Assignment3_stat359

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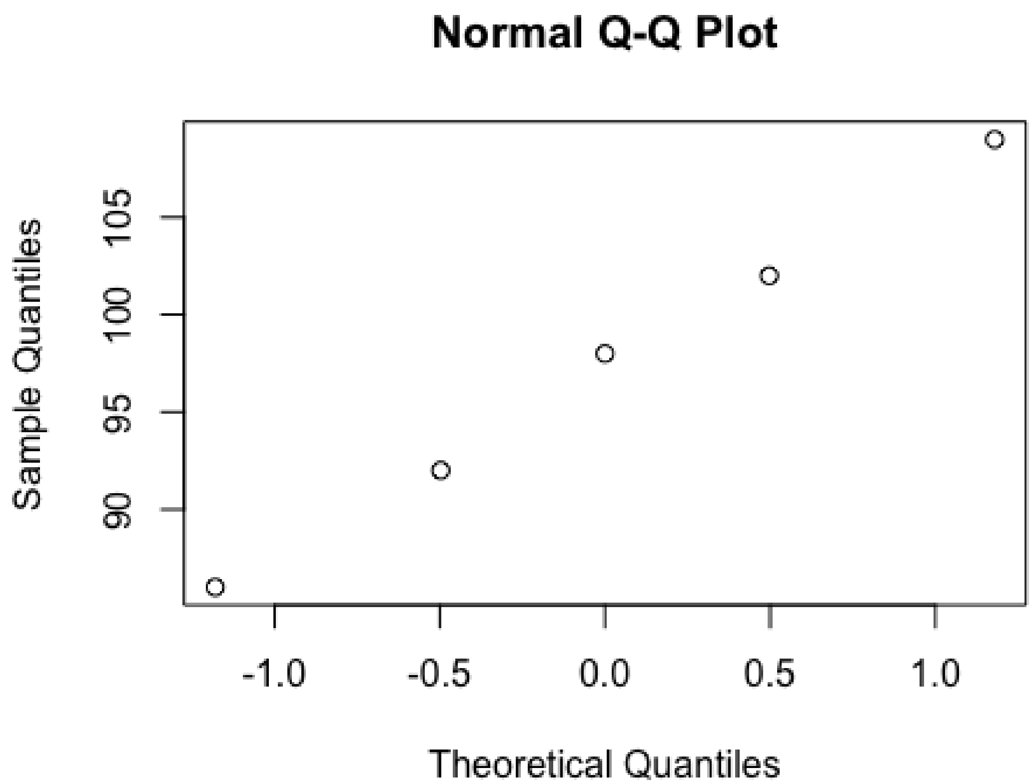
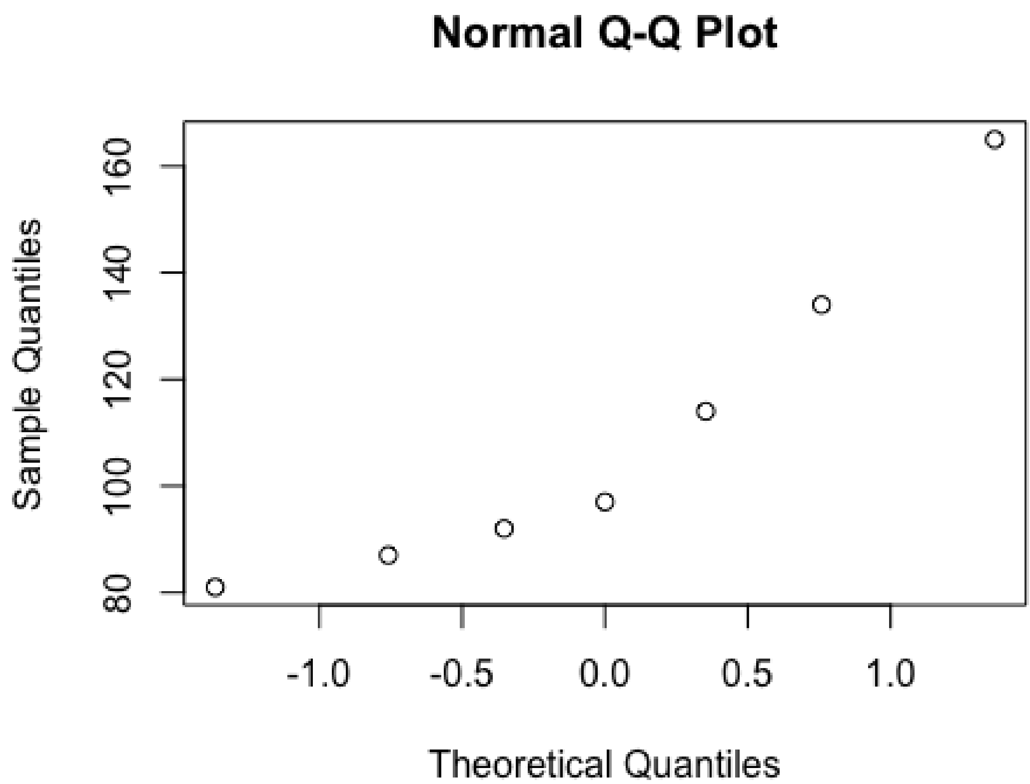
#1. The following data represent the running times of films produced by #two motion-picture companies: #Test the hypothesis that the average running time of films produced by company #2 exceeds the average running time of films produced by company 1 by 10 #minutes against the one-sided alternative that the difference is less than 10 #minutes. Use a 0.1 level of significance. Please consider carefully assumptions #made on the data.

```
#Since both of the sample sizes are pretty small, and we do not know sigmas,
#I use t distribution.
#Test the hypothesis that the average running time of films produced by
company
#2 exceeds the average running time of films produced by company 1 by 10
#minutes against the one-sided alternative that the difference is less than
10
#minutes. Use a 0.1 level of significance. Please consider carefully
assumptions
#made on the data.
c1<-c(102, 86, 98, 109, 92)
c2<-c(81, 165, 97, 134, 92, 87, 114)
summary(c1)

##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    86.0    92.0    98.0    97.4   102.0   109.0

summary(c2)

##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    81.0    89.5    97.0   110.0   124.0   165.0

boxplot(c1,c2, names = c("Company 1", "Company 2"),
         main = "Running time of films",sub = "Written by Koki")
```


```
#According to the boxplots, means are the almost the same,but the range of
the
#data from Company 2 is much larger than the data from company 1
qqnorm(c1)
```


Normal Q-Q Plot
Sample Quantiles
90
95
100
105
-1.0
-0.5
0.0
0.5
1.0
Theoretical Quantiles

```
qqnorm(c2)
```




```
#There is a streighrt line in both of qq plots which means these data are
#Normally distributed
#To decide which t-test I will use, I need to know if the sample
#variance of 2 different data sets are the same or not
var.test(c1,c2,alternative = "two.sided",conf.level = 0.90)

##
##  F test to compare two variances
##
## data:  c1 and c2
## F = 0.086277, num df = 4, denom df = 6, p-value = 0.03298
## alternative hypothesis: true ratio of variances is not equal to 1
## 90 percent confidence interval:
##  0.01903033 0.53173886
## sample estimates:
## ratio of variances
##         0.08627737

#Since P value = 0,003298 <= a = 0.1, this is a significant evidence against
Ho.
#Therefore, the variance is different.
#Since the variance is different, I use Welch's t-test
```

```r
t.test(c1,c2,alternative = "less",mu = 10, var.equal = FALSE,conf.level =
0.90)
```

```
##
##  Welch Two Sample t-test
##
## data:  c1 and c2
## t = -1.8689, df = 7.3756, p-value = 0.05085
## alternative hypothesis: true difference in means is less than 10
## 90 percent confidence interval:
##      -Inf 4.420568
## sample estimates:
## mean of x mean of y
##      97.4     110.0
```

```r
#Since the p-value = 0.05085 <= a = 0.1, we reject Ho.
#There is a significant evidence that the average running time of films
produced
#by company 2 exceeds the average running time of films produced by company 1
#by 10 minutes against the one-sided alternative that the difference is less
#than 10 minutes
```

#Question 2 #Six different machines are being considered for use in manufacturing rubber #seals. The machines are being compared with respect to tensile strength of the #product. A random sample of four seals from each machine is used to #determine whether the mean tensile strength varies from machine to #machine. The following are the tensile-strength measurements in kilograms #per square centimeter 10E-01.

```r
#k = 6, n = 4, N =24, a = 0.05

#an analysis of variance at the 0.05 significance level.
#The hypothesis is Ho: u1 = u2 = ...= u6 Ha: at least one u is different
dataframe<-data.frame(strength = c(17.5, 16.9,15.8,18.6,16.4,19.2,17.7,15.4,
20.3,15.7,17.8,18.9,14.6,16.7,20.8,18.9,17.5,19.2,
16.5,20.5,18.3,16.2,17.5,20.1),
Machines= c("M1","M1","M1","M1","M2","M2","M2","M2","M3","M3","M3","M3","M4",
            "M4","M4","M4","M5","M5","M5","M5","M6","M6","M6","M6"))
dataframe
```

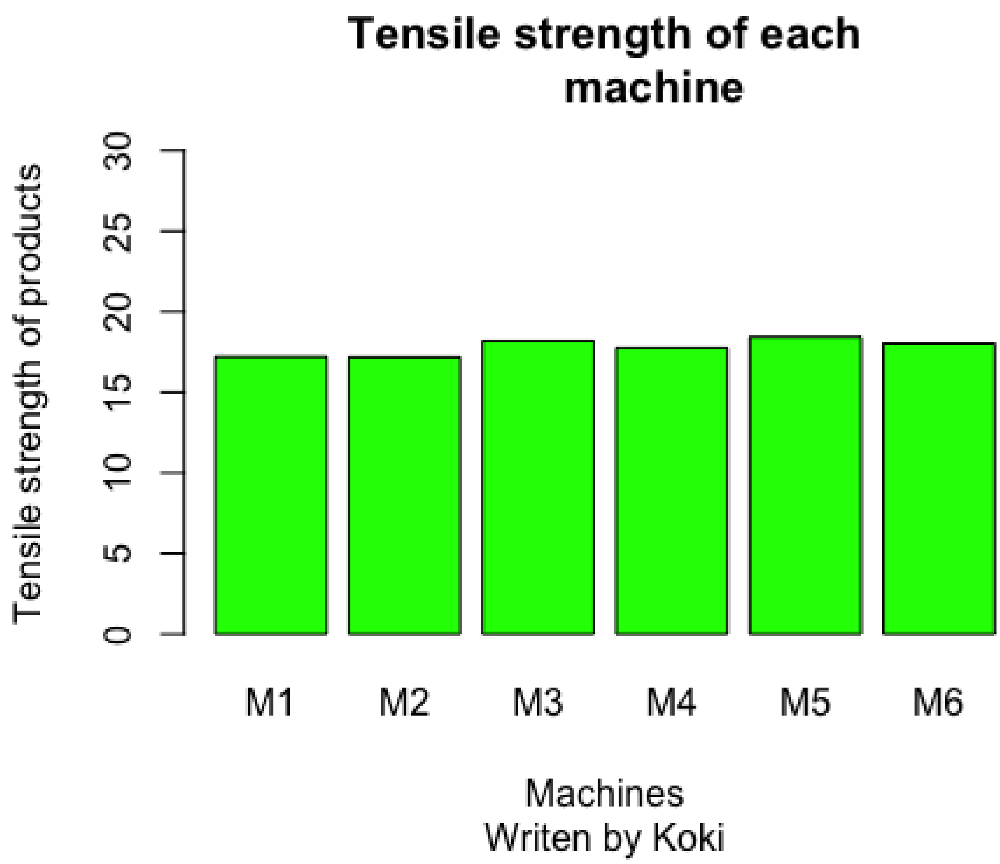
```
##    strength Machines
## 1      17.5       M1
## 2      16.9       M1
## 3      15.8       M1
## 4      18.6       M1
## 5      16.4       M2
## 6      19.2       M2
## 7      17.7       M2
## 8      15.4       M2
## 9      20.3       M3
## 10     15.7       M3
```

```
## 11     17.8       M3
## 12     18.9       M3
## 13     14.6       M4
## 14     16.7       M4
## 15     20.8       M4
## 16     18.9       M4
## 17     17.5       M5
## 18     19.2       M5
## 19     16.5       M5
## 20     20.5       M5
## 21     18.3       M6
## 22     16.2       M6
## 23     17.5       M6
## 24     20.1       M6
```

```
attach(dataframe)
Strength<-tapply(strength,Machines,mean)
Strength
```

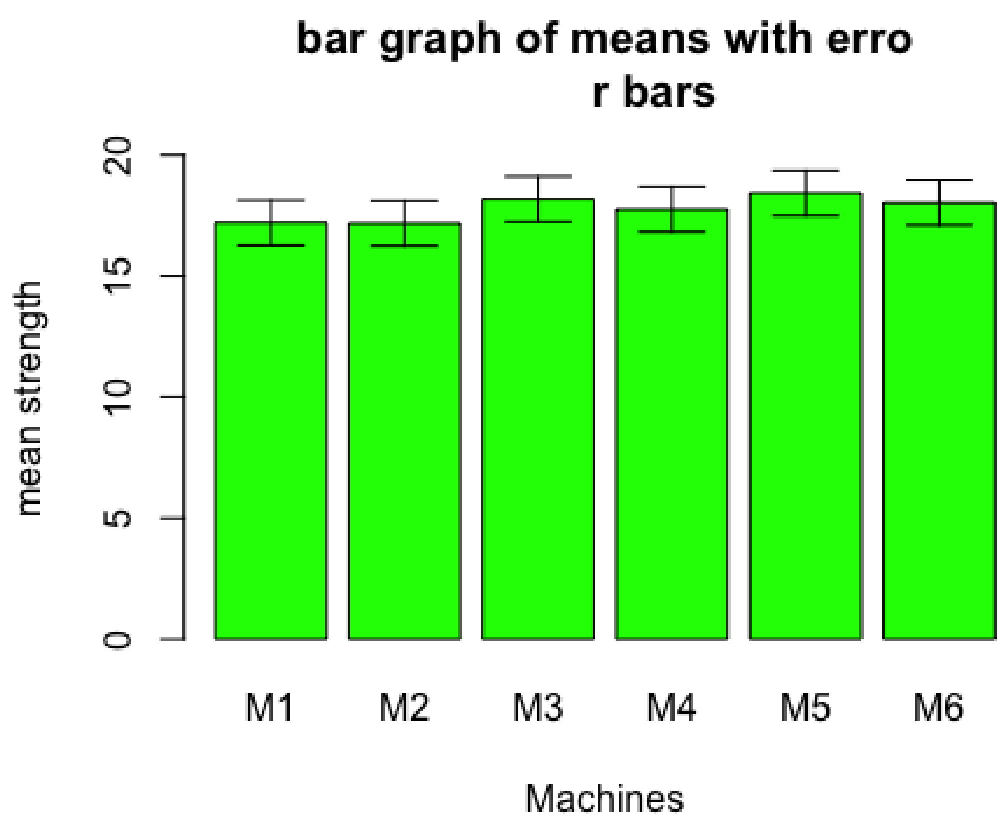
```
##     M1     M2     M3     M4     M5     M6
## 17.200 17.175 18.175 17.750 18.425 18.025
```

```
#par(mfrow=c(2,3))
barplot(Strength,col = "Green", ylim = c(0,30),main = "Tensile strength of
each
        machine",xlab = "Machines",
        ylab = "Tensile strength of products", sub = "Writen by Koki")
```

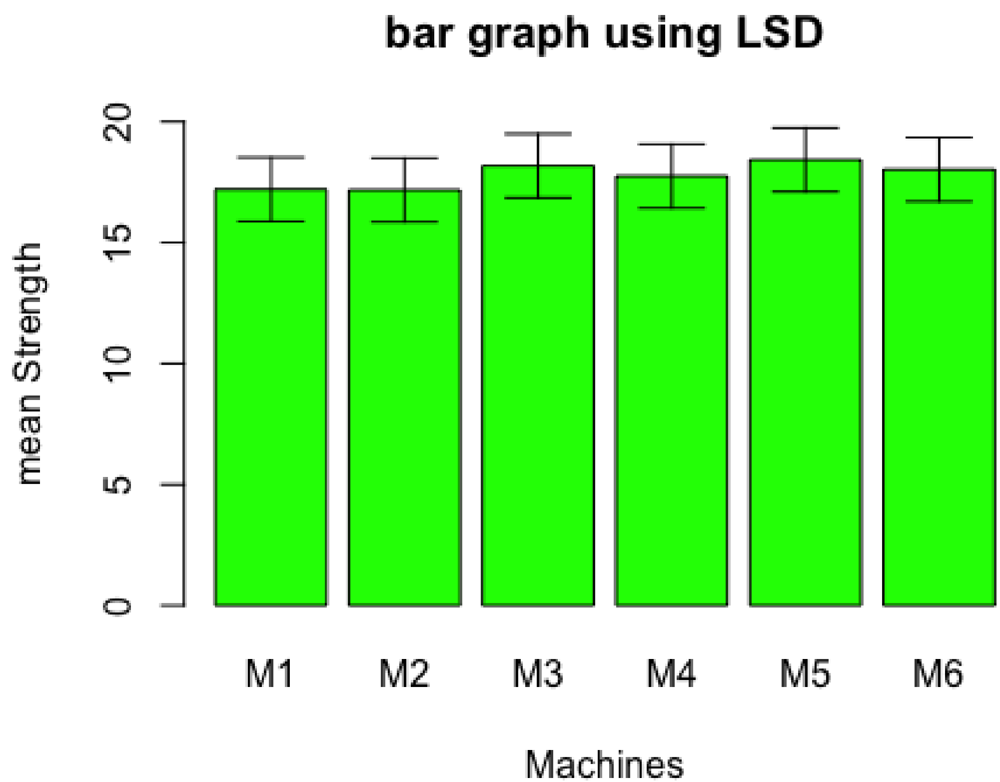



```
#The means of tensile strength of products for the 4 different
#machines are the almost same


error.bars<-function(y,z){
  x<-barplot(y, plot=F)
  n<-length(y)
  for (i in 1:n)
  {
    arrows(x[i],y[i]-z[i],x[i],y[i]+z[i],code=3,angle=90,length=0.15)
  }
}
sigma.hat<-summary.lm(aov(strength~Machines))$sigma
sigma.hat

## [1] 1.865476

table(Machines)

## Machines
## M1 M2 M3 M4 M5 M6
##  4  4  4  4  4  4
```

```
se.mean<-sigma.hat/sqrt(4)
se.mean

## [1] 0.9327379

barplot(Strength, col="green", ylim=c(0,20),main = "bar graph of means with erro
        r bars",ylab="mean strength", xlab = "Machines")
bar.half.width<-rep(se.mean,6)
error.bars(Strength,bar.half.width)
```

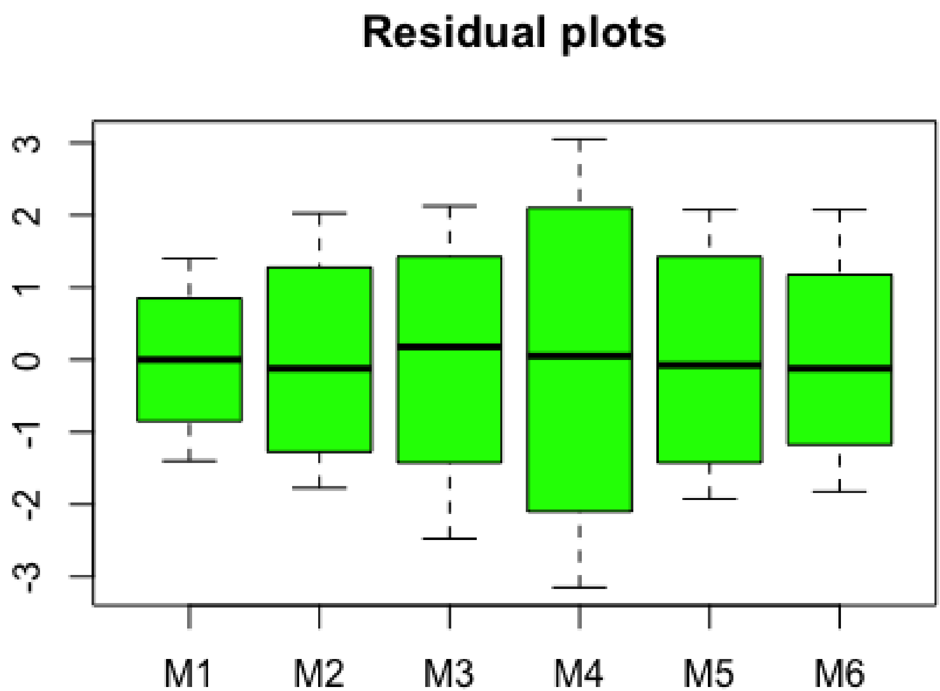



```
#According to the barplot with error bars, it is clear that the error bars are
#overlaped. This means all means seem to be the same.

#For certainly, I also use the least significant difference method.

LSD<-2*sqrt(2)*se.mean
LSD.bars<-rep(LSD,6)/2
barplot(Strength, col="green", ylim=c(0,20),main = "bar graph using LSD",ylab=
          "mean Strength", xlab ="Machines")
error.bars(Strength,LSD.bars)
```

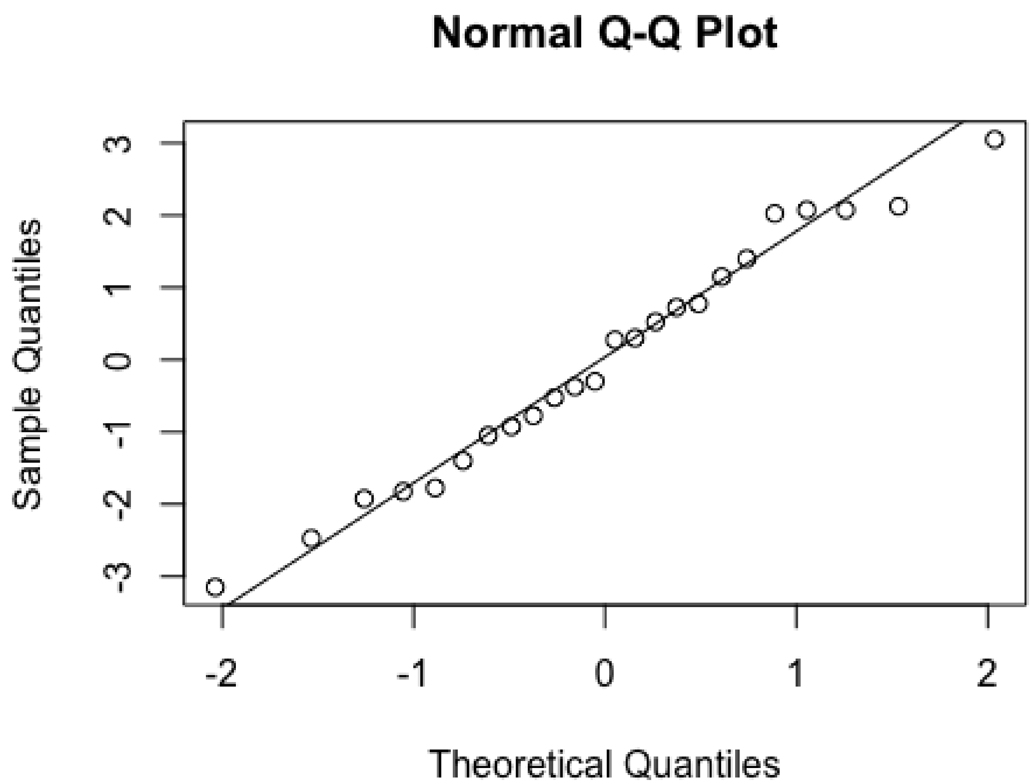



```
#From this graph using LSD, I can see that the error bars are overlaped as
well.
#so There is not significant difference among means of the strength
#from different Machines


summary(aov(strength~Machines))

##              Df Sum Sq Mean Sq F value Pr(>F)
## Machines      5   5.34   1.068   0.307  0.902
## Residuals    18  62.64   3.480

#According to the ANOVA table, the p-value is 0.902.
#Since the p-value >= 0.05 = a, we fail to reject Ho.
#There is a insignificant evidence that at least one mean of 6 machines are
#different.


resid.plant<-resid(aov(strength~Machines))
boxplot(resid.plant[Machines=="M1"],resid.plant[Machines=="M2"],
        resid.plant[Machines=="M3"],resid.plant[Machines=="M4"],
        resid.plant[Machines=="M5"],resid.plant[Machines=="M6"],
        main = "Residual plots",
```

```
        names=c('M1','M2','M3','M4','M5', 'M6'),
        col="green")
```




```
qqnorm(resid.plant)
qqline(resid.plant)
```

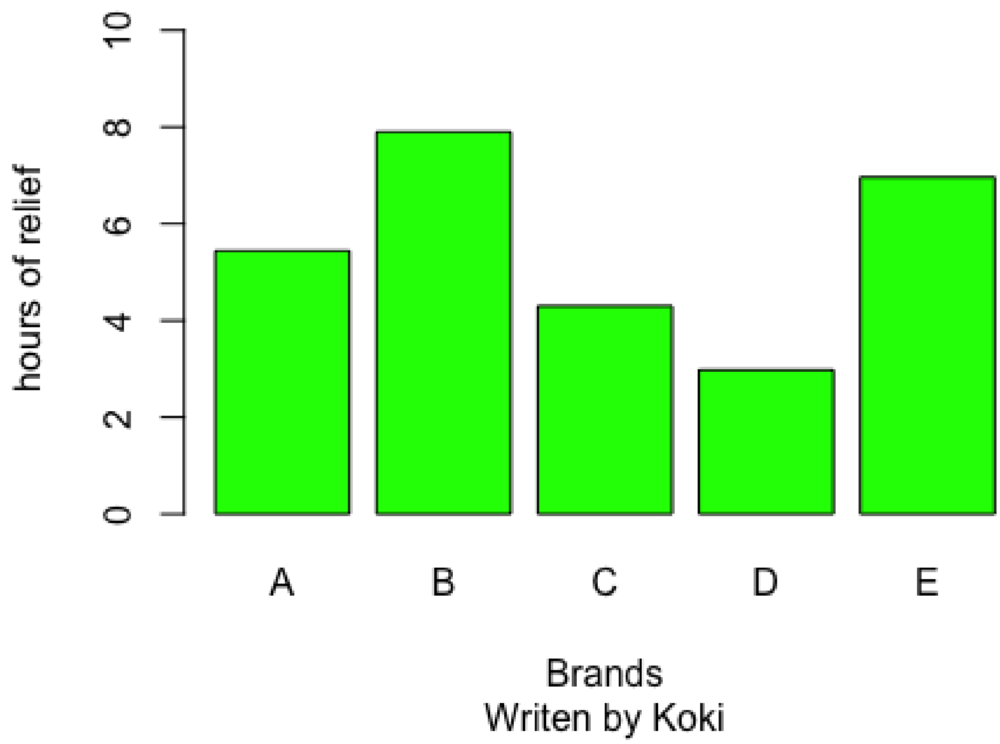



```
#According to the qq plot of residuals, there is a clear streight line on the
#graph. This means the residuals are normally distributed.
```

#Q3 #The data in the following table represent the number of hours of relief #provided by five different brands of headache tablets administered to 25 #ubjects experiencing fevers of 38 degrees Celsius or more. Perform the #analysis of variance and test the hypothesis at the 0.05 level of significance #that the mean number of hours of relief provided by the tablets is the same for #all five brands. Discuss the results.

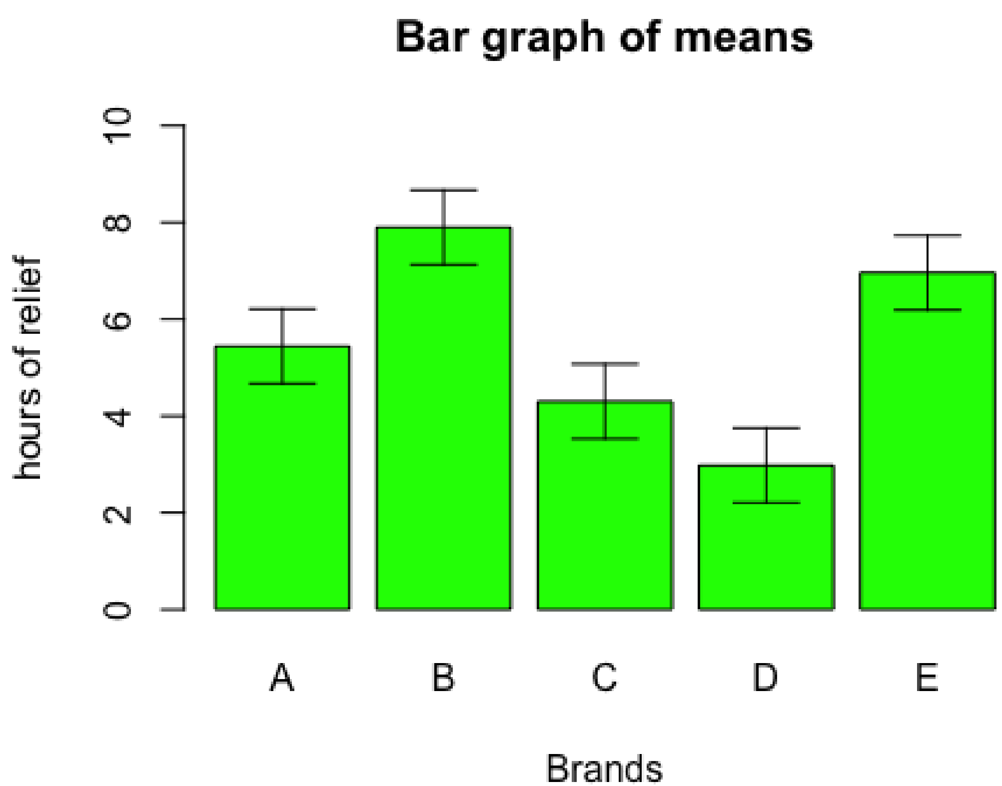
```
data_hours<-data.frame(Hours = c(5.2,4.7,8.1,6.2,3.0,9.1,7.1,8.2,6.0,9.1,
                                  3.2,5.8,2.2,3.1,7.2,2.4,3.4,4.1,1.0,4.0,
                                  7.1,6.6,9.3,4.2,7.6),
                      Brands=
c("A","A","A","A","A","B","B","B","B","B","C","C","C",

"C","C","D","D","D","D","D","E","E","E","E","E"))



attach(data_hours)
mhours<-tapply(Hours,Brands,mean)
#par(mfrow=c(2,3))
```

```r
barplot(mhours,col = "Green", ylim = c(0,10),xlab = "Brands",
        ylab = "hours of relief ", sub = "Writen by Koki")
```

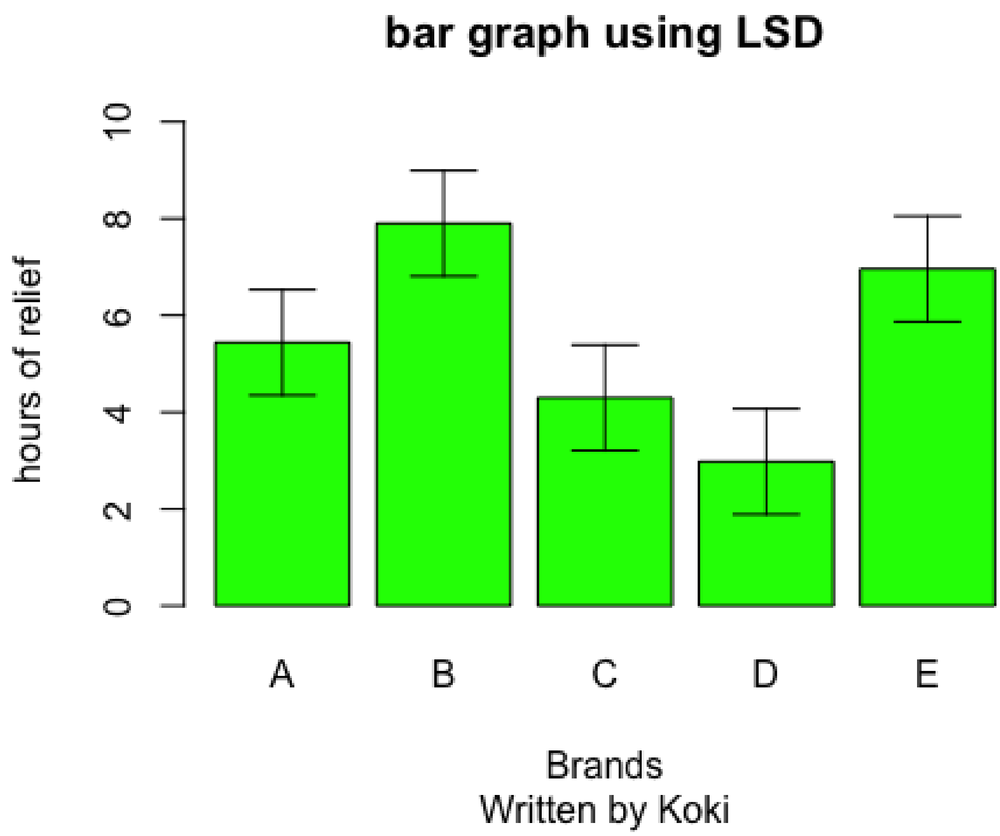



```r
#From the bar graph, it is clear that the means of brand c and d are much
#smaller than others.

error.bars<-function(y,z){
  x<-barplot(y, plot=F)
  n<-length(y)
  for (i in 1:n)
  {
    arrows(x[i],y[i]-z[i],x[i],y[i]+z[i],code=3,angle=90,length=0.15)
  }
}
sigma.hat<-summary.lm(aov(Hours~Brands))$sigma
sigma.hat

## [1] 1.725283

table(Brands)

## Brands
## A B C D E
## 5 5 5 5 5
```

```
se.mean<-sigma.hat/sqrt(5)
se.mean

## [1] 0.7715698

barplot(mhours, col="green", ylim=c(0,10),main = "Bar graph of means"
        ,ylab="hours of relief", xlab = "Brands")
bar.half.width<-rep(se.mean,6)
error.bars(mhours,bar.half.width)
```

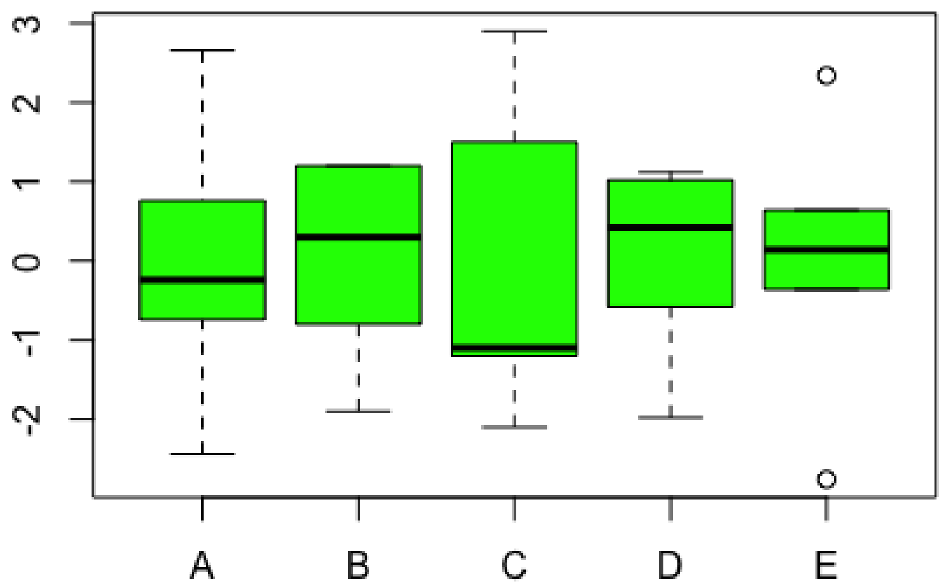



```
#According to the barplot with error bars, it is clear that the error bars of
C
#and D are quite small and do not overlap with the other error bars.
#This means all means seem not to be the same.

#For certainly, I also use the least significant difference method.

LSD<-2*sqrt(2)*se.mean
LSD.bars<-rep(LSD,6)/2
barplot(mhours, col="green", ylim=c(0,10),main = "bar graph using LSD",
        ylab="hours of relief ", xlab =
          "Brands", sub = "Written by Koki")
error.bars(mhours,LSD.bars)
```

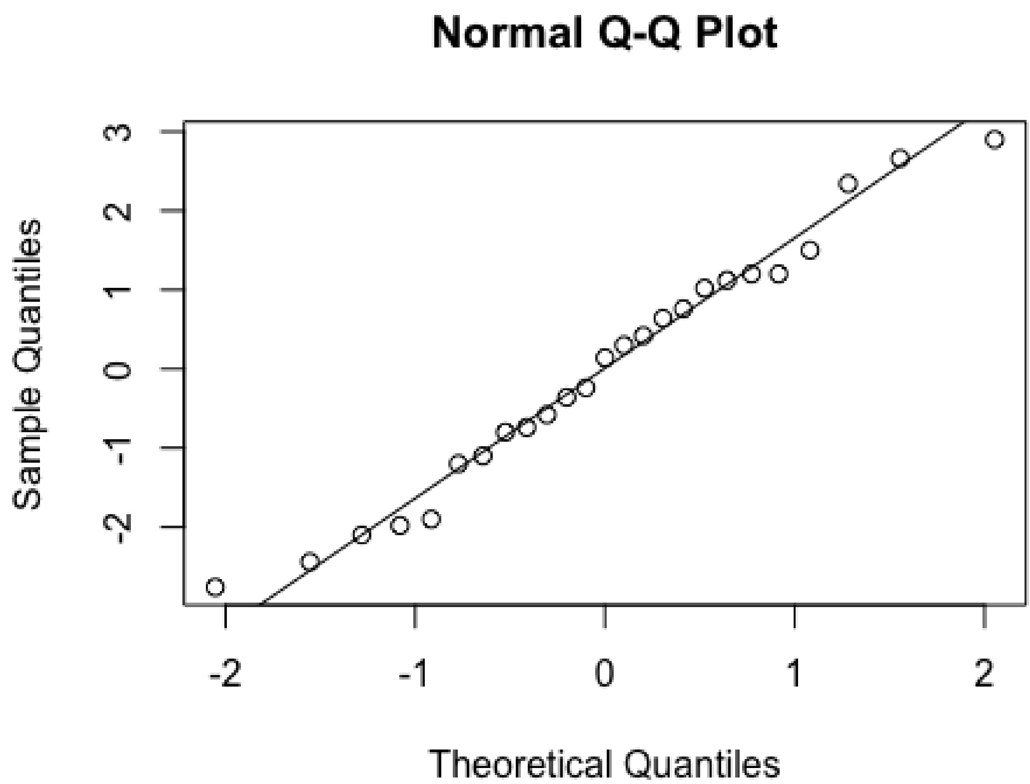



```
#From this graph, I can see that the all error bars are not overlaped as
well.
#The means from brands B and E are pretty large compared to the means from
#brands C and D. This means means of C and D are not the same as the means
#of B and E.


summary(aov(Hours~Brands))

##              Df Sum Sq Mean Sq F value Pr(>F)
## Brands        4  78.42  19.605   6.587 0.0015 **
## Residuals    20  59.53   2.977
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#According to the ANOVA table, the p-value is 0.0015.
#Since the p-value >= 0.05 = a, we reject Ho.
#There is a significant evidence that at least one mean that the number of
hours
#of relief provided by five different brands of headache tablets is different


resid.plant<-resid(aov(Hours~Brands))
```

```
boxplot(resid.plant[Brands=="A"],resid.plant[Brands=="B"],
        resid.plant[Brands=="C"],resid.plant[Brands=="D"],
        resid.plant[Brands=="E"],
        names=c('A','B','C','D','E'),
        col="green")
```




```
#From the residual plots, we can see that mean of c is pretty low.
#Also there is outliers in graph E.


qqnorm(resid.plant)
qqline(resid.plant)
```




```
#From the qq plot, the data make the stright line.
#This means the data of residuals is normally distributed.
```