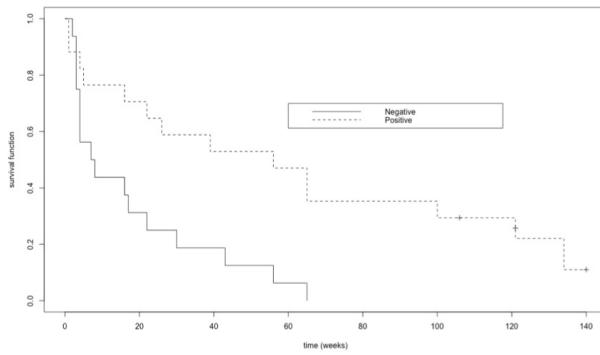

This question wasn't answered

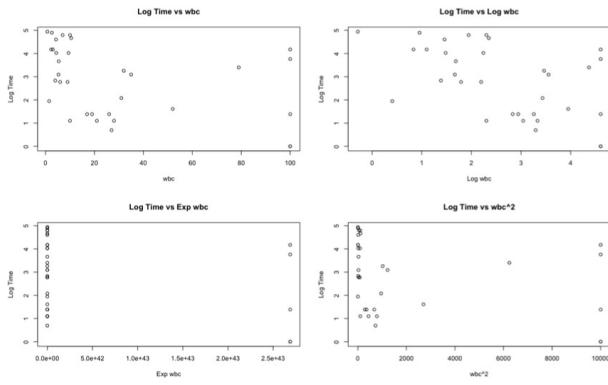
STAT886 A4Q2

- (a) ● Kaplan-Meier plot: the influence of AG to survival time.



Comment: The KM graph shows that both tests showed similar survival trend at the beginning before 4 weeks but showed great difference later. Patients with positive test related to white blood cell characteristics tend to have bigger probability to live longer. Also, there are more censored points in positive group.

- Scatter plots for wbc and functions of wbc (Here is light censor)



Comment: Here, we tried log time versus wbc, log wbc, exp wbc and wbc². Only the scatter

plot "Log Time vs Log wbc" shows a more linear decreasing pattern than other scatter plots, suggesting that there might be some relationship between the survival time and log(wbc).

(b)

- Model1: We firstly fit the parametric regression model with AG and log(wbc), the fit results are shown below:

Call:

```
survreg(formula = Surv(time, status) ~ as.factor(AG) + log(wbc),
        data = p42)
```

	Value	Std. Error	z	p
(Intercept)	3.841	0.534	7.19	6.6e-13
as.factor(AG)1	1.177	0.427	2.76	0.0058
log(wbc)	-0.366	0.150	-2.45	0.0143
Log(scale)	0.112	0.147	0.77	0.4442

Scale= 1.12

Weibull distribution

Loglik(model)= -132.5 Loglik(intercept only)= -140.3

Chisq= 15.69 on 2 degrees of freedom, p= 0.00039

Number of Newton-Raphson Iterations: 6

n= 33

Both AG and log(wbc) are significant since the p-value is 0.0058 and 0.0143, which are smaller than 0.05. The global p-value is 0.00039, which is far from 0.05, indicating that the model fits the data well.

- Then we want to check whether it's possible to reduce the covariate, and we fit one model with AG only and another model with log(wbc) only.

- Model2: With AG only:

Call:

```
survreg(formula = Surv(time, status) ~ as.factor(AG), data = p42)
```

	Value	Std. Error	z	p
(Intercept)	2.800	0.305	9.17 < 2e-16	
as.factor(AG)1	1.459	0.437	3.34	0.00085
Log(scale)	0.172	0.149	1.16	0.24650

Scale= 1.19

Weibull distribution

Loglik(model)= -135.5 Loglik(intercept only)= -140.3

Chisq= 9.63 on 1 degrees of freedom, p= 0.0019

Number of Newton-Raphson Iterations: 5

n= 33

We do the LR test: Is Model 2 better than Model 1?

$$\lambda_{obs} = 2 * (-132.5 + 135.5) = 6$$

which follows a chi-square distribution with df=1, the corresponding p-value is 0.01430588<0.05, suggesting that we could reject the null hypothesis and Model 1 is better.

- Model 3: with log(wbc) only:

Call:

```
survreg(formula = Surv(time, status) ~ log(wbc), data = p42)
```

	Value	Std. Error	z	p
(Intercept)	4.854	0.500	9.71	<2e-16
log(wbc)	-0.500	0.165	-3.03	0.0024
Log(scale)	0.222	0.146	1.52	0.1277

Scale= 1.25

Weibull distribution

Loglik(model)= -136 Loglik(intercept only)= -140.3

Chisq= 8.77 on 1 degrees of freedom, p= 0.0031

Number of Newton-Raphson Iterations: 5

n= 33

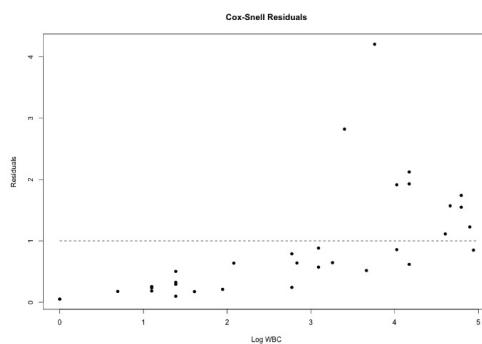
We do the LR test: Is Model 3 better than Model 1?

$$\lambda_{obs} = 2 * (-132.5 + 136) = 7$$

which follows a chi-square distribution with df=1, the corresponding p-value is 0.008150972<0.05, suggesting that we could reject the null hypothesis and Model 1 is better.

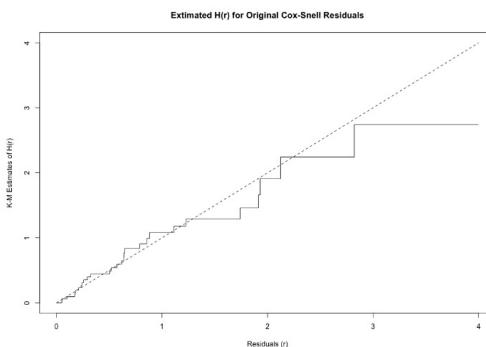
Therefore, Model 1 with AG and log(wbc) is the best parametric regression model to the data.

(c)



another con-snell plot -1

Comment: The Cox-Snell residuals plot agree reasonably well with the expected behavior, which looks like $\text{Exp}(1)$ observations. So the model 1 fits data really well.



Comment: The K-M estimated $H(r)$ for original Cox-Snell residuals shows a similar trend as the line $y=x$, which means the model 1 fits the data well.

(d)

Final model:

Call:

`survreg(formula = Surv(time, status) ~ as.factor(AG) + log(wbc),`

`data = p42)`

	Value	Std. Error	z	p
(Intercept)	3.841	0.534	7.19	6.6e-13
as.factor(AG)1	1.177	0.427	2.76	0.0058
log(wbc)	-0.366	0.150	-2.45	0.0143
Log(scale)	0.112	0.147	0.77	0.4442

Scale= 1.12

Weibull distribution

Loglik(model)= -132.5 Loglik(intercept only)= -140.3

Chisq= 15.69 on 2 degrees of freedom, p= 0.00039

Number of Newton-Raphson Iterations: 6

n= 33

Final model:

$$\log(\text{time}) = 3.841 + 1.177 * I(\text{AG} = 1) - 0.366 * \log(\text{wbc})$$

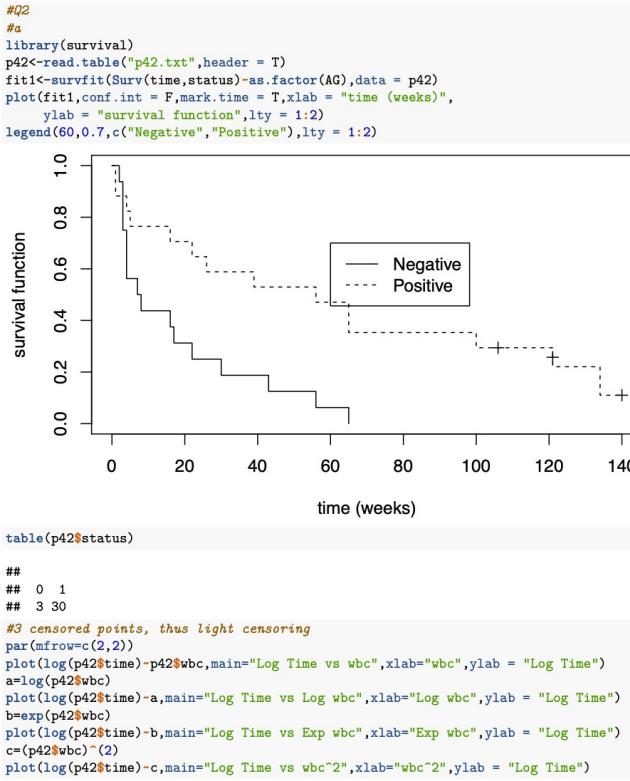
$\hat{\beta}_0 = 3.841$: When ag test is negative and white blood cell count at diagnosis is 0, the average failure time is $3.841 - E[\text{EV}] = 3.841 - 0.58 = 3.261$. The $\hat{\beta}_0$ here includes the expected log failure

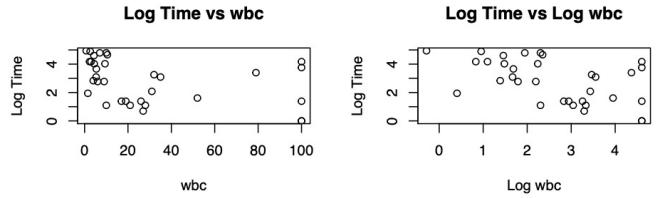
time and the E[EV].

$\beta_1 = 1.177$: for the same log(wbc) value, the positive AG test will lead to 1.177 unit increase in log failure time compared to the negative AG test.

$\beta_2 = -0.366$: for the same AG test results, an unit of increase on log(wbc) will lead to a 0.366 unit decrease in log failure time.

Appendix for A4Q2





```
#b
fit2<-survreg(Surv(time,status)-as.factor(AG)+log(wbc),data = p42)
summary(fit2)

##
## Call:
## survreg(formula = Surv(time, status) ~ as.factor(AG) + log(wbc),
## data = p42)
##          Value Std. Error      z      p
## (Intercept) 3.841    0.534  7.19 6.6e-13
## as.factor(AG)1 1.177    0.427  2.76  0.0058
## log(wbc)   -0.366    0.150 -2.45  0.0143
## Log(scale)   0.112    0.147  0.77  0.4442
##
## Scale= 1.12
##
## Weibull distribution
## Loglik(model)= -132.5  Loglik(intercept only)= -140.3
## Chisq= 15.69 on 2 degrees of freedom, p= 0.00039
## Number of Newton-Raphson Iterations: 6
## n= 33

fit3<-survreg(Surv(time,status)-as.factor(AG),data = p42)
summary(fit3)

##
## Call:
## survreg(formula = Surv(time, status) ~ as.factor(AG), data = p42)
##          Value Std. Error      z      p
## (Intercept) 2.800    0.305  9.17 < 2e-16
```

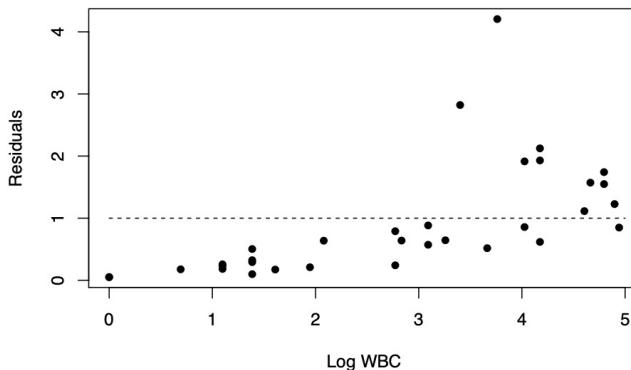
```

## as.factor(AG)1 1.459      0.437 3.34 0.00085
## Log(scale)       0.172      0.149 1.16 0.24650
##
## Scale= 1.19
##
## Weibull distribution
## Loglik(model)= -135.5   Loglik(intercept only)= -140.3
## Chisq= 9.63 on 1 degrees of freedom, p= 0.0019
## Number of Newton-Raphson Iterations: 5
## n= 33
fit4<-survreg(Surv(time,status)-log(wbc),data = p42)
summary(fit4)

##
## Call:
## survreg(formula = Surv(time, status) ~ log(wbc), data = p42)
##          Value Std. Error     z      p
## (Intercept) 4.854    0.500  9.71 <2e-16
## log(wbc)    -0.500    0.165 -3.03 0.0024
## Log(scale)   0.222    0.146  1.52 0.1277
##
## Scale= 1.25
##
## Weibull distribution
## Loglik(model)= -136   Loglik(intercept only)= -140.3
## Chisq= 8.77 on 1 degrees of freedom, p= 0.0031
## Number of Newton-Raphson Iterations: 5
## n= 33
#still need keep all in
#c
par(mfrow=c(1,1))
sig<-fit2$scale
v<-p42$log(wbc)
b<-fit2$coefficients
mu<-b[1]+b[3]*log(v)+b[2]*p42$AG
r<-exp((log(p42$time)-mu)/sig)
plot(log(p42$time),r,main="Cox-Snell Residuals",xlab = "Log WBC",
     ylab = "Residuals",pch=16)
lines(seq(0,5,0.2),rep(1,26),lty=2)

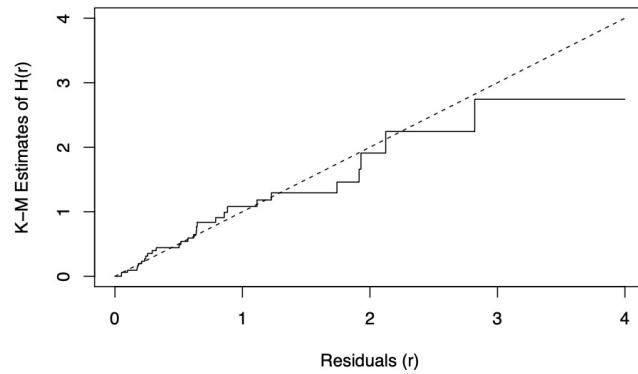
```

Cox-Snell Residuals



```
fit.r<-survfit(Surv(r,p42$status)-1)
plot(fit.r,fun = "cunhaz",conf.int = F,xlim=c(0,4),ylim=c(0,4),
     xlab = "Residuals (r)",ylab = "K-M Estimates of H(r)",
     main="Estimated H(r) for Original Cox-Snell Residuals")
lines(0:4,0:4,lty=2)
```

Estimated $H(r)$ for Original Cox-Snell Residuals

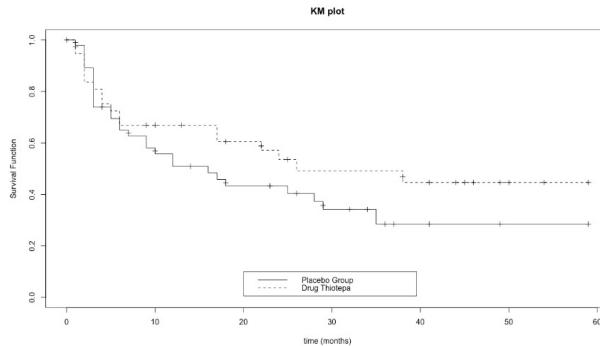


```
#d
summary(fit2)

##
## Call:
## survreg(formula = Surv(time, status) ~ as.factor(AG) + log(wbc),
##   data = p42)
##           Value Std. Error      z      p
## (Intercept) 3.841    0.534  7.19 6.6e-13
## as.factor(AG)1 1.177    0.427  2.76  0.0058
## log(wbc)     -0.366    0.150 -2.45  0.0143
## Log(scale)    0.112    0.147  0.77  0.4442
##
## Scale= 1.12
##
## Weibull distribution
## Loglik(model)= -132.5  Loglik(intercept only)= -140.3
## Chisq= 15.69 on 2 degrees of freedom, p= 0.00039
## Number of Newton-Raphson Iterations: 6
## n= 33
```

STAT886 A4Q3

- Graphical exploration



Comment: We firstly plot the KM plot for comparing the treatment groups. The graph shows that both placebo and drug thiotepa groups show similar survival trends before 6 months. After that point, there is some slight difference between them.

- Fit Cox regression models:

- Model 1: Cox regression model with group, size and number

```
Call:
coxph(formula = Surv(time, status) ~ as.factor(Group) + number +
size, data = q3)
```

n= 86, number of events= 47

	coef	exp(coef)	se(coef)	z	Pr(> z)
as.factor(Group)2	-0.52598	0.59097	0.31583	-1.665	0.0958 .
number	0.23818	1.26894	0.07588	3.139	0.0017 **
size	0.06961	1.07209	0.10156	0.685	0.4931

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

	exp(coef)	exp(-coef)	lower .95	upper .95
as.factor(Group)2	0.591	1.6921	0.3182	1.097
number	1.269	0.7881	1.0936	1.472
size	1.072	0.9328	0.8786	1.308

Concordance= 0.631 (se = 0.044)

Likelihood ratio test= 9.92 on 3 df, p=0.02

Wald test = 10.53 on 3 df, p=0.01

Score (logrank) test = 11.12 on 3 df, p=0.01

The fit result shows that the p-value of number is 0.0017<0.05, indicating that number is a significant covariate. The p-value of group is 0.0958, which is slightly larger than 0.05, suggesting that while it may not be statistically significant, it still plays some role in the fitting. As for the size, the p-value is 0.4931, which is far from 0.05, indicating that we may delete it in the model. So here we try model 2 with group and number only.

■ Model 2: Cox regression model with group and number

```
Call:  
coxph(formula = Surv(time, status) ~ as.factor(Group) + number,  
      data = q3)  
  
n= 86, number of events= 47  
  
              coef exp(coef) se(coef)      z Pr(>|z|)  
as.factor(Group)2 -0.51218   0.59919  0.31299 -1.636  0.10176  
number          0.23079   1.25960  0.07542  3.060  0.00221 **  
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
              exp(coef) exp(-coef) lower .95 upper .95  
as.factor(Group)2  0.5992    1.6689    0.3244    1.107  
number            0.7939    1.0865    1.460
```

what are the model setup -5

Score (logrank) test = 10.73 on 2 df, p=0.003

Likelihood ratio test= 9.47 on 2 df, p=0.009

Wald test = 10.15 on 2 df, p=0.006

Score (logrank) test = 10.73 on 2 df, p=0.005

Firstly, we want to know whether model 1 is better than model 2 using likelihood ratio test:

$$\lambda_{obs} = 2 * (180.4023 - 180.1783) = 0.448$$

which follows chi-square distribution with df=1, then we get the p-value is 0.5032863>0.05, indicating that we could not reject the null hypothesis and model 1 is not better than model 2.

Secondly, in model 2, the p-value of number is 0.00221<0.05, and the p-value of group is 0.10176>0.05, suggesting that we could consider move group out. So we try the model 3 with number only.

■ Model 3: Cox regression model with number

```
Call:  
coxph(formula = Surv(time, status) ~ number, data = q3)
```

n= 86, number of events= 47

```
              coef exp(coef) se(coef)      z Pr(>|z|)  
number 0.20120   1.22287  0.07068 2.846  0.00442 **
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
exp(coef) exp(-coef) lower .95 upper .95
number 1.223 0.8178 1.065 1.405

Concordance= 0.604 (se = 0.041)
Likelihood ratio test= 6.7 on 1 df, p=0.01
Wald test = 8.1 on 1 df, p=0.004
Score (logrank) test = 8.46 on 1 df, p=0.004

Firstly, we want to know whether Model 2 is better than Model 3 using likelihood ratio test:

$$\lambda_{obs} = 2 * (181.7882 - 180.4023) = 2.7718$$

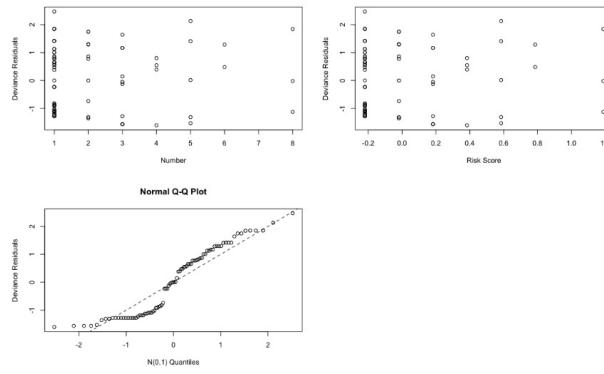
which follows chi-square distribution with df=1, and the corresponding p-value is 0.09593822>0.05, suggesting that we could not reject the null hypothesis and Model 2 is not better than Model 3.

Secondly, in Model 3, the p-value of number is 0.00442<0.05, suggesting that this term is statistically significant. And the global p-values are all smaller than 0.05, suggesting that this model fits data well.

Therefore, Model 3 is our final model.

- Model checking and residual analysis

Since deviance residuals are useful for assessing both PH assumption and model adequacy, we use deviance residuals to do the model checking and residual analysis.



Comment: The censoring rate is $39/(39+47)=0.45>0.4$. Therefore, we expect to see a large number of residuals are close to 0, which distorts the $N(0,1)$ distribution shape. But residuals

should still mostly fall between [-2,2] and be roughly symmetric in range. Here, in the first and second plots, the points are located not really symmetrically while most of them are between -2 and 2. Both of them don't behave perfectly like random observations from $N(0,1)$.

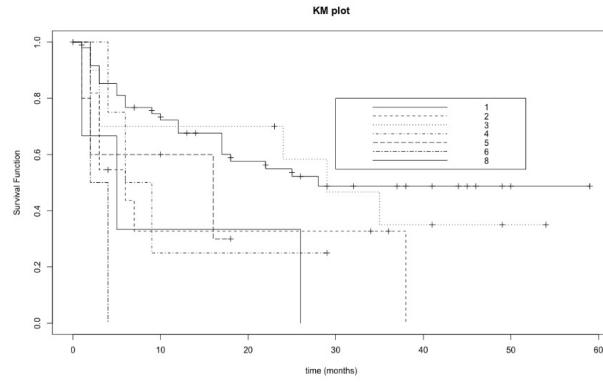
The Q-Q plot agrees roughly with the straight line $y=x$, but fits poorly with it. So we think the residuals are not normally distributed.

- Conclusion

To sum up, the cox model with "number" has the best performance among these models, but the residual analysis shows that the Cox regression model does not fit the data well.

Only have one estimated coefficient in the final model that is 0.20120, $\exp(\beta)=1.22287$. 0.20120 is the log hazard ratio for a one more tumor at initial diagnosis and 1.22287 is the hazard ratio for a one more tumor at initial diagnosis, which suggests an increased risk.

Here we still plot a K-M plot w.r.t number (here we only have number = 1,2,3,4,5,6,8), the relationships are truly complicated.



Appendix for A4Q3

```

library(survival)
#input the data
q3<-read.table("bladder.txt",header = F,col.names = c("Group","futime",
"number","size","r1","r2","r3","r4"),na.strings = "",fill = T)
q3$time=q3$r1
q3$status=1
for (i in 1:nrow(q3)){
  if (is.na(q3$r1[i])){
    q3$time[i]=q3$futime[i]
    q3$status[i]=0
  }
  else if (q3$r1[i] >q3$futime[i]){
    q3$time[i]=q3$futime[i]
    q3$status[i]=0
  }
}
plot(log(q3$time),q3$size)

```

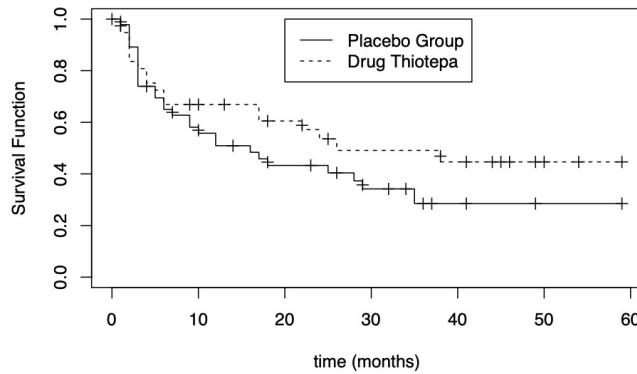
A scatter plot with the x-axis labeled $\log(q3\$/time)$ and the y-axis labeled $q3\$/size$. The x-axis ranges from 0 to 4 with major ticks at 0, 1, 2, 3, and 4. The y-axis ranges from 1 to 7 with major ticks at 1, 2, 3, 4, 5, 6, and 7. There are approximately 50 data points represented by open circles. The points show a general upward trend, indicating that as the log of time increases, the size tends to increase.

```

#K-M
fit.q3km<-survfit(Surv(time,status)-as.factor(Group),data = q3)
plot(fit.q3km,conf.int = F,mark.time = T,xlab = "time (months)",
     ylab = "Survival Function",lty = 1:2,main="KM plot")
legend(20,1.0,c("Placebo Group","Drug Thiotepe"),lty=1:2)

```

KM plot



```
#cox with all covariates
fit.q31<-coxph(Surv(time,status)-as.factor(Group)+number+size,data = q3)
summary(fit.q31)

## Call:
## coxph(formula = Surv(time, status) ~ as.factor(Group) + number +
##       size, data = q3)
##
##   n= 86, number of events= 47
##
##           coef exp(coef) se(coef)      z Pr(>|z|)
## as.factor(Group)2 -0.52598  0.59097 0.31583 -1.665  0.0958 .
## number          0.23818  1.26894 0.07588  3.139  0.0017 **
## size            0.06961  1.07209 0.10156  0.685  0.4931
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##           exp(coef) exp(-coef) lower .95 upper .95
## as.factor(Group)2  0.591     1.6921  0.3182  1.097
## number           1.269     0.7881  1.0936  1.472
## size             1.072     0.9328  0.8786  1.308
##
## Concordance= 0.631  (se = 0.044 )
## Likelihood ratio test= 9.92  on 3 df,  p=0.02
## Wald test           = 10.53  on 3 df,  p=0.01
## Score (logrank) test = 11.12  on 3 df,  p=0.01
fit.q31$loglik

## [1] -185.1376 -180.1783
```

```

fit.q32<-coxph(Surv(time,status)-as.factor(Group)+number,data = q3)
summary(fit.q32)

## Call:
## coxph(formula = Surv(time, status) ~ as.factor(Group) + number,
##       data = q3)
##
##   n= 86, number of events= 47
##
##           coef exp(coef) se(coef)      z Pr(>|z|)
## as.factor(Group)2 -0.51218   0.59919  0.31299 -1.636  0.10176
## number          0.23079   1.25960  0.07542  3.060  0.00221 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##           exp(coef) exp(-coef) lower .95 upper .95
## as.factor(Group)2   0.5992    1.6689   0.3244   1.107
## number            1.2596    0.7939   1.0865   1.460
##
## Concordance= 0.633  (se = 0.043 )
## Likelihood ratio test= 9.47  on 2 df,  p=0.009
## Wald test           = 10.15  on 2 df,  p=0.006
## Score (logrank) test = 10.73  on 2 df,  p=0.005
fit.q32$loglik

## [1] -185.1376 -180.4023
pchisq(2*(180.4023-180.1783),1,lower.tail = F)

## [1] 0.5032863
fit.q33<-coxph(Surv(time,status)-number,data = q3)
summary(fit.q33)

## Call:
## coxph(formula = Surv(time, status) ~ number, data = q3)
##
##   n= 86, number of events= 47
##
##           coef exp(coef) se(coef)      z Pr(>|z|)
## number 0.20120   1.22287  0.07068 2.846  0.00442 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##           exp(coef) exp(-coef) lower .95 upper .95
## number     1.223     0.8178    1.065     1.405
##
## Concordance= 0.604  (se = 0.041 )
## Likelihood ratio test= 6.7  on 1 df,  p=0.01
## Wald test           = 8.1  on 1 df,  p=0.004
## Score (logrank) test = 8.46  on 1 df,  p=0.004
fit.q33$loglik

## [1] -185.1376 -181.7882

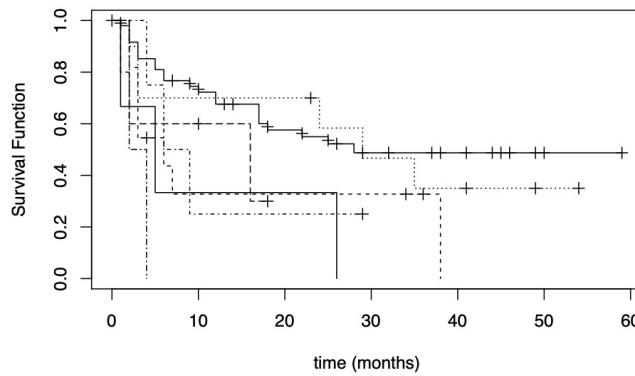
```

```

pchisq(2*(181.7882-180.4023),1,lower.tail = F)
## [1] 0.09593822
#only number covariate
fit.q3km2<-survfit(Surv(time,status)-as.factor(number),data = q3)
plot(fit.q3km2,conf.int = F,mark.time = T,xlab = "time (months)",
ylab = "Survival Function",lty = 1:7,main="KM plot")

```

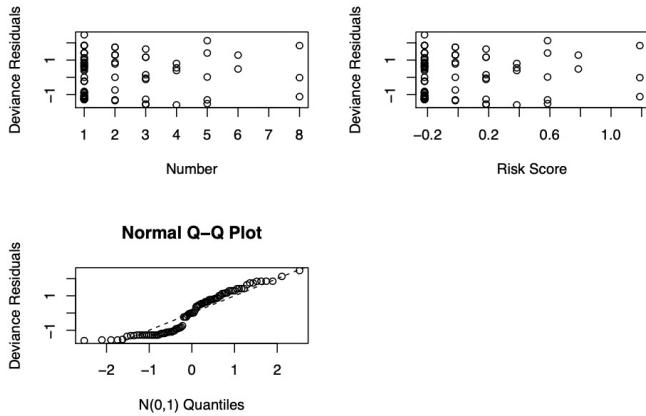
KM plot



```

##model checking & residual analysis
fit.res<-resid(fit.q33,type = "deviance")
par(mfrow=c(2,2))
plot(q3$number,fit.res,ylab = "Deviance Residuals",xlab = "Number")
plot(predict(fit.q33),fit.res,ylab = "Deviance Residuals",xlab = "Risk Score")
qqnorm(fit.res,ylab = "Deviance Residuals",xlab = "N(0,1) Quantiles")
abline(0,1,lty=2)

```



A4 Q4 a

The null hypothesis $H_0: S_1(t) = S_2(t) = \dots = S_G(t)$ for all t

Alternative hypothesis $H_A: \text{At least one of the } S_i(t) \text{ is different for some } t,$
where $i = 1, 2, \dots, G$

Let $t_1 < t_2 < \dots < t_K$ be the distinct failure times of both groups. Then the weighted log-rank statistic for testing H_0 is: (take group G_1 as the reference)

$$U_i = \sum_{j=1}^K W(t_j) [d_{i..}(t_j) - \frac{Y_{i..}(t_j)}{Y_{..}(t_j)} d_{..}(t_j)], \text{ where } i = 1, 2, \dots, G-1$$

$$U = \begin{pmatrix} U_1 \\ U_2 \\ \vdots \\ U_{G-1} \end{pmatrix}, \text{ where } W(t_j) \text{ is a common weight shared by each group.}$$

$d_{i..}(t_j)$ is the observed # of failures in group i at t_j

$Y_{i..}(t_j)$ is # at risk at t_j in group i

$Y_{..}(t_j)$ is # at risk at t_j in all groups

$d_{..}(t_j)$ is # of failures in all groups at t_j .

$$V = V_{\alpha}(U) = \begin{pmatrix} \sigma_{11} & \sigma_{12} & \cdots & \sigma_{1G-1} \\ \sigma_{21} & \sigma_{22} & \cdots & \sigma_{2G-1} \\ \vdots & \ddots & \ddots & \vdots \\ \sigma_{G-11} & \sigma_{G-12} & \cdots & \sigma_{(G-1)(G-1)} \end{pmatrix}_{(G-1) \times (G-1)}$$

where the variance is:

$$\sigma_{ii} = \sum_{j=1}^K W(t_j)^2 \frac{Y_{i..}(t_j)}{Y_{..}(t_j)} \left(1 - \frac{Y_{i..}(t_j)}{Y_{..}(t_j)} \right) \left(\frac{Y_{..}(t_j) - d_{..}(t_j)}{Y_{..}(t_j) - 1} \right) d_{..}(t_j)$$

The covariance is

$$\sigma_{ig} = - \sum_{j=1}^K W(t_j)^2 \frac{Y_{i..}(t_j)}{Y_{..}(t_j)} \frac{Y_{g..}(t_j)}{Y_{..}(t_j)} \left(\frac{Y_{..}(t_j) - d_{..}(t_j)}{Y_{..}(t_j) - 1} \right) d_{..}(t_j) \quad \text{if } i \neq g$$

for $i, g = 1, 2, \dots, G-1$

And the asymptotic distribution for $W^2 = U^\top V^{-1} U \approx \chi^2_{G-1}$,
for the purpose of testing the null hypothesis that all groups have the
same survival time distribution.

(b)

- Compare two treatments

Null hypothesis $H_0: S_1(t) = S_2(t)$ for all t ;

Alternative hypothesis $H_a: S_1(t) \neq S_2(t)$ for some t ;

Where $S_1(t)$ and $S_2(t)$ is the survival function for each treatment, then we did log rank test (weight=1), the results are shown below,

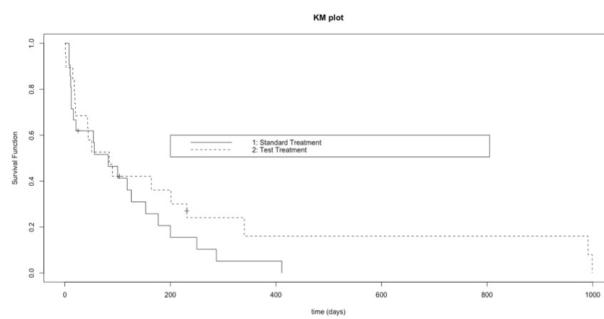
Call:

```
survdiff(formula = Surv(time, status) ~ as.factor(trt), data = q4)
```

	N	Observed	Expected	$(O-E)^2/E$	$(O-E)^2/V$
as.factor(trt)=1	21	20	16.7	0.668	1.3
as.factor(trt)=2	19	17	20.3	0.547	1.3

Chisq= 1.3 on 1 degrees of freedom, p= 0.3

The p-value is 0.3>0.05, indicating that there is no evidence against the null hypothesis. Thus, there is no significant difference between the survival time in these two treatments.



Comment: the KM plot also confirms the result we get before. Two treatments show similar survival function curves. The distributions of treatments are similar when survival time is between 0 and 100, while the distributions are slightly different for the two treatment groups when survival time > 100. But in general, they are similar.

- Compare four cell types

Null hypothesis: $H_0: S_1(t) = S_2(t) = S_3(t) = S_4(t)$ for all t ;

Alternative hypothesis $H_a: At\ least\ one\ of\ the\ S_i(t)\ is\ different\ for\ some\ t$;

Where $S_1(t)$, $S_2(t)$, $S_3(t)$ and $S_4(t)$ is the survival function for each treatment, then we did log rank test (weight=1), the results are shown below,

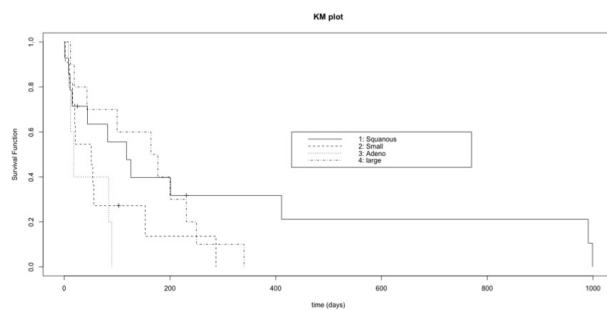
Call:

```
survdiff(formula = Surv(time, status) ~ as.factor(celltype),
          data = q4)
```

	N	Observed	Expected	$(O-E)^2/E$	$(O-E)^2/V$
as.factor(celltype)=1	14	12	16.72	1.330	2.825
as.factor(celltype)=2	11	10	6.93	1.356	1.771
as.factor(celltype)=3	5	5	2.18	3.651	4.099
as.factor(celltype)=4	10	10	11.17	0.123	0.187

Chisq= 7.4 on 3 degrees of freedom, p= 0.06

The p-value is 0.06>0.05, there is weak evidence to reject the null hypothesis. Therefore, the four cell types have similar survival distribution while some slight difference may exist.



Comment: The KM plot shows similar results as log rank test. The distributions of four cell types are similar when survival time is between 0 and 50, while the distributions are slightly different for them when survival time is larger than 50. More specifically, type 1 and type 2 show more similar trends and type 3 and type 4 show similar trends before time=210.

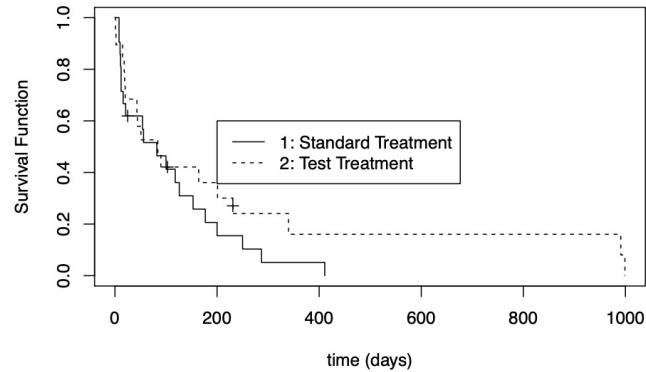
well done **20**

Appendix for A4Q4

```
#b
library(survival)
q4<-read.table(file = "eg541.txt",header = T)
logrk<-survdiff(Surv(time,status)-as.factor(trt),data = q4)
logrk

## Call:
## survdiff(formula = Surv(time, status) ~ as.factor(trt), data = q4)
##
##          N Observed Expected (O-E)^2/E (O-E)^2/V
## as.factor(trt)=1 21      20     16.7   0.668    1.3
## as.factor(trt)=2 19      17     20.3   0.547    1.3
##
##   Chisq= 1.3 on 1 degrees of freedom, p= 0.3
fit.q41<-survfit(Surv(time,status)-as.factor(trt),data = q4)
plot(fit.q41,conf.int = F,mark.time = T,xlab = "time (days)",
     ylab = "Survival Function",lty = 1:2,main="KM plot")
legend(200,0.6,c("1: Standard Treatment","2: Test Treatment"),lty=1:2)
```

KM plot



```
#no
#####
logrk2<-survdiff(Surv(time,status)-as.factor(celltype),data = q4)
```

```

logrk2

## Call:
## survdiff(formula = Surv(time, status) ~ as.factor(celltype),
##           data = q4)
##
##          N Observed Expected (O-E)^2/E (O-E)^2/V
## as.factor(celltype)=1 14      12   16.72     1.330    2.825
## as.factor(celltype)=2 11      10    6.93     1.356    1.771
## as.factor(celltype)=3  5       5    2.18     3.651    4.099
## as.factor(celltype)=4 10      10   11.17     0.123    0.187
##
##  Chi-sq= 7.4 on 3 degrees of freedom, p= 0.06
fit.q42<-survfit(Surv(time,status)-as.factor(celltype),data = q4)
plot(fit.q42,conf.int = F,mark.time = T,xlab = "time (days)",
     ylab = "Survival Function",lty = 1:4,main="KM plot")
legend(430,1.0,c("1: Squamous","2: Small","3: Adeno","4: large"),lty=1:4)

```

KM plot

