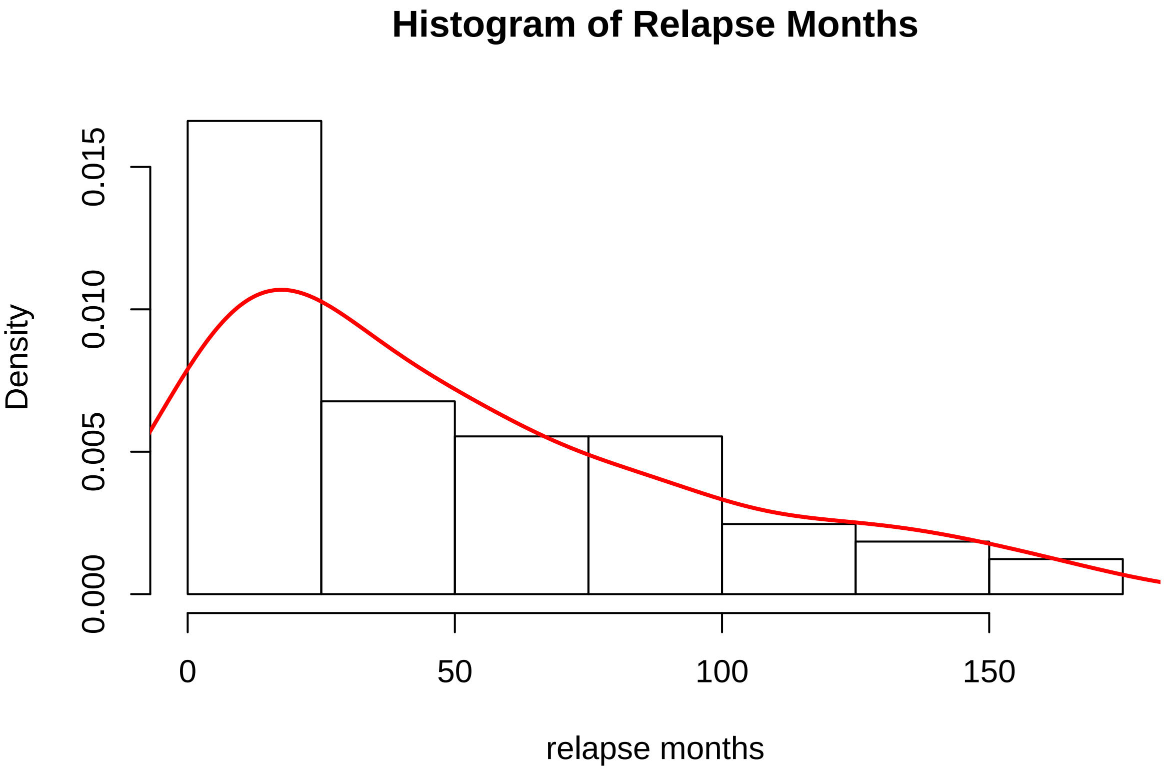
```
saveRDS(kmpdf,"kmplotdf.rds")
```

###Plot the density of survival month and relapse month

```
hist(kmpdf$survival_month,breaks =seq(0,250,25) ,freq=FALSE,xlim=c(0,250),
     main="Histogram of Survival Months",xlab= "survival months")
lines(density(kmpdf$survival_month),lwd=2,col=2)
```



```
hist(kmpdf$relapse_month,breaks =seq(0,175,25) ,freq=FALSE,xlim=c(0,175),
     main="Histogram of Relapse Months",xlab= "relapse months")
lines(density(kmpdf$relapse_month,na.rm = TRUE),lwd=2,col=2)
```



The distribution of survival months is quite normal, even though it's left skewed a little bit, which means that more observations than expected have short survival months. There are only 65 observations that has the relapse months data. The histogram shows that the data maybe follow a poission distribution with a small parameter λ.

```r
attach(kmpdf)
```

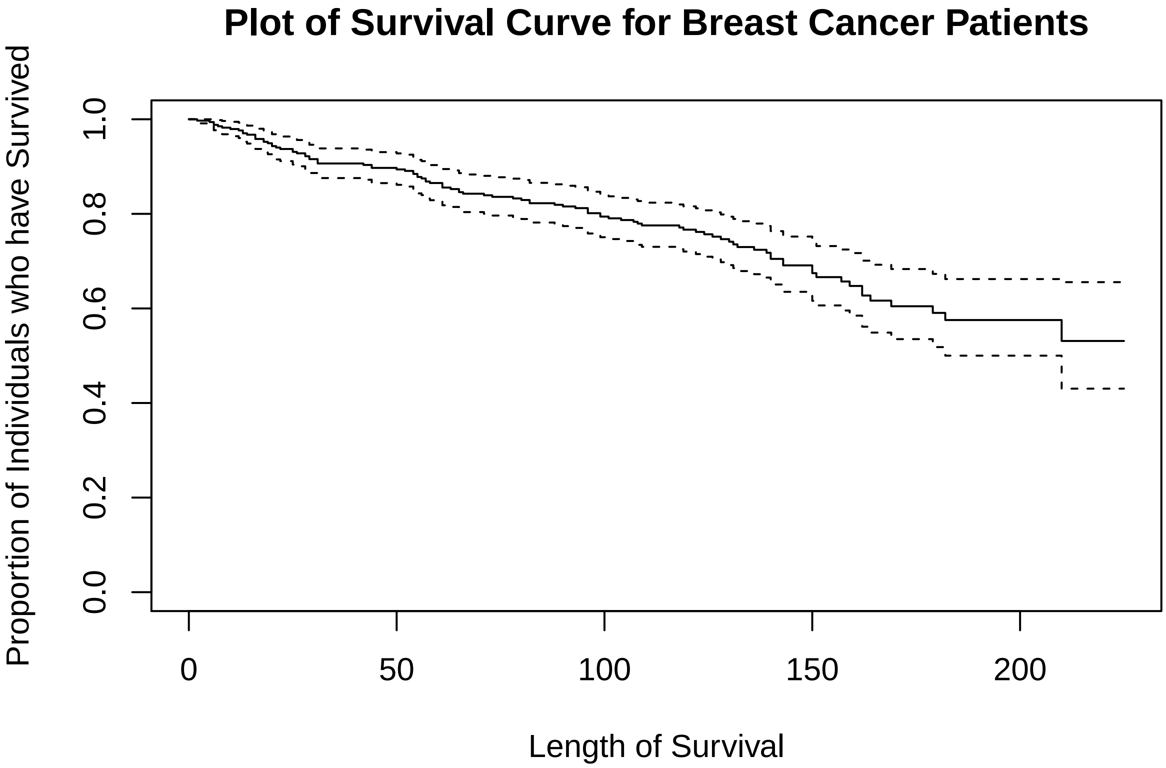
Kaplan Meier Curves

####Overall Compare the survival distribution to examine whether or not there is an association between features and length of survival

```r
surv.all<-survfit(Surv(survival_month,survival)~1)
summary(surv.all)
```

```
## Call: survfit(formula = Surv(survival_month, survival) ~ 1)
##
##  time n.risk n.event survival std.err lower 95% CI upper 95% CI
##     2    340       1    0.997 0.00294        0.991        1.000
##     5    339       1    0.994 0.00415        0.986        1.000
##     6    336       2    0.988 0.00587        0.977        1.000
##     7    333       1    0.985 0.00656        0.972        0.998
##     8    332       1    0.982 0.00718        0.968        0.996
##    10    331       1    0.979 0.00774        0.964        0.995
##    12    330       1    0.976 0.00827        0.960        0.993
##    13    327       2    0.970 0.00923        0.952        0.989
##    14    324       1    0.967 0.00968        0.949        0.987
##    16    322       3    0.958 0.01090        0.937        0.980
##    18    318       2    0.952 0.01163        0.930        0.975
##    19    315       1    0.949 0.01198        0.926        0.973
##    20    313       2    0.943 0.01265        0.919        0.968
##    21    310       1    0.940 0.01297        0.915        0.966
##    22    308       1    0.937 0.01328        0.911        0.964
##    25    307       2    0.931 0.01388        0.904        0.959
##    26    305       1    0.928 0.01417        0.901        0.956
##    28    304       2    0.922 0.01472        0.893        0.951
##    29    300       2    0.916 0.01525        0.886        0.946
##    31    298       3    0.907 0.01599        0.876        0.938
##    42    291       1    0.903 0.01624        0.872        0.936
##    44    289       2    0.897 0.01672        0.865        0.931
##    50    282       1    0.894 0.01696        0.861        0.928
##    52    281       1    0.891 0.01719        0.858        0.925
##    54    279       2    0.884 0.01765        0.850        0.920
##    55    277       2    0.878 0.01810        0.843        0.914
##    56    275       1    0.875 0.01831        0.840        0.911
##    57    273       2    0.868 0.01873        0.832        0.906
##    58    271       1    0.865 0.01893        0.829        0.903
##    61    270       3    0.856 0.01952        0.818        0.895
##    63    265       1    0.852 0.01971        0.815        0.892
##    65    261       2    0.846 0.02009        0.807        0.886
##    66    259       1    0.843 0.02028        0.804        0.883
##    71    255       1    0.839 0.02047        0.800        0.880
##    73    252       1    0.836 0.02065        0.796        0.877
##    78    250       1    0.833 0.02084        0.793        0.874
##    80    249       1    0.829 0.02102        0.789        0.871
##    82    246       2    0.823 0.02139        0.782        0.866
##    88    241       1    0.819 0.02157        0.778        0.862
##    90    237       1    0.816 0.02175        0.774        0.859
##    93    232       1    0.812 0.02194        0.770        0.856
##    96    227       3    0.801 0.02251        0.758        0.847
##    99    223       2    0.794 0.02287        0.751        0.840
##   101    218       1    0.791 0.02306        0.747        0.837
##   104    213       1    0.787 0.02324        0.743        0.834
##   107    211       1    0.783 0.02343        0.739        0.830
##   108    208       1    0.779 0.02362        0.734        0.827
##   109    205       1    0.776 0.02381        0.730        0.824
##   118    174       1    0.771 0.02408        0.725        0.820
##   119    170       1    0.767 0.02437        0.720        0.816
##   122    161       1    0.762 0.02468        0.715        0.812
##   124    152       1    0.757 0.02502        0.709        0.807
##   126    149       1    0.752 0.02536        0.704        0.803
##   128    144       1    0.746 0.02572        0.698        0.799
##   130    136       1    0.741 0.02611        0.692        0.794
##   131    133       1    0.735 0.02650        0.685        0.789
##   132    131       1    0.730 0.02688        0.679        0.784
##   136    125       1    0.724 0.02729        0.672        0.779
##   139    115       1    0.718 0.02777        0.665        0.774
##   140    111       2    0.705 0.02874        0.651        0.763
##   143    103       2    0.691 0.02977        0.635        0.752
##   150     84       2    0.675 0.03125        0.616        0.739
##   151     80       1    0.666 0.03197        0.606        0.732
##   157     72       1    0.657 0.03284        0.596        0.725
##   159     70       1    0.648 0.03369        0.585        0.717
##   162     64       2    0.627 0.03554        0.561        0.701
##    164      58       1    0.616 0.03654        0.549        0.692
##    169      52       1    0.605 0.03771        0.535        0.683
##    179      43       1    0.591 0.03937        0.518        0.673
##    182      39       1    0.575 0.04117        0.500        0.662
##    210      13       1    0.531 0.05703        0.430        0.656
```

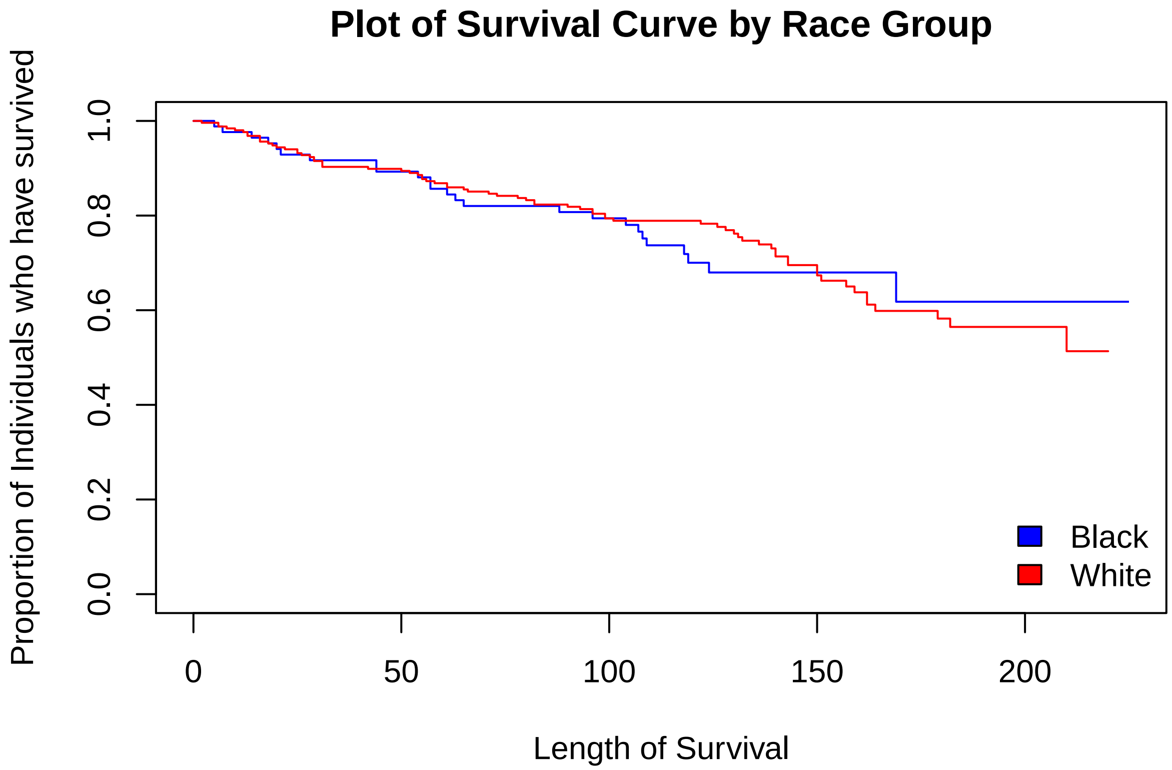
```
plot(surv.all,main="Plot of Survival Curve for Breast Cancer Patients",xlab= "Length of Survival", ylab=
```



For the 341 people in the dataset, 97 people were uncensored(followed for the entire time, until occurence of event). Since the data has not yet dropped to 50% survival at the end of the available data, there is an NA value for median survival. The following summary goes through each time point in the study in which an individual was lost to follow up or died and re-computes the total number of people still at risk (n.risk), the number of events at that time point (n.event), the proportion of individuals who survived up until that point (survival) and the standard error (std.err) and 95% confidence interval (lower 95% CI, upper 95% CI) for the proportion of individuals who survived at that point. This plot shows the survival curve (also known as a Kaplan-Meier plot), the proportion of individual who have survived up until that particular time as a solid black line and the 95% confidence interval (the dashed lines).

####Race

```
surv.race<-survfit(Surv(survival_month,survival)~race)
plot(surv.race,col=c("blue","red"),ylim = c(0,1),
     main="Plot of Survival Curve by Race Group",
     xlab = "Length of Survival",ylab= "Proportion of Individuals who have survived")
legend("bottomright",legend=c("Black","White"),fill=c("blue","red"),bty="n")
```



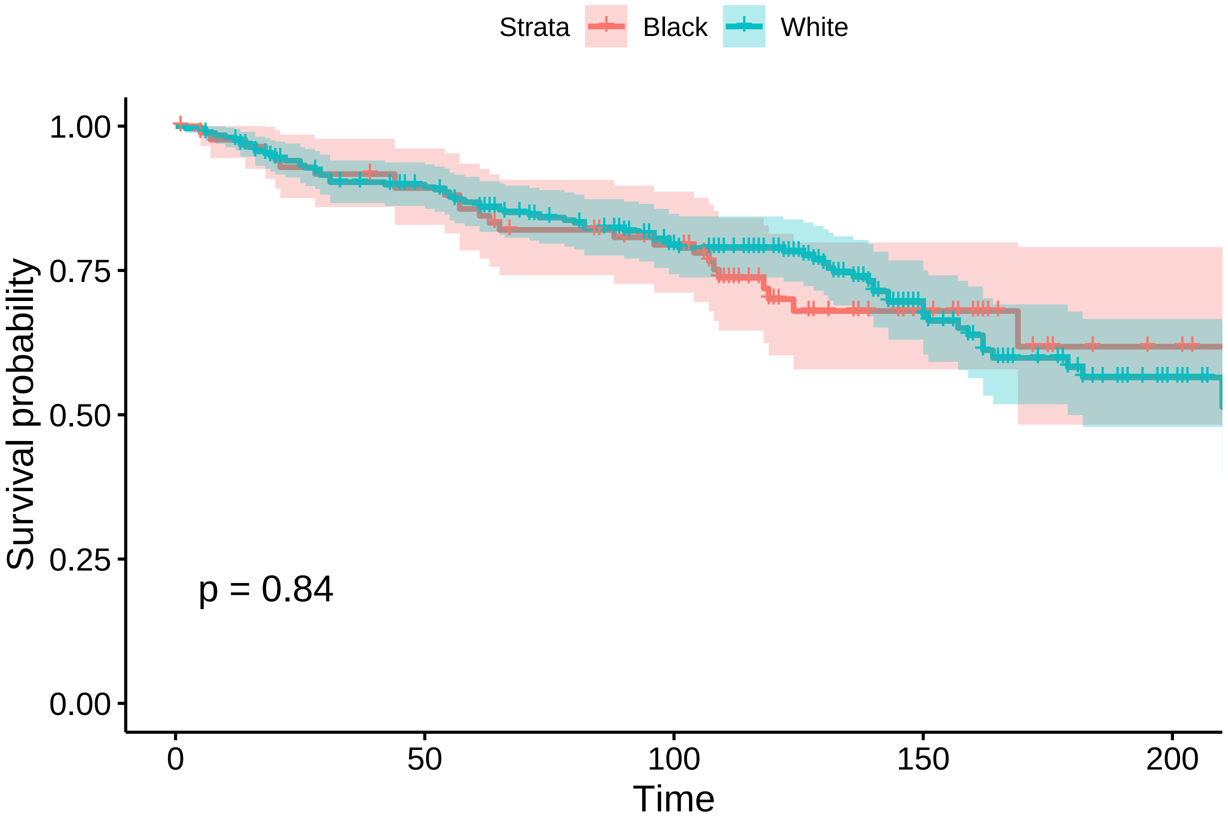
```
#Since the levels are "Black","White"
survdiff(Surv(survival_month,survival)~race)
```

```
## Call:
## survdiff(formula = Surv(survival_month, survival) ~ race)
##
##                N Observed Expected (O-E)^2/E (O-E)^2/V
## race=Black  87       25     24.1   0.02996    0.0401
## race=White 254       72     72.9   0.00993    0.0401
##
##  Chisq= 0  on 1 degrees of freedom, p= 0.8
```

The 95% confidence interval of survival time for those on maintained chemotherapy is (, NA); NA in this case means infinity. A 95% upper confidence limit of NA/infinity is common in survival analysis due to the fact that the data is skewed.

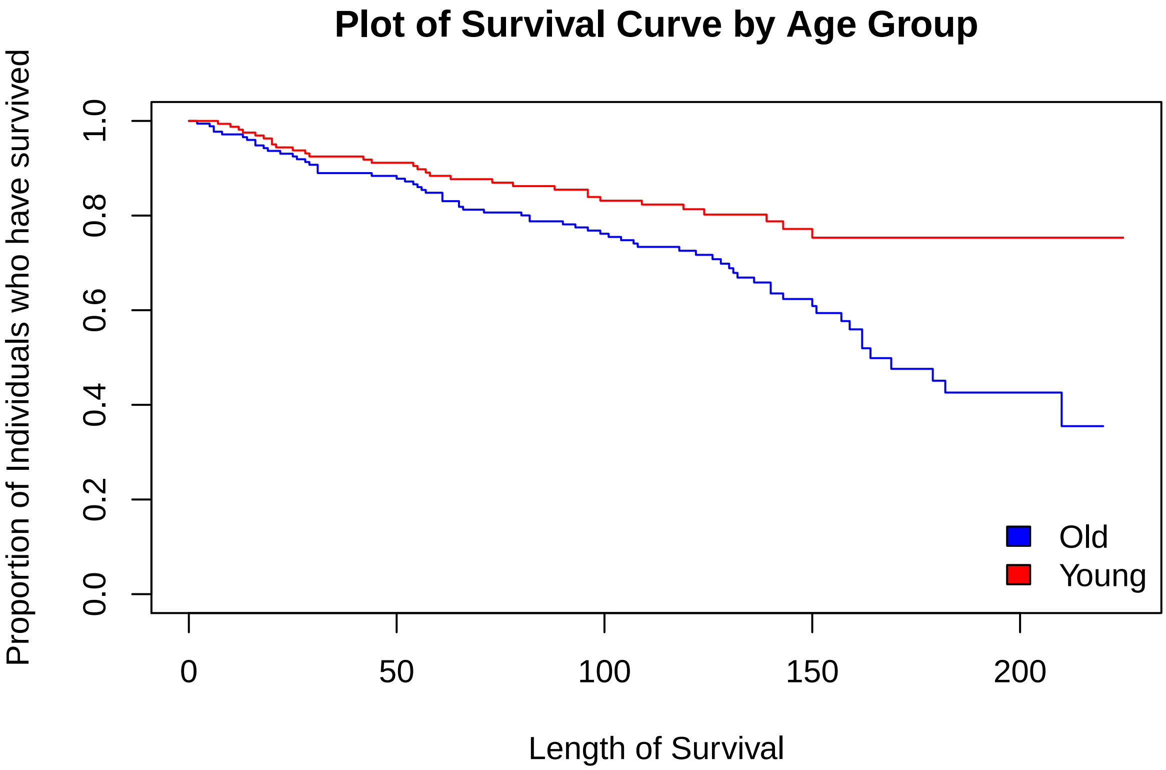
Using `survminer` package to plot.

```
ggsurvplot(surv.race,data=kmpdf,censor.size=4,conf.int=TRUE,pval=TRUE,
           legend.labs= c("Black","White"))
```



####Age

```
surv.age<-survfit(Surv(survival_month,survival)~age)
plot(surv.age,col=c("blue","red"),ylim = c(0,1),
     main="Plot of Survival Curve by Age Group",
     xlab = "Length of Survival",ylab= "Proportion of Individuals who have survived")
legend("bottomright",legend=c("Old","Young"),fill=c("blue","red"),bty="n")
```



log-rank test H0: There is no difference in the survival function between those who were young and those who were old

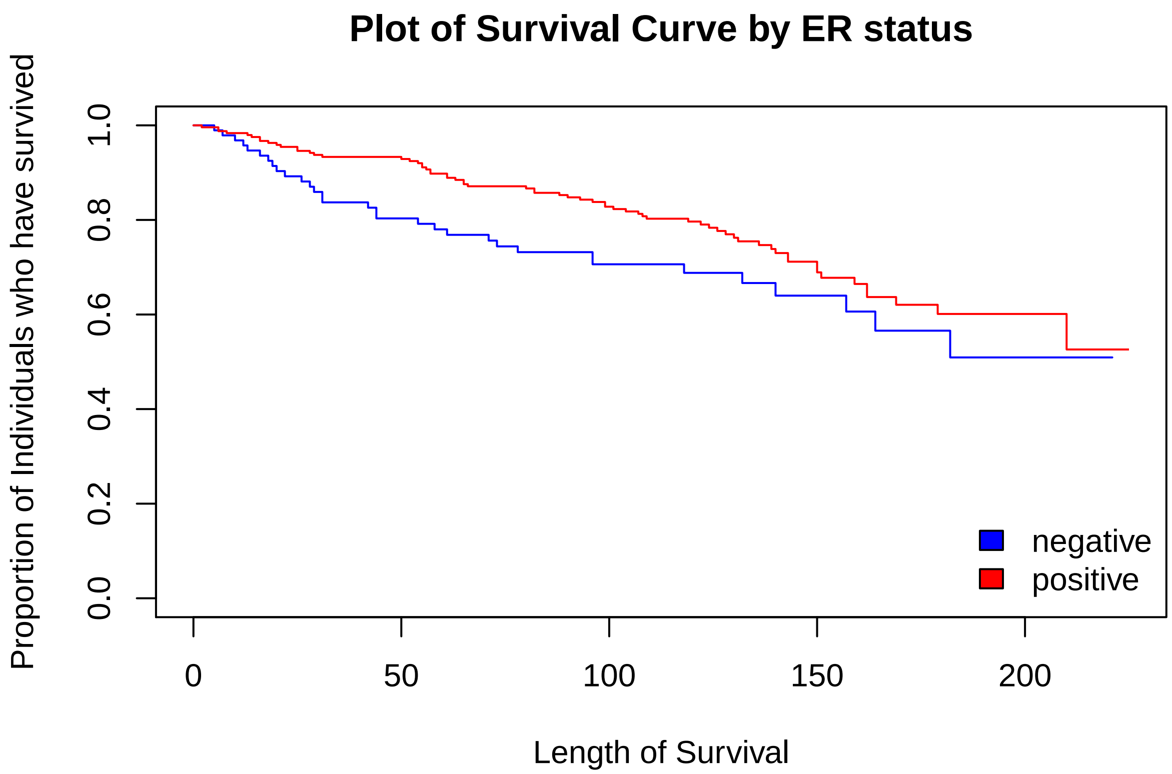
```
survdiff(Surv(survival_month,survival)~age)
```

```
## Call:
## survdiff(formula = Surv(survival_month, survival) ~ age)
##
##              N Observed Expected (O-E)^2/E (O-E)^2/V
## age=old   177       66     49.7      5.35        11
## age=young 164       31     47.3      5.62        11
##
##  Chisq= 11  on 1 degrees of freedom, p= 9e-04
```

```
#reject H0
```

####ER: estrogen receptor status

```
surv.ER<-survfit(Surv(survival_month,survival)~ER)
plot(surv.ER,col=c("blue","red"),ylim = c(0,1),
     main="Plot of Survival Curve by ER status",
     xlab = "Length of Survival",ylab= "Proportion of Individuals who have survived")
legend("bottomright",legend=c("negative","positive"),fill=c("blue","red"),bty="n")
```



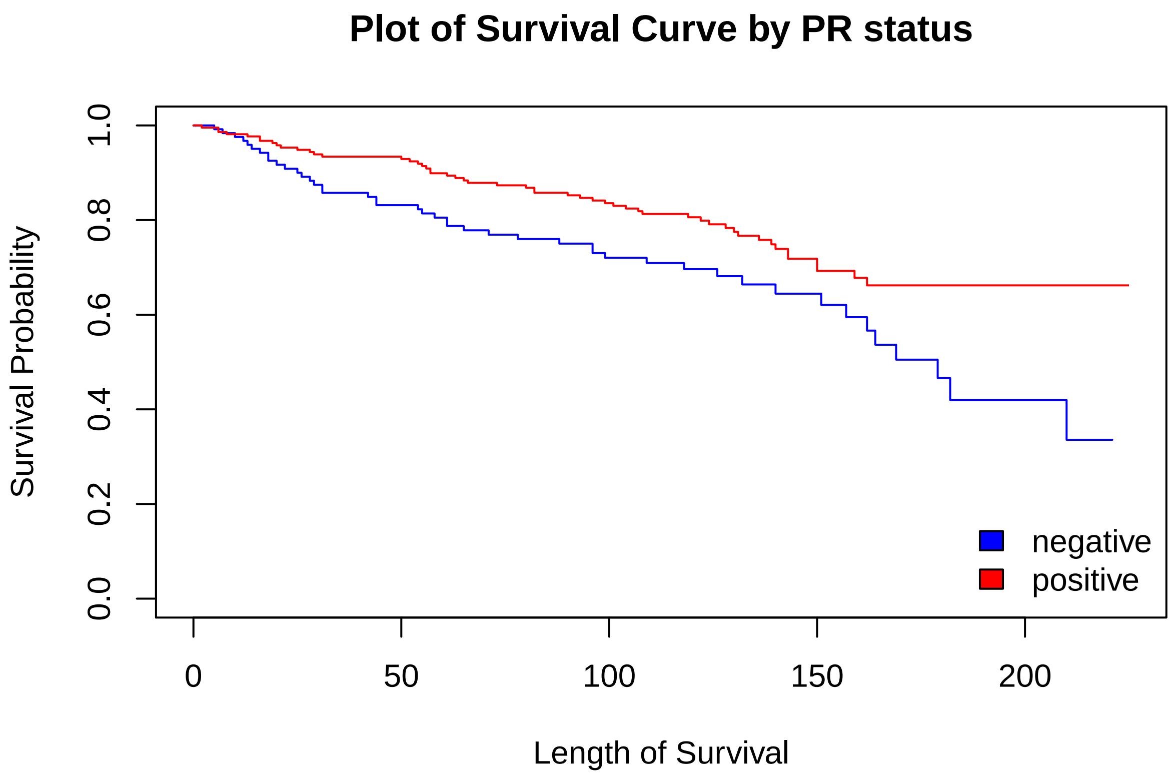
```
#levels = 0,1 0 means negative, 1 means positive

survdiff(Surv(survival_month,survival)~ER) #not reject
```

```
## Call:
## survdiff(formula = Surv(survival_month, survival) ~ ER)
##
##         N Observed Expected (O-E)^2/E (O-E)^2/V
## ER=0  95       32     24.6     2.252      3.03
## ER=1 246       65     72.4     0.764      3.03
##
##  Chisq= 3  on 1 degrees of freedom, p= 0.08
```

####PR progesterone receptor status

```
surv.PR<-survfit(Surv(survival_month,survival)~PR)
plot(surv.PR,col=c("blue","red"),ylim = c(0,1),
     main="Plot of Survival Curve by PR status",
     xlab = "Length of Survival",ylab= "Survival Probability")
legend("bottomright",legend=c("negative","positive"),fill=c("blue","red"),bty="n")
```



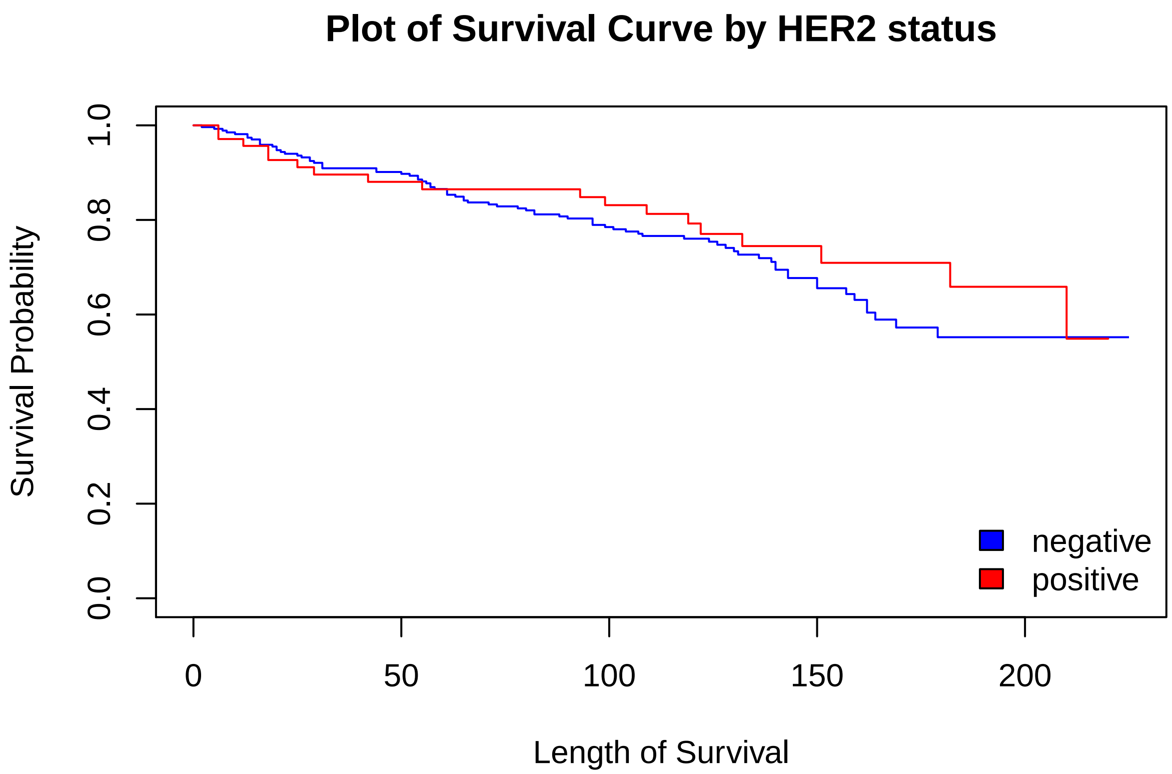
```
#levels = 0,1 0 means negative, 1 means positive

survdiff(Surv(survival_month,survival)~PR)
```

```
## Call:
## survdiff(formula = Surv(survival_month, survival) ~ PR)
##
##        N Observed Expected (O-E)^2/E (O-E)^2/V
## PR=0 125       45     32.4      4.92      7.43
## PR=1 216       52     64.6      2.47      7.43
##
##  Chisq= 7.4  on 1 degrees of freedom, p= 0.006
```

####HER2 (human epidermal growth factor receptor 2) status positive means: When a breast cell has abnormally high levels of the HER2 gene or the HER2 protein, it is called `HER2- positive`. Most patients with metastatic breast cancer have HER2-negative breast cancer.

```
surv.HER2<-survfit(Surv(survival_month,survival)~HER2)
plot(surv.HER2,col=c("blue","red"),ylim = c(0,1),
     main="Plot of Survival Curve by HER2 status",
     xlab = "Length of Survival",ylab= "Survival Probability")
legend("bottomright",legend=c("negative","positive"),fill=c("blue","red"),bty="n")
```



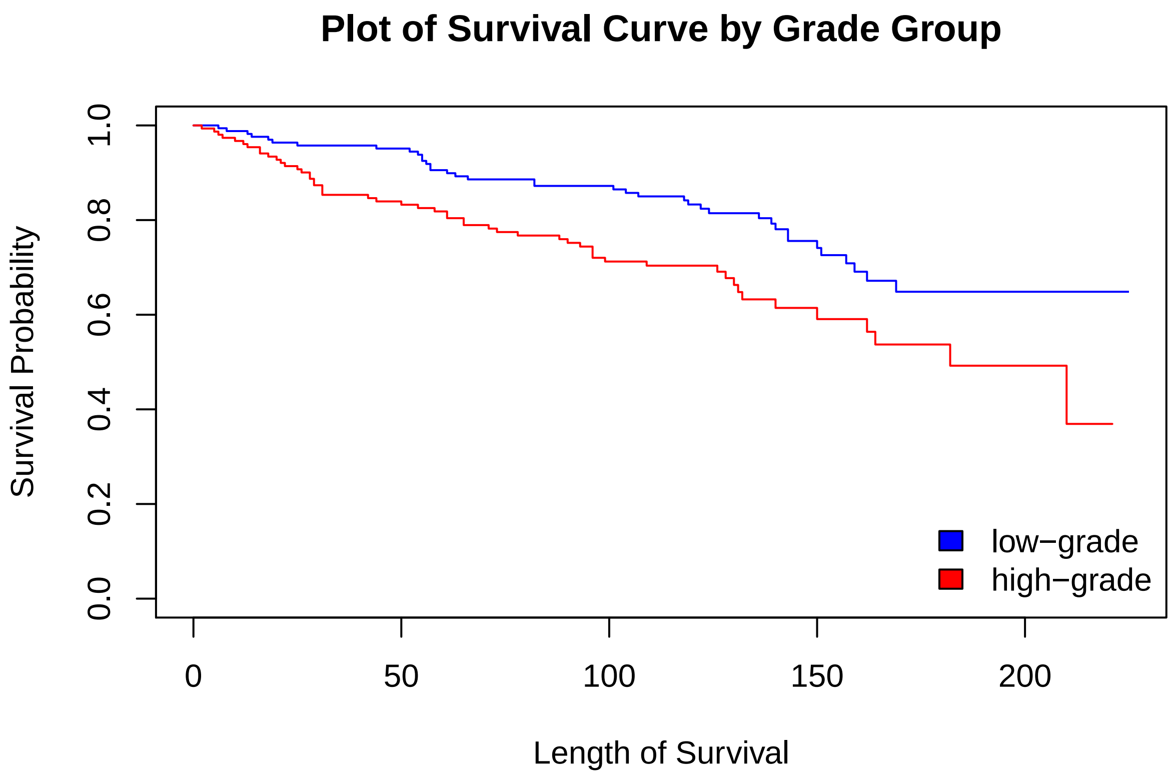
```
#levels = 0,1. 0 means negative, 1 means positive

survdiff(Surv(survival_month,survival)~HER2)
```

```
## Call:
## survdiff(formula = Surv(survival_month, survival) ~ HER2)
##
##          N Observed Expected (O-E)^2/E (O-E)^2/V
## HER2=0 271       79     75.7     0.147     0.676
## HER2=1  70       18     21.3     0.521     0.676
##
##  Chisq= 0.7  on 1 degrees of freedom, p= 0.4
```

####grade: The overall grade of the tumor specimen at definitive surgery 0 means low grade, 1 means high grade. Low-grade cancer cells (also known as well-differentiated cancer cells) look more like normal cells and tend to grow and spread more slowly than high-grade cancer cells(poorly differentiated or undifferentiated cancer cells.).

```
surv.grade<-survfit(Surv(survival_month,survival)~grade)
plot(surv.grade,col=c("blue","red"),ylim = c(0,1),
     main="Plot of Survival Curve by Grade Group",
     xlab = "Length of Survival",ylab= "Survival Probability")
legend("bottomright",legend=c("low-grade","high-grade"),fill=c("blue","red"),bty="n")
```

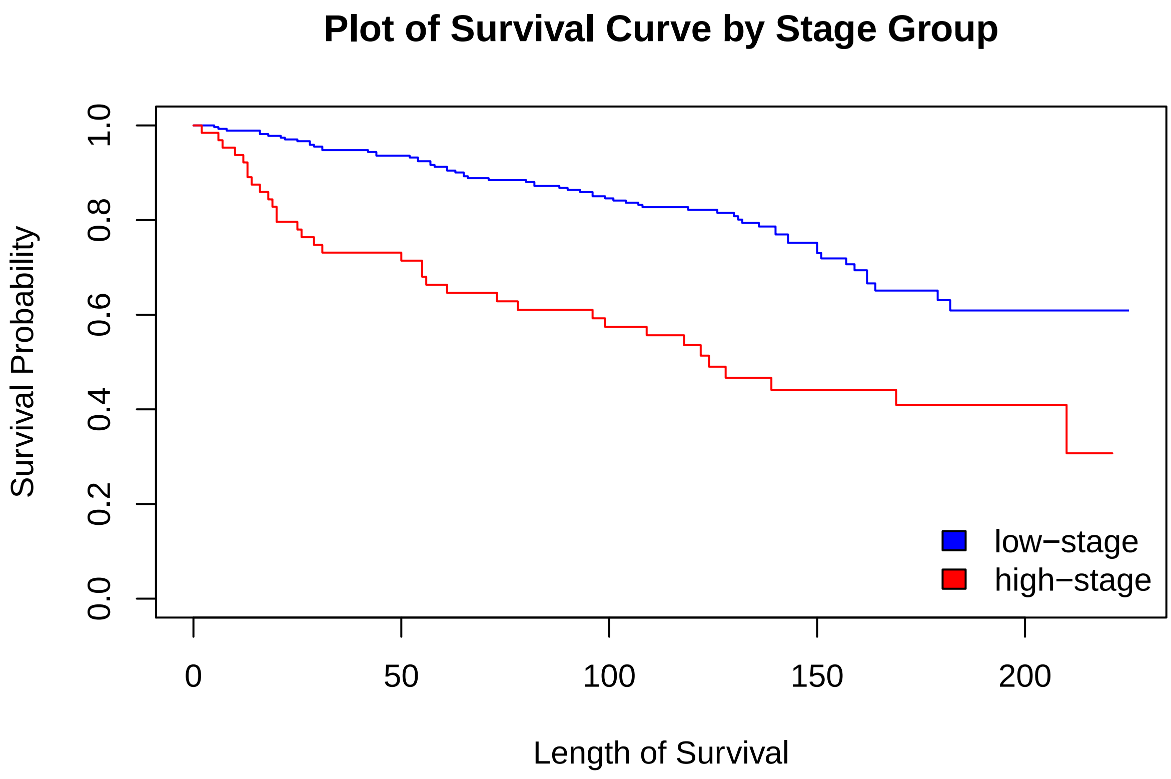


```
survdiff(Surv(survival_month,survival)~grade)
```

```
## Call:
## survdiff(formula = Surv(survival_month, survival) ~ grade)
##
## n=323, 18 observations deleted due to missingness.
##
##           N Observed Expected (O-E)^2/E (O-E)^2/V
## grade=0 169       38       52      3.79      8.95
## grade=1 154       53       39      5.06      8.95
##
##  Chisq= 9  on 1 degrees of freedom, p= 0.003
```

####stage 0 means low stage, 1 means high stage. Lower grade cancers are typically less aggressive and have a better prognosis. The more abnormal the cells look and organize themselves, the higher the cancer's grade. Cancer cells with a high grades tend to be more aggressive.

```
surv.stage<-survfit(Surv(survival_month,survival)~stage)
plot(surv.stage,col=c("blue","red"),ylim = c(0,1),
     main="Plot of Survival Curve by Stage Group",
     xlab = "Length of Survival",ylab= "Survival Probability")
legend("bottomright",legend=c("low-stage","high-stage"),fill=c("blue","red"),bty="n")
```

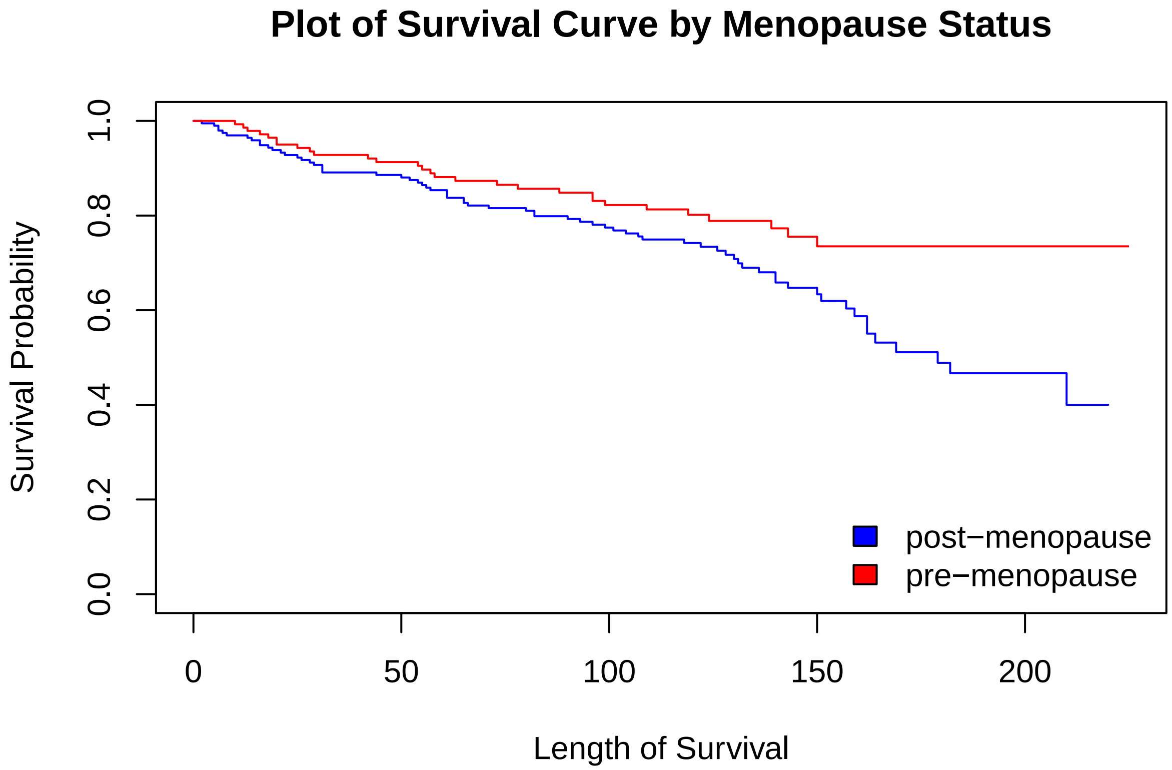


```
survdiff(Surv(survival_month,survival)~stage)
```

```
## Call:
## survdiff(formula = Surv(survival_month, survival) ~ stage)
##
##             N Observed Expected (O-E)^2/E (O-E)^2/V
## stage=0 277       63     81.1      4.02      24.7
## stage=1  64       34     15.9     20.45      24.7
##
##  Chisq= 24.7  on 1 degrees of freedom, p= 7e-07
```

####menopause: subject's menopausal status at diagnosis 0 means post-menopause, 1 means pre-menopause

```
surv.menopause<-survfit(Surv(survival_month,survival)~menopause)
plot(surv.menopause,col=c("blue","red"),ylim = c(0,1),
     main="Plot of Survival Curve by Menopause Status",
     xlab = "Length of Survival",ylab= "Survival Probability")
legend("bottomright",legend=c("post-menopause","pre-menopause"),fill=c("blue","red"),bty="n")
```



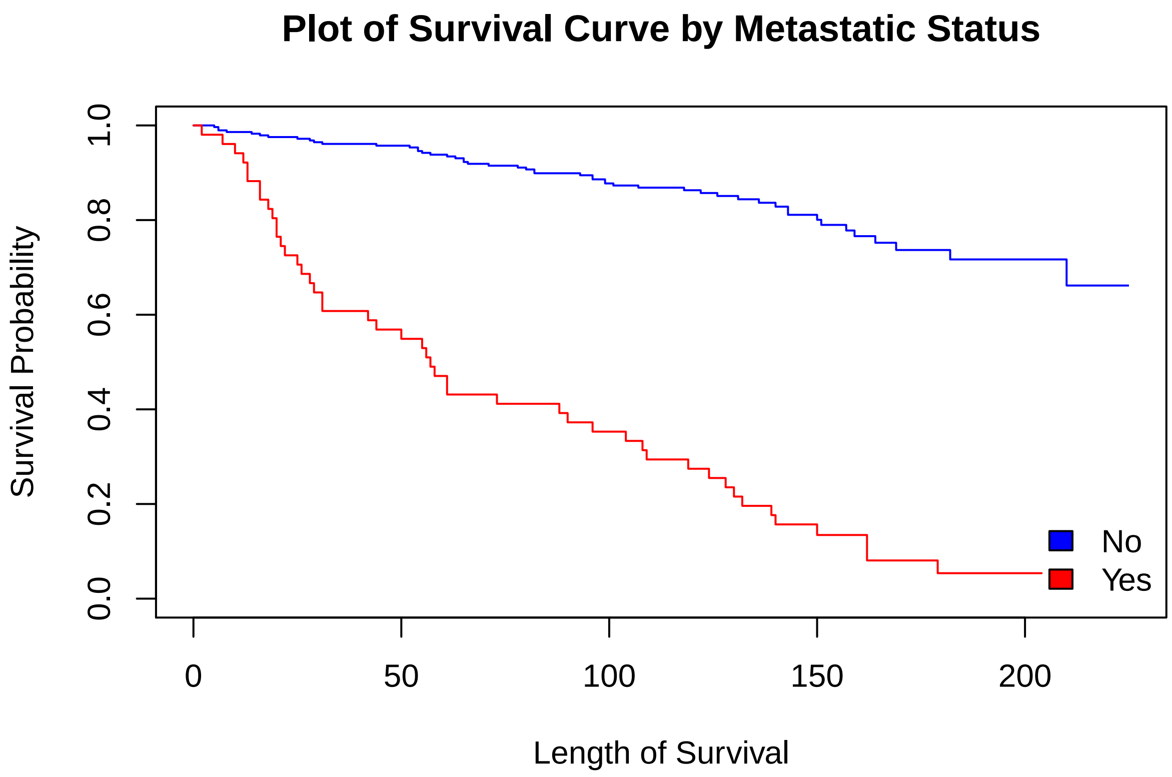
```
survdiff(Surv(survival_month,survival)~menopause)
```

```
## Call:
## survdiff(formula = Surv(survival_month, survival) ~ menopause)
##
##                  N Observed Expected (O-E)^2/E (O-E)^2/V
## menopause=0 198       68     55.5      2.79      6.56
## menopause=1 143       29     41.5      3.74      6.56
##
##  Chisq= 6.6  on 1 degrees of freedom, p= 0.01
```

This plot looks quite similar to the plot of survival curve by age, Since all old patients are most-menopause and most of young patients are pre-menopause. However, the p-value is not signifiant.

####metastatic: Has the subject been diagnosed with metastatic/distant disease?

```
surv.metastatic<-survfit(Surv(survival_month,survival)~metastatic)
plot(surv.metastatic,col=c("blue","red"),ylim = c(0,1),
     main="Plot of Survival Curve by Metastatic Status",
     xlab = "Length of Survival",ylab= "Survival Probability")
legend("bottomright",legend=c("No","Yes"),fill=c("blue","red"),bty="n")
```



```
survdiff(Surv(survival_month,survival)~metastatic)
```

```
## Call:
## survdiff(formula = Surv(survival_month, survival) ~ metastatic)
##
##                    N Observed Expected (O-E)^2/E (O-E)^2/V
## metastatic=No    290       50     87.4        16       163
## metastatic=Yes    51       47      9.6       146       163
##
##  Chisq= 163  on 1 degrees of freedom, p= <2e-16
```

```
table(grade,metastatic)
```

```
##      metastatic
## grade  No Yes
##     0 155  14
##     1 120  34
```

```
table(survival,metastatic)
```

```
##         metastatic
## survival  No Yes
##        0 240   4
##        1  50  47
```

The metastatic feature is dominant in survival. There are 51 patients who were diagonised with metastatic/distant disease and only 4 of them survived at the censored time.

Include age, PR, in the report results section.