

# ice cream and frog data

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## Ice Cream

### DATA

```
data<-read.csv("final.csv",header=T)
y<-data[,2]
A<-factor(data[,3]) #Time
B<-factor(data[,4]) #Milk Type
block<-factor(data[,5]) #user
data
```

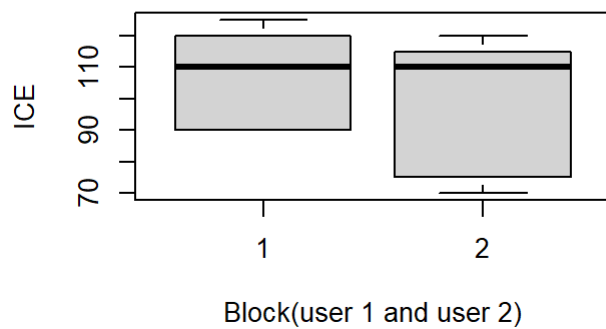
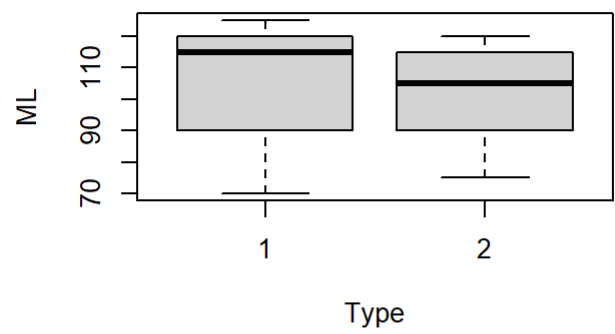
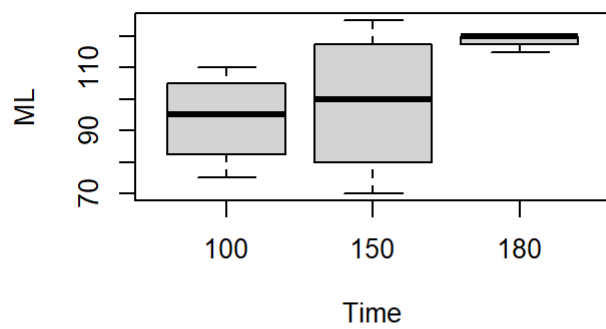
Order <int>	ML <int>	Minute <int>	Type <int>	block <int>
2	120	180	1	1
1	120	180	2	1
7	120	180	1	2
11	115	180	2	2
4	125	150	1	1
5	90	150	2	1
10	70	150	1	2
8	110	150	2	2
6	90	100	1	1
3	100	100	2	1

1-10 of 12 rows

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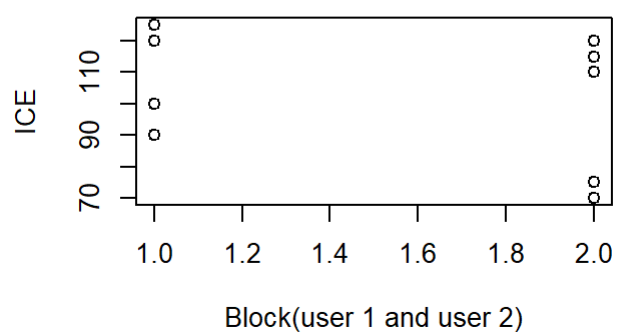
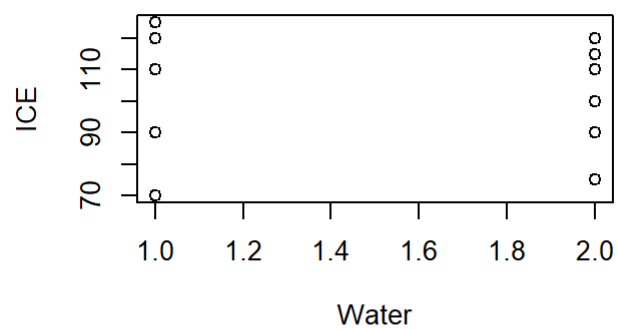
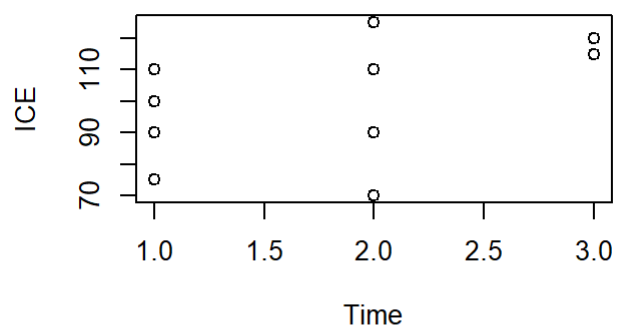
### BOX PLOT

```
par(mfrow=c(2,2))
plot(A,y,xlab="Time",ylab="ML") #Time
plot(B,y,xlab="Type",ylab="ML") #Milk Type
plot(block,y,xlab="Block(user 1 and user 2)",ylab="ICE") #user 1 and 2
par(mfrow=c(1,1))
```



## QQPLOT

```
par(mfrow=c(2,2))
plot(as.numeric(A),y,xlab="Time",ylab="ICE")
plot(as.numeric(B),y,xlab="Water",ylab="ICE")
plot(as.numeric(block),y,xlab="Block(user 1 and user 2)",ylab="ICE")
par(mfrow=c(1,1))
```



## ANOVA analysis

```
r1t<-aov(y~A*B+block)
summary(r1t)
```

##	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## A	2	1400.0	700.0	1.692	0.275
## B	1	52.1	52.1	0.126	0.737
## block	1	168.8	168.8	0.408	0.551
## A:B	2	116.7	58.3	0.141	0.872
## Residuals	5	2068.7	413.7		

ALL P-Value > 0.05, thus these factor is nonsignificant.

## Residual Plot

```
e<-rlt$residuals
y.hat<-rlt$fitted.values
ord<-data[,1]

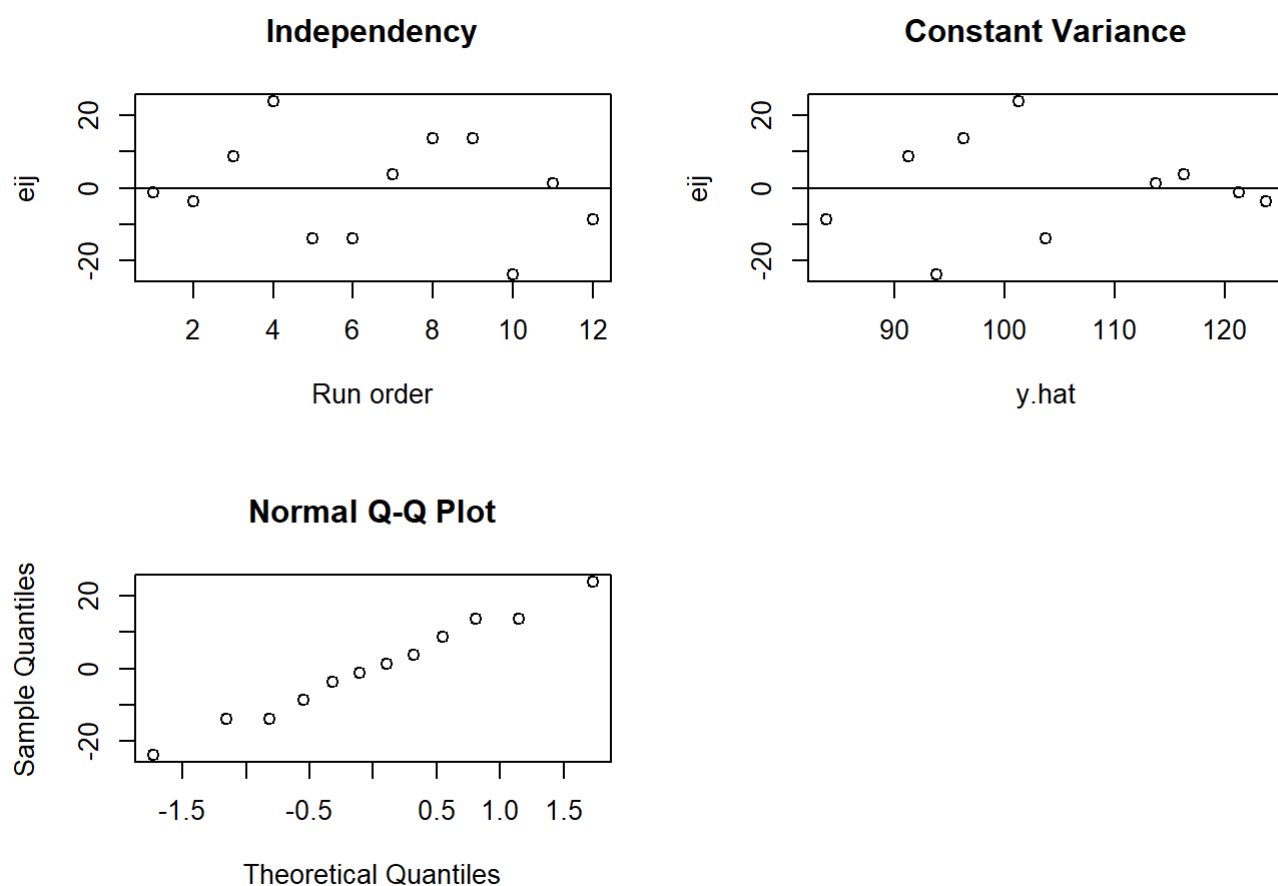
par(mfrow=c(2,2))

plot(ord,e,xlab="Run order",ylab="eij",main = "Independency" )
abline(0,0)

plot(y.hat,e,xlab="y.hat",ylab="eij" , main = "Constant Variance")
abline(0,0)

qqnorm(e)

par(mfrow=c(1,1))
```



The points are not uniformly distributed at 0, so Non-Constant Variance.

## shapiro test

```
shapiro.test(e)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  e
## W = 0.9853, p-value = 0.9969
```

# Frog

## Data

```
data<-read.csv("frog.csv",header=T)

y<-data[,2]
A<-factor(data[,3]) #number of pin
B<-factor(data[,4]) #Type(Big and Small)
C<-factor(data[,5]) #Fold
data
```

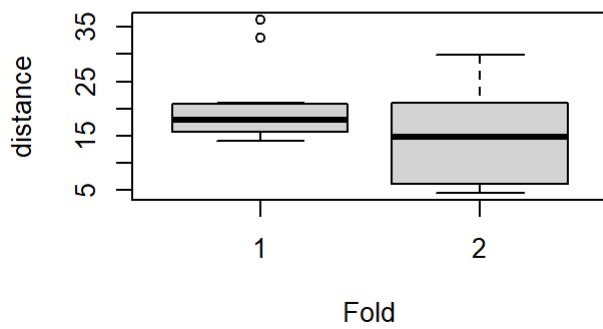
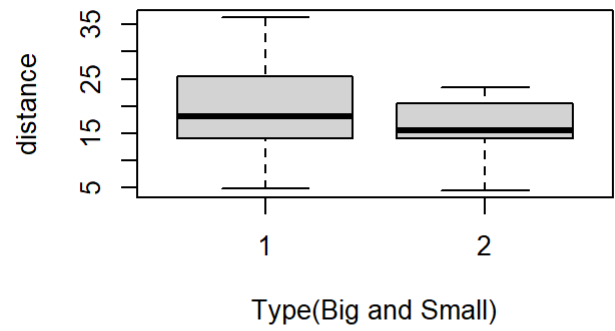
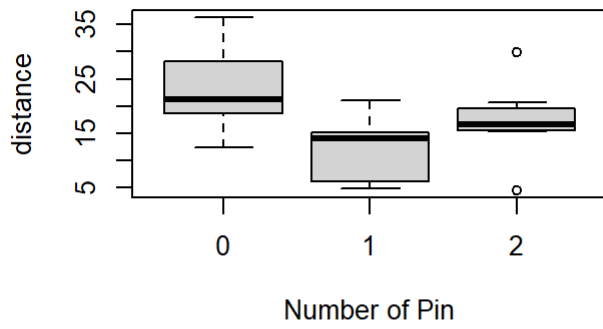
Order <int>	distance <dbl>	Pin <int>	type <int>	fold <int>
13	33.0	0	1	1
23	36.3	0	1	1
15	20.0	0	1	2
24	12.5	0	1	2
7	17.4	0	2	1
14	20.3	0	2	1
21	23.5	0	2	2
16	22.0	0	2	2
4	21.0	1	1	1
22	16.1	1	1	1

1-10 of 24 rows

Previous **1** 2 3 Next

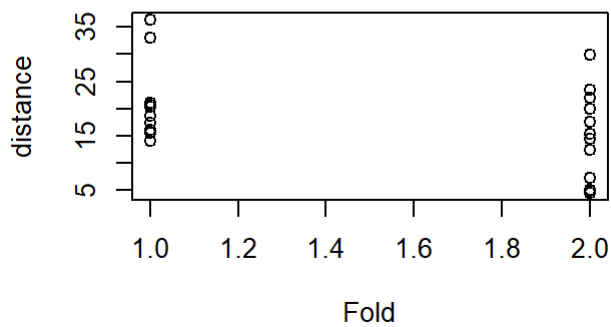
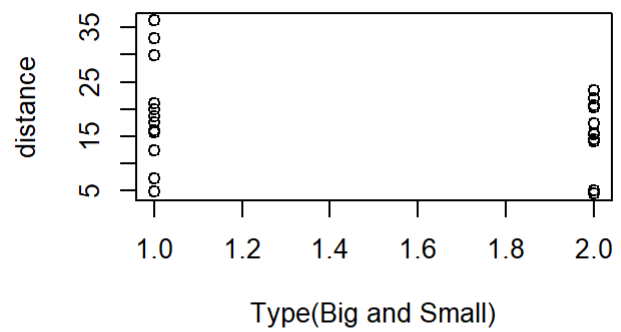
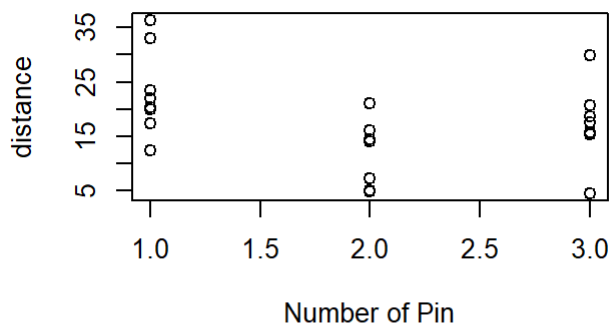
## Frog BOX PLOT

```
par(mfrow=c(2,2))
plot(A,y,xlab="Number of Pin",ylab="distance")
plot(B,y,xlab="Type(Big and Small)",ylab="distance") # type1: small frog, type2: big frog
plot(C,y,xlab="Fold",ylab="distance")
par(mfrow=c(1,1))
```



## Frog QQ PLOT

```
par(mfrow=c(2,2))
plot(as.numeric(A),y,xlab="Number of Pin",ylab="distance")
plot(as.numeric(B),y,xlab="Type(Big and Small)",ylab="distance")
plot(as.numeric(C),y,xlab="Fold",ylab="distance")
par(mfrow=c(1,1))
```



## ANOVA analysis

```
r1t<-aov(y~A*B*C)
summary(r1t)
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## A             2   489.2   244.58   11.838 0.00145 **
## B             1    87.4    87.40    4.230 0.06212 .
## C             1   182.6   182.60    8.838 0.01164 *
## A:B           2    38.1    19.04    0.922 0.42427
## A:C           2    65.3    32.63    1.579 0.24608
## B:C           1    42.1    42.14    2.039 0.17877
## A:B:C         2   349.0   174.50    8.446 0.00513 **
## Residuals    12   247.9    20.66
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The P-value of factor B(frog size), interaction AB, interaction AC and interaction BC is smaller than 0.05. That means these factor are nonsignificant.

## PLOT

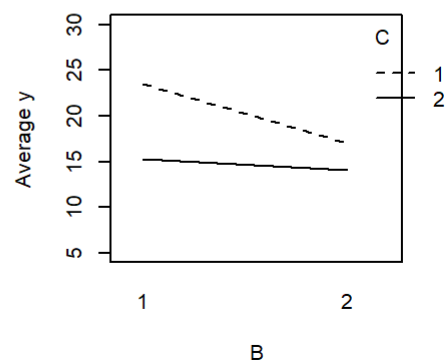
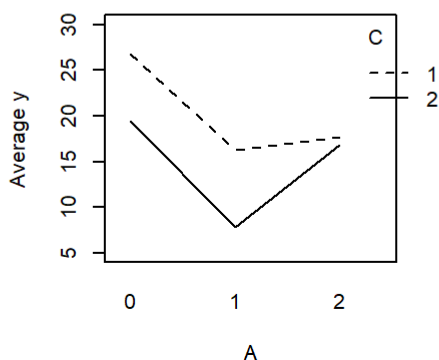
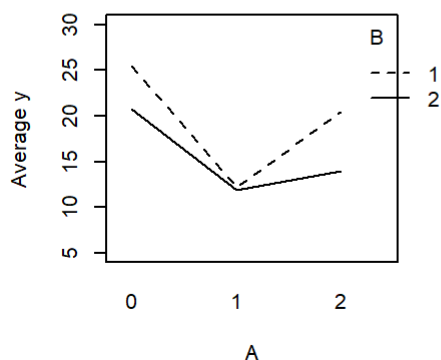
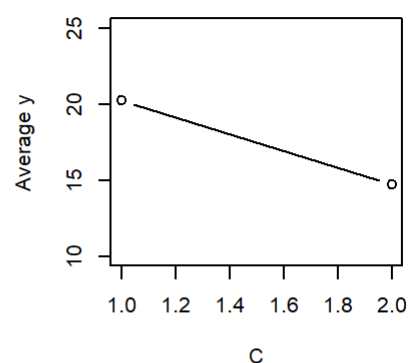
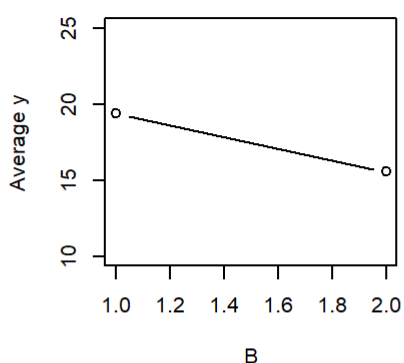
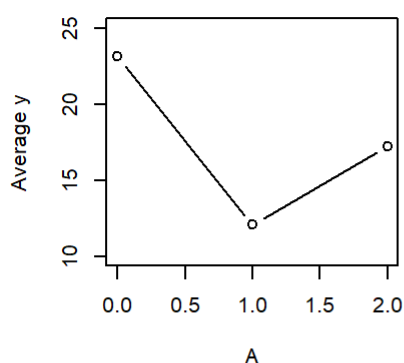
```
par(mfrow=c(2,3))
```

```
Ai.bar<-tapply(y,A,mean)
plot(names(Ai.bar),Ai.bar,type="b",xlab="A",ylab="Average y",ylim=c(10,25))
```

```
Bi.bar<-tapply(y,B,mean)
plot(names(Bi.bar),Bi.bar,type="b",xlab="B",ylab="Average y",ylim=c(10,25))
```

```
Ci.bar<-tapply(y,C,mean)
plot(names(Ci.bar),Ci.bar,type="b",xlab="C",ylab="Average y",ylim=c(10,25))
```

```
interaction.plot(A,B,y,xlab="A",ylab="Average y",ylim=c(5,30))
interaction.plot(A,C,y,xlab="A",ylab="Average y",ylim=c(5,30))
interaction.plot(B,C,y,xlab="B",ylab="Average y",ylim=c(5,30))
```



```
par(mfrow=c(1,1))
```

The degree of influence of each factor is  $A > B > C$ .

## Residual PLOT



```
e<-rlt$residuals
y.hat<-rlt$fitted.values
ord<-data[,1]

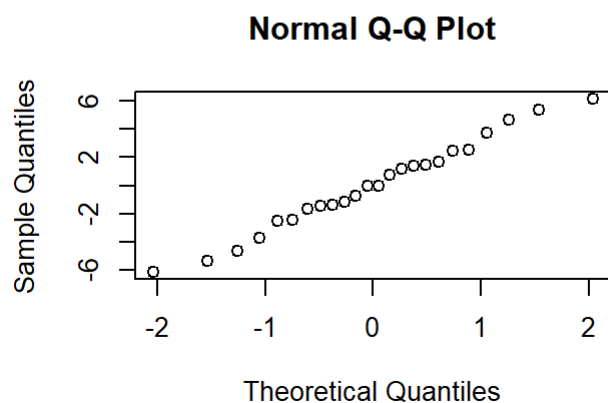
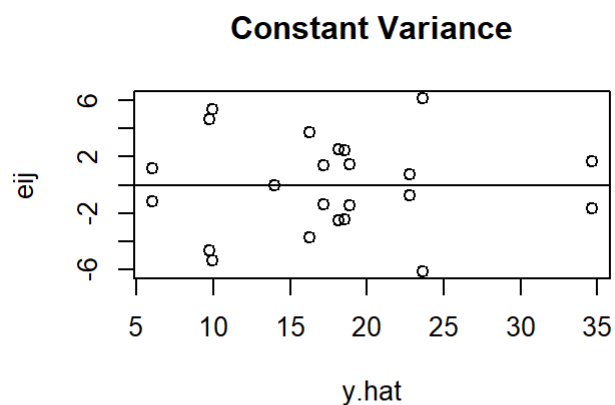
par(mfrow=c(2,2))

plot(ord,e,xlab="Run order",ylab="eij",main = "Independency")
abline(0,0)

plot(y.hat,e,xlab="y.hat",ylab="eij", main = "Constant Variance")
abline(0,0)

qqnorm(e)

par(mfrow=c(1,1))
```



## shapiro test

```
shapiro.test(e)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  e
## W = 0.98377, p-value = 0.9539
```

Delete the factor B(frog size), interaction AB, interaction AC and interaction BC.

(After) ANOVA analysis

```
r1t.1<-aov(y~A+C)
summary(r1t.1)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## A              2  489.2   244.58    5.895 0.00971 **
## C              1  182.6   182.60    4.401 0.04882 *
## Residuals     20  829.8    41.49
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(After) Residual PLOT

```
e<-r1t.1$residuals
y.hat<-r1t.1$fitted.values
ord<-data[,1]

par(mfrow=c(2,2))

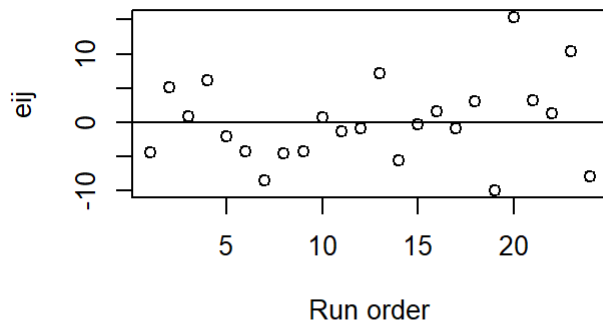
plot(ord,e,xlab="Run order",ylab="eij",main = "Independency")
abline(0,0)

plot(y.hat,e,xlab="y.hat",ylab="eij", main = "Constant Variance")
abline(0,0)

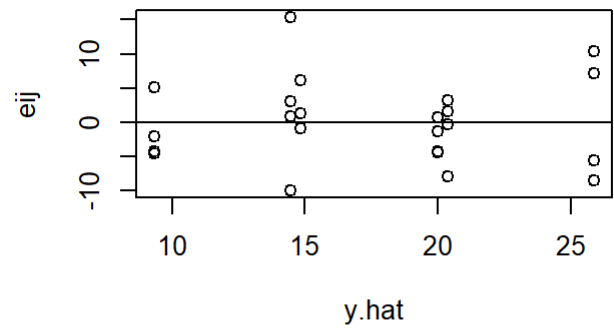
qqnorm(e)

par(mfrow=c(1,1))
```

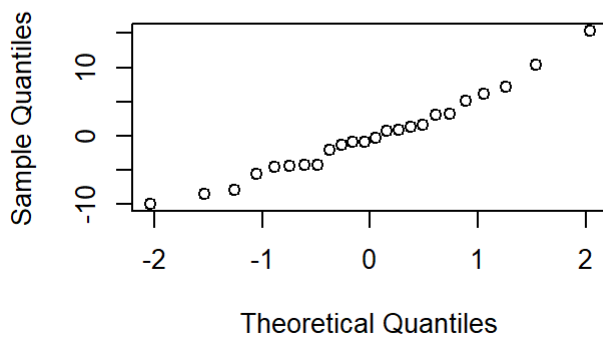
**Independency**



**Constant Variance**



**Normal Q-Q Plot**



(After) shapiro test

```
shapiro.test(e)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  e  
## W = 0.96942, p-value = 0.6527
```

**Conclusion**

```
cbind(A,B,C,y.hat)
```

```
##      A B C      y.hat
## 1  1 1 1 25.883333
## 2  1 1 1 25.883333
## 3  1 1 2 20.366667
## 4  1 1 2 20.366667
## 5  1 2 1 25.883333
## 6  1 2 1 25.883333
## 7  1 2 2 20.366667
## 8  1 2 2 20.366667
## 9  2 1 1 14.833333
## 10 2 1 1 14.833333
## 11 2 1 2  9.316667
## 12 2 1 2  9.316667
## 13 2 2 1 14.833333
## 14 2 2 1 14.833333
## 15 2 2 2  9.316667
## 16 2 2 2  9.316667
## 17 3 1 1 19.983333
## 18 3 1 1 19.983333
## 19 3 1 2 14.466667
## 20 3 1 2 14.466667
## 21 3 2 1 19.983333
## 22 3 2 1 19.983333
## 23 3 2 2 14.466667
## 24 3 2 2 14.466667
```

The big frog with one fold and small frog with one fold are the farthest.