

Problem 3

3.b

```
sl=read.table("SleepRem.txt", header = TRUE)
anova(aov(sl$values~sl$ind))
```

Analysis of Variance Table

Response: sl\$values

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
sl\$ind	3	5881.7	1960.58	21.093	8.322e-06 ***
Residuals	16	1487.1	92.95		

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

From the resulting table we see that the P-value of 8.3222×10^{-6} is far less than the .05 level of significance, therefore we conclude that we should reject the null hypothesis.

##3.c

```
rem_aov<-aov(sl$values~sl$ind)
resids<-rem_aov$resid
shapiro.test(resids)
```

Shapiro-Wilk normality test

data: resids

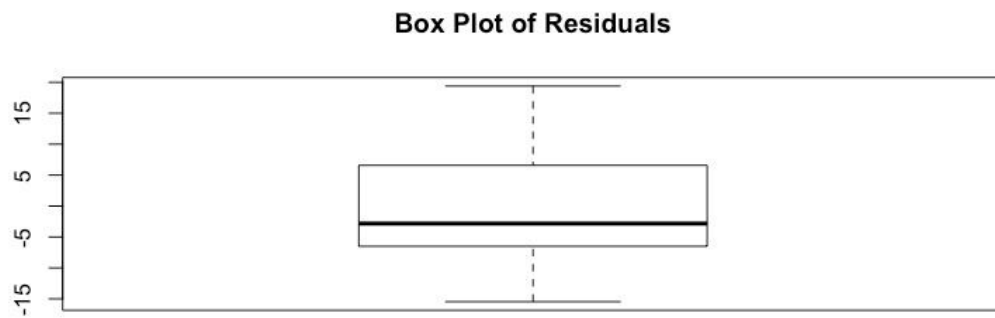
W = 0.92585, p-value = 0.1285

Here, we can see that the p-value of 0.1285 is greater than the .05 level of significance.

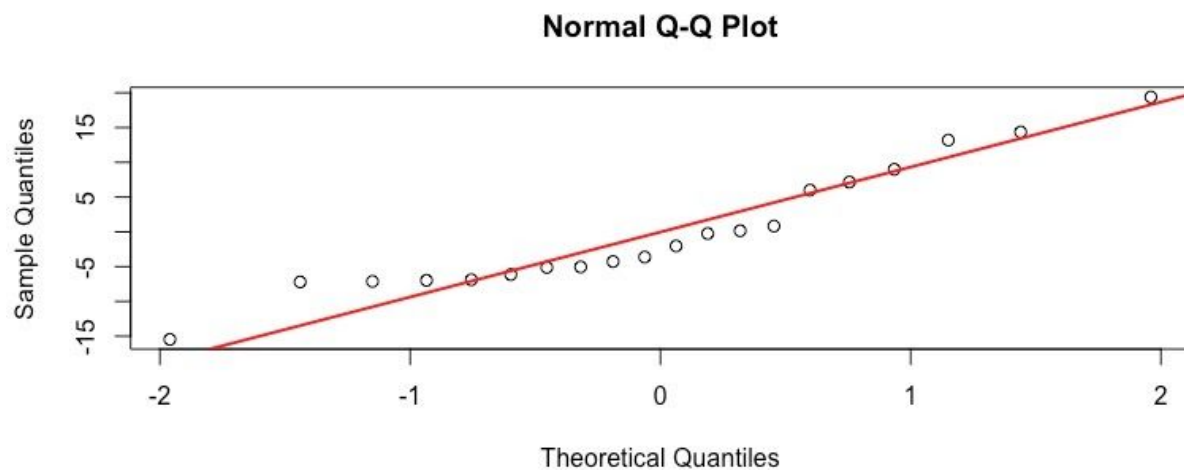
This implies that our normality assumption is not disproved by the data.

##Boxplot and Q-Q plot:

```
boxplot(resids, main = "Box Plot of Residuals")
```



```
qqnorm(resids, main = "Normal Q-Q Plot")
qqline(resids, col = "RED", lwd = 2)
```



From the above two graphs, we can reasonably conclude that the normality assumption is satisfied to a usable extent.

6.b

```
pc = read.table("PorousCarbon.txt", header = T)
carbon_aov = aov(pc$values~as.factor(pc$temp))
anova(carbon_aov)
```

Analysis of Variance Table

```
Response: pc$values
              Df Sum Sq Mean Sq F value
as.factor(pc$temp)  3  4.4474  1.48246   11.437
Residuals          16  2.0740  0.12963
              Pr(>F)
as.factor(pc$temp) 0.0002958 ***
Residuals
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From the resulting table we see that the p-value of .0002958 is less than the .05 level of significance, therefore we conclude that we should reject the null hypothesis.

##Also, the test-statistic given is an F-value of 11.437.

6.c

```
carbon_aov <- aov(pc$values~pc$temp)
resids <- carbon_aov$resid
shapiro.test(resids)
```

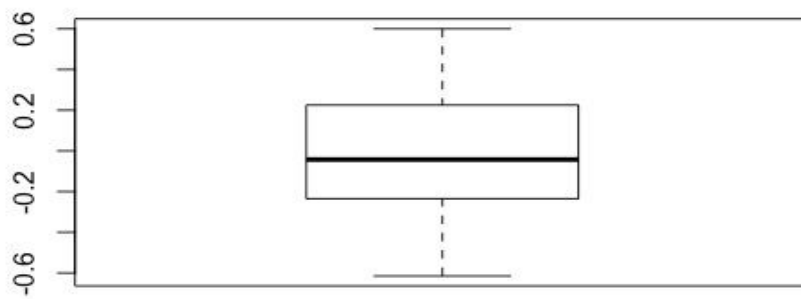
Shapiro-Wilk normality test

```
data: resids
W = 0.97345, p-value = 0.8255
```

The resulting p-value of 0.8225 is greater than the significance level of 0.05 implying that our assumption of normality is not disproved by the data.

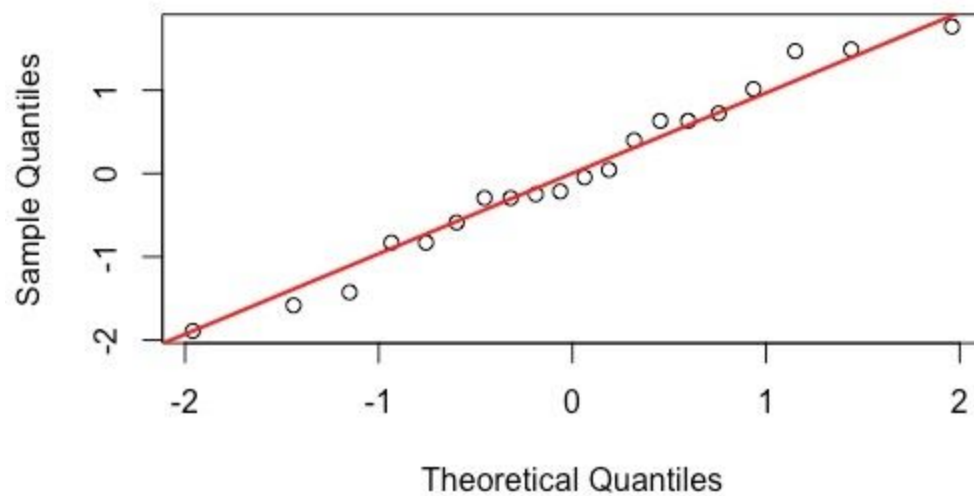
```
boxplot(resids, main = "Box Plot of Residuals")
```

Box Plot of Residuals



```
stdresids=rstandard(carbon_aov)
qqnorm(stdresids, main = "Normal Q-Q Plot")
qqline(stdresids, col = "RED", lwd = 2)
```

Normal Q-Q Plot



```
##in addition
fit=fitted.values(carbon_aov)
plot(residuals, fit)
```

Part B - Problem 4

##4.a

```
pc=read.table("PorousCarbon.txt", header = TRUE)
TukeyHSD(aov(pc$values~as.factor(pc$temp)), conf.level=0.95)
```

```
  Tukey multiple comparisons of means
    95% family-wise confidence level
```

```
Fit: aov(formula = pc$values ~ as.factor(pc$temp))
```

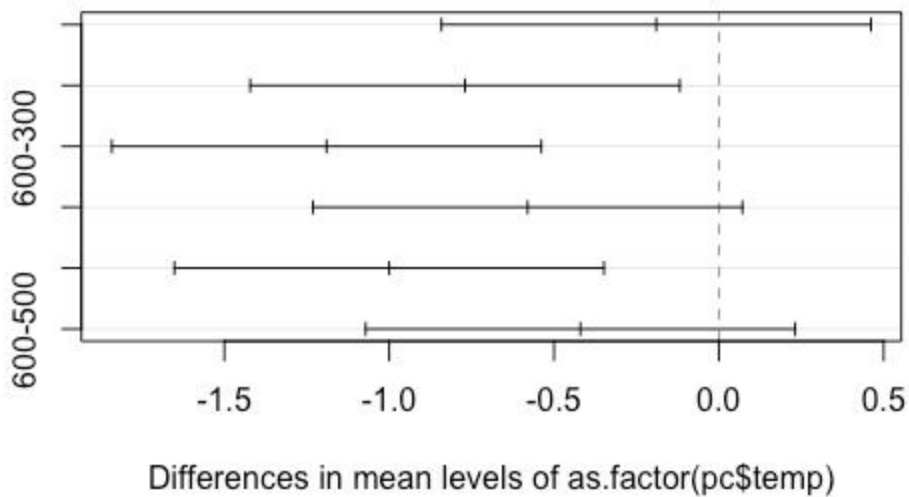
```
$`as.factor(pc$temp)`
      diff      lwr      upr    p adj
400-300 -0.19 -0.8414712  0.46147124 0.8373903
500-300 -0.77 -1.4214712 -0.11852876 0.0179499
600-300 -1.19 -1.8414712 -0.53852876 0.0004366
500-400 -0.58 -1.2314712  0.07147124 0.0900085
600-400 -1.00 -1.6514712 -0.34852876 0.0023107
600-500 -0.42 -1.0714712  0.23147124 0.2897872
```

from the output table, we can see that the 2nd, 3rd and 5th outputs are significant at the experiment wise level of .05

##From the output of the c

```
plot(TukeyHSD(aov(pc$values~as.factor(pc$temp)),
conf.level=0.95))
```

95% family-wise confidence level



```
a=subset(pc, temp=="300")
u1=mean(a$values)
u1
```

```
[1] 7.43
```

```
b=subset(pc, temp == "400")
u2=mean(b$values)
U2
```

```
[1] 7.24
```

```
c=subset(pc, temp == "500")
u3=mean(c$values)
U3
```

```
[1] 6.66
```

```
d=subset(pc, temp == "600")
u4=mean(d$values)
```

U4

[1] 6.24

```
## in increasing order, we have: u4, u3, u2, and u1
## from this ordering, we can infer that u4 does not
## significantly differ from u3
## and u2 does not significantly differ from u4
```