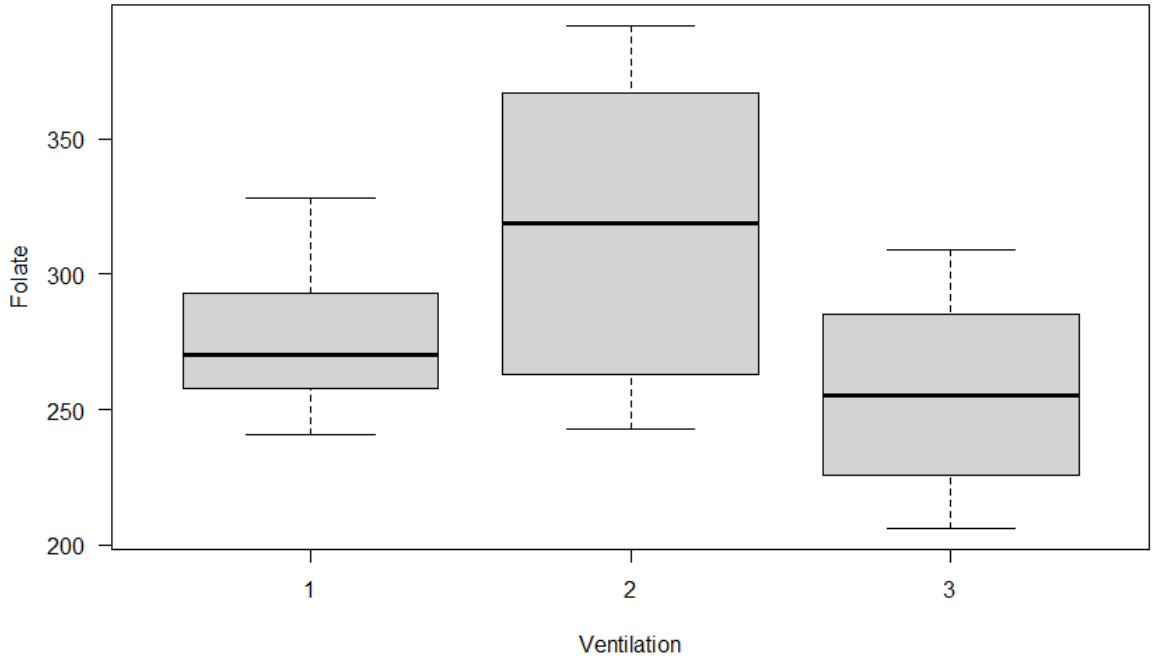
Question 1



It will be assumed that ventilation method 1 and 3 are quite similar due to the amount of overlap between them. There is a noticeable amount of overlap between the three methods, the second method has a wider variance in the folate level of patients

	Estimate	Std. Error	2.5 %	97.5 %
(Intercept)	278.00000	20.44662	235.20474	320.79526
ventilation2	38.62500	26.06443	-15.92847	93.17847
ventilation3	-21.55556	25.50141	-74.93063	31.81952

From the above confidence interval output for the coefficients of the predictors, it is noticed that method 1 is used as baseline; the mean red cell folate level in patients receiving method 1 ventilation during anaesthesia is 278 and the 95% interval is 235.2 to 320.8

- The mean red cell folate level if using ventilation method 2 is higher than method 1 by 38.63
- But not significantly higher as its 95% interval of -15.93 to 93.82 includes 0
- The mean red cell folate level of using ventilation method 3 is less than method 1 by 21.56 and its 95% interval of -74.93 to 31.82 includes 0; therefore, it is not significantly lower

However, we cannot explicitly compare between ventilation method 2 and 3, therefore, this estimate can be done by using Contrast method to compare the mean of using method 2 to method 3 and find out if there is a difference between both.

- Compare mean of red cell folate level of method 2 and method 3

H0: $\mu 2 = \mu 3$

$\mu 2 - \mu 3 = 0$

$0*\mu 1 + 1*\mu 2 - 1*\mu 3 = 0$

Coefficients of the contrast are then (0, 1, -1)

- Compare mean of red cell folate level of method 1 to method 2 and 3

H0: $\mu 1 = \mu 2 + \mu 3$

$\mu 1 - \mu 2 - \mu 3 = 0$

$1*\mu 1 - 1*\mu 2 - 1*\mu 3 = 0$

Coefficient of contrast is (1, -1, -1); therefore, the orthogonal set refers to a contrast of $\mu 1$ against $\mu 2$ and $\mu 3$

C1 = (0, 1, -1), C2 = (1, -1, -1)

To test for orthogonality:

- **C1 * C2**
  (0, 1, -1) * (1, -1, -1)
  (0*1) + (1*1) + (-1*1) = 0; therefore, the contrast is orthogonal

	Estimate	Std. Error	2.5 %	97.5 %
(Intercept)	282.267361	11.63455	257.915964	306.61876
m2_v_m31	30.090278	11.10797	6.841029	53.33953
orth_set1	-4.267361	11.63455	-28.618758	20.08404

The above output is the 95% interval output of a new model created using the 2 contrast and the output can be interpreted as:

- The intercept is the average across the 3 groups and is estimated as 282.27
- Coefficient of m2_v_m3 is 30.09 implies that the differences between mean red cell folate level of patients receiving method 1 to method 2.
- Also, their difference is significantly higher than the ground mean (intercept) because the 95% confidence interval (6.84 to 43.34) does not include 0

Analysis of Variance Table

Response: folate

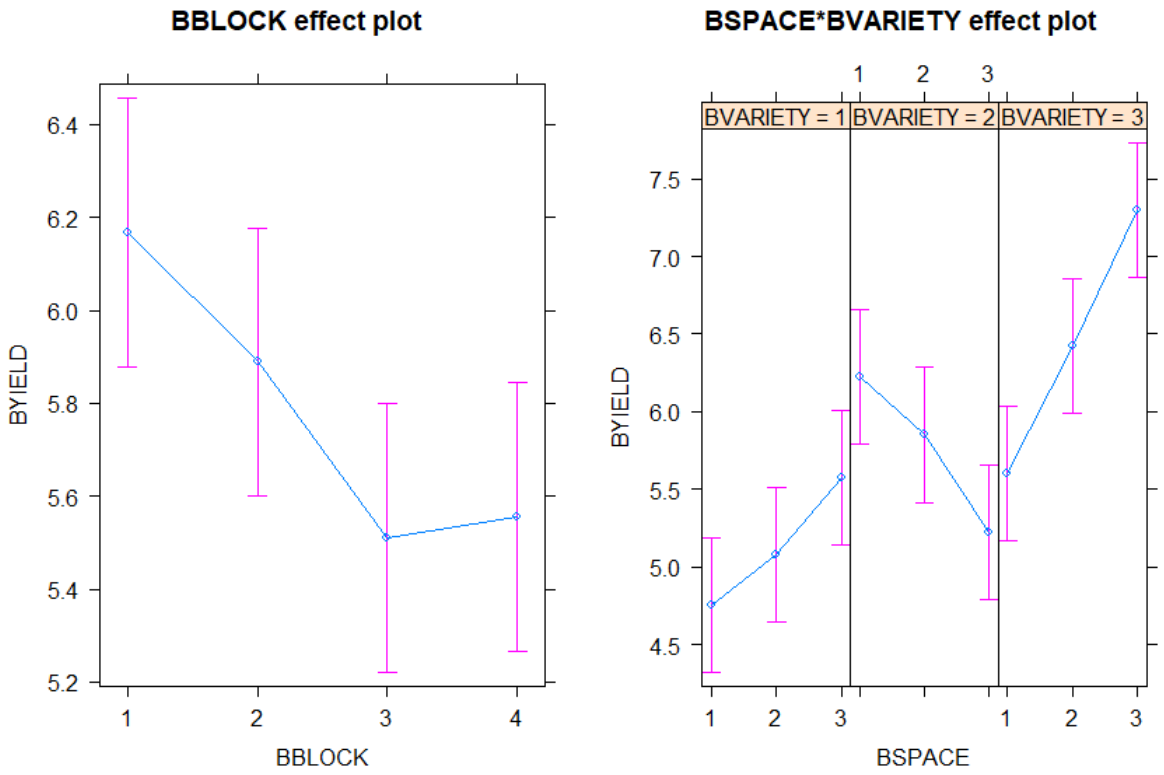
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
m2_v_m3	1	15235	15234.6	7.2881	0.0142 *
orth_set	1	281	281.2	0.1345	0.7178
Residuals	19	39716	2090.3		

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

From the ANOVA output, it will be seen that with a p value of 0.0142 which is less than 0.05, the difference between method 2 and 3 is significant (m2_v_m3)

The orth_set is the orthogonal set and with a p value of 0.7178, the set is not significant. No significant difference between the mean of method 1 and the average of the remaining 2 methods (2 and 3)

Question 2



From the above exploratory plot,

- It is seen from the BBLOCK effect plot on the left that the mean BYIELD for **block 1** is more when compared to the other 3 blocks and the lowest BBYIELD is given by **block 2**.
- The BSPACE*BVARIETY effect plot on the right shows the effect of the 3 variety on the yield when different row spacing is applied.
    - For Variety 1, it would be seen that the BYIELD increases as the BSPACE increases. There is some form of significant overlap in the amount of yield gotten from different row spaces.
    - For Variety 2, the yield reduces as the as BSPACE increases; also, a significant amount of overlap between row spaced can be assumed to give similar yield
    - Variety 3 gives the highest BYIELD in all row spaces compared to other Variety types; it is seen that BYIELD in the 3 different row spaces give high yield that can be assumed as significantly different from each other because there is little or no overlap in the yield for different spaces.

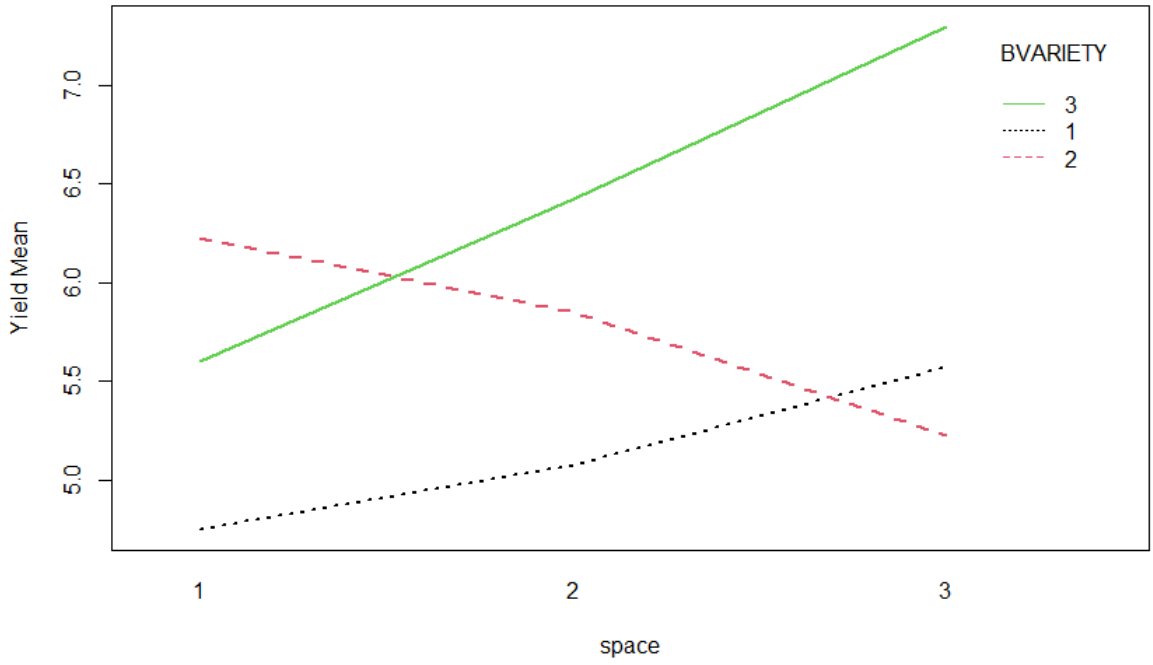
```
Call:
lm(formula = BYIELD ~ BBLOCK + BSPACE * BVARIETY, data = barley)

Residuals:
    Min      1Q  Median      3Q     Max
-0.6111 -0.2535 -0.0625  0.2938  0.6694

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)         5.1361     0.2427  21.162  < 2e-16 ***
BBLOCK2            -0.2778     0.1982  -1.402 0.173792
BBLOCK3            -0.6556     0.1982  -3.308 0.002953 **
BBLOCK4            -0.6111     0.1982  -3.084 0.005081 **
BSPACE2             0.3250     0.2972   1.093 0.285088
BSPACE3             0.8250     0.2972   2.775 0.010511 *
BVARIETY2           1.4750     0.2972   4.962 4.58e-05 ***
BVARIETY3           0.8500     0.2972   2.860 0.008642 **
BSPACE2:BVARIETY2  -0.7000     0.4204  -1.665 0.108877
BSPACE3:BVARIETY2  -1.8250     0.4204  -4.341 0.000222 ***
BSPACE2:BVARIETY3   0.5000     0.4204   1.189 0.245909
BSPACE3:BVARIETY3   0.8750     0.4204   2.081 0.048227 *
---
Signif. codes:  0 â€˜***â€™ 0.001 â€˜**â€™ 0.01 â€˜*â€™ 0.05 â€˜.â€™
0.1 â€˜ â€™ 1

Residual standard error: 0.4204 on 24 degrees of freedom
Multiple R-squared:  0.8386, Adjusted R-squared:  0.7646
F-statistic: 11.34 on 11 and 24 DF,  p-value: 5.173e-07
```

The above output is the fitted model taking into consideration the block, space, variety types and the interaction between the space and variety types. The output shows that:

- BVariety 2 and 3 have an estimated yield that is significantly higher than variety 1 as their p-values are both greater than 0.05
- Both Bspace 2 and 3 have highere estimated yield than Bspace 1 but only Bspace 3 produces a significantly yield returns which is higher than Bspace 1.
- Block 1 has a higher estimated yield when compared to the remaining block. Block 3 and 4 are significantly lower than block 1 in estimated yield. Although, the estimated yield in block 2 is lower than block 1, but the difference is not significant
- About 76.46% of the variability is explained by the model.

The model equation is given by:

$$\begin{aligned}\mathrm{E}(\mathbf{BYIELD}) = {} & 5.1361 - 0.2778(\mathbf{BBLOCK2}) - 0.6556(\mathbf{BBLOCK3}) - 0.6111(\mathbf{BBLOCK4}) \\ & + 0.325(\mathbf{BSPACE2}) + 0.825(\mathbf{BSPACE3}) + 1.475(\mathbf{BVARIETY2}) \\ & + 0.85(\mathbf{BVARIETY3}) - 0.7(\mathbf{BSPACE2}{:}\,\mathbf{BVARIETY2}) \\ & - 1.825(\mathbf{BSPACE3}{:}\,\mathbf{BVARIETY2}) + 0.5(\mathbf{BSPACE2}{:}\,\mathbf{BVARIETY3}) \\ & + 0.875(\mathbf{BSPACE3}{:}\,\mathbf{BVARIETY3})\end{aligned}$$



The above diagram shows the mean yield of different variety types at different row spaces:

For row space 1, it would be seen that Variety 2 produces the highest mean yield and Variety 1 had the lowest yield. While in row space 2, the mean yield for variety 2 decreases and variety produces more yield, while variety 1 slowly increases. Lastly, in row space 3, variety 2 has the lowest yield as variety 1 produces more yield than 2; but the most yield is gotten from variety 3 which continues to increase rapidly.

Therefore, it can be concluded that variety 2 is best suited for row space of 1 when trying to get the maximum yield, but variety 3 is most preferable in row space 2 and 3 as it produces the most yield

```
Analysis of Variance Table

Response: BYIELD
                Df  Sum Sq Mean Sq F value    Pr(>F)
BBLOCK           3  2.5564  0.8521  4.8221   0.00912 **
BSPACE           2  1.5506  0.7753  4.3872   0.02377 *
BVARIETY         2 10.2739  5.1369 29.0694 3.872e-07 ***
BSPACE:BVARIETY  4  7.6544  1.9136 10.8289 3.679e-05 ***
Residuals       24  4.2411  0.1767
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

From the ANOVA output above, it will be seen that BBLOCK is significant to the model, also, row space (BSPACE), variety (BVARIETY) and the interaction of the space and variety is significant to the model as it explains a significant amount of variance with p-values less than 0.05.

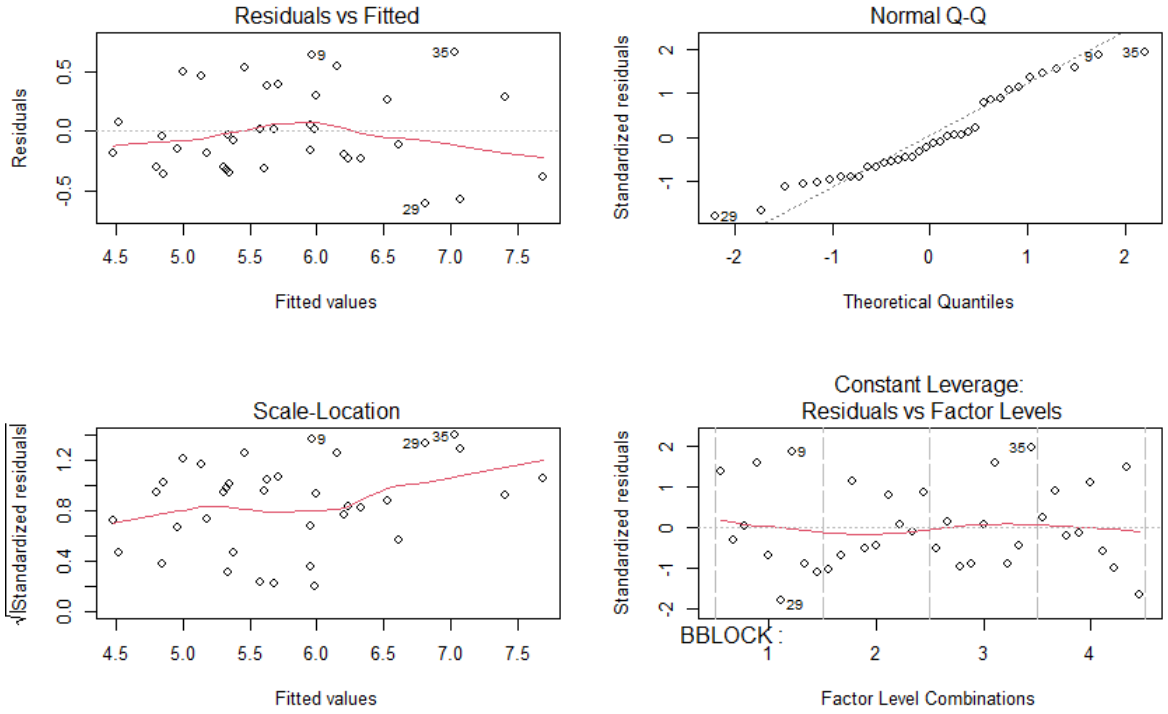
H_0: Residuals are normally distributed

```
        Shapiro-Wilk normality test

data:  lmod$residuals

W = 0.94702, p-value = 0.08429
```

The above output tests the residuals to confirm that it is normally distributed; with a p value > 0.05, the null hypothesis is accepted, therefore, the residuals are normally distributed.

```
mean(lmod$residuals)

[1] -5.393906e-18
```

The above result confirms the assumption that the mean of the residuals is 0



From the assumption plot above, it can be seen that the Residuals plot shows that the residuals have a constant variance around 0. The residual is also assumed to be normally distributed as seen in Normal Q-Q plot. The residual vs Factor level shows a random pattern of residuals across the 4 blocks.

R CODE

```
setwd("C:/Users/olley/Downloads/Documents/statistics/410 ANOVA
Factorial")
#install.packages("effects")
library(dae)
library(effects)
barley = read.table("Barley.txt", header=T)
str(barley)
barley$BBLOCK = as.factor(barley$BBLOCK)
barley$BSPACE = as.factor(barley$BSPACE)
barley$BVARIETY = as.factor(barley$BVARIETY)
str(barley)

# Linear model
lmod <- lm(BYIELD~BBLOCK+BSPACE*BVARIETY, data = barley)
plot(allEffects(lmod))
summary(lmod)
anova(lmod)

interaction.plot(barley$BSPACE,barley$BVARIETY,barley$BYIELD,
                 col= c(1,2,3),lwd=2,xlab="space",ylab="Yield Mean",
                 trace.label = "BVARIETY")

?interaction.plot

print(allEffects(lmod))

par(mfrow=c(2,2))
plot(lmod)
par(mfrow=c(1,1))

boxplot(lmod$residuals)

shapiro.test(lmod$residuals)

mean(lmod$residuals)
```

```
setwd("C:/Users/olley/Downloads/Documents/statistics")
folate = read.table("folate.txt", header=T)
str(folate)
folate$ventilation <- as.factor(folate$ventilation)

plot(folate$folate~folate$ventilation,las=1,xlab="Ventilation",ylab="Fo
late")

df <- as.data.frame(cbind(method=c(1,2,3), mean =
round(tapply(folate$folate,folate$ventilation,mean),2)))
df
model <- lm(folate~ventilation,data = folate)
summary(model)
source("Rfunctions.R")

# Interpret Coefficient
```

```
betaCI(model)


m2_v_m3 <- C(folate$ventilation,c(0,1,-1),1)
orth_set <- C(folate$ventilation,c(1,-1,-1),1)

new_model <- lm(folate~m2_v_m3+orth_set,data = folate)
betaCI(new_model)


anova(new_model)
```