4.) We can do Tukey's procedure by using r as pictured below

```
PROBLEMS  33    OUTPUT   DEBUG CONSOLE   TERMINAL

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

Fit: aov(formula = values ~ as.factor(temp), data = poredata)

$`as.factor(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

>
```

Before analyzing the table above we first have to state the null hypothesis : $H_o : \mu_i = \mu_j$. We can

reject this hypothesis if the range given by the table doesn't contain 0. We can see that the 1st,

4th and 6th pair (400-300, 500-400, and 600-500) do contain 0 , meaning that we cannot say that

those means are significantly different from each other . We can plot this and see more

graphically how they are not so different :

95% family-wise confidence level

Differences in mean levels of as.factor(temp)
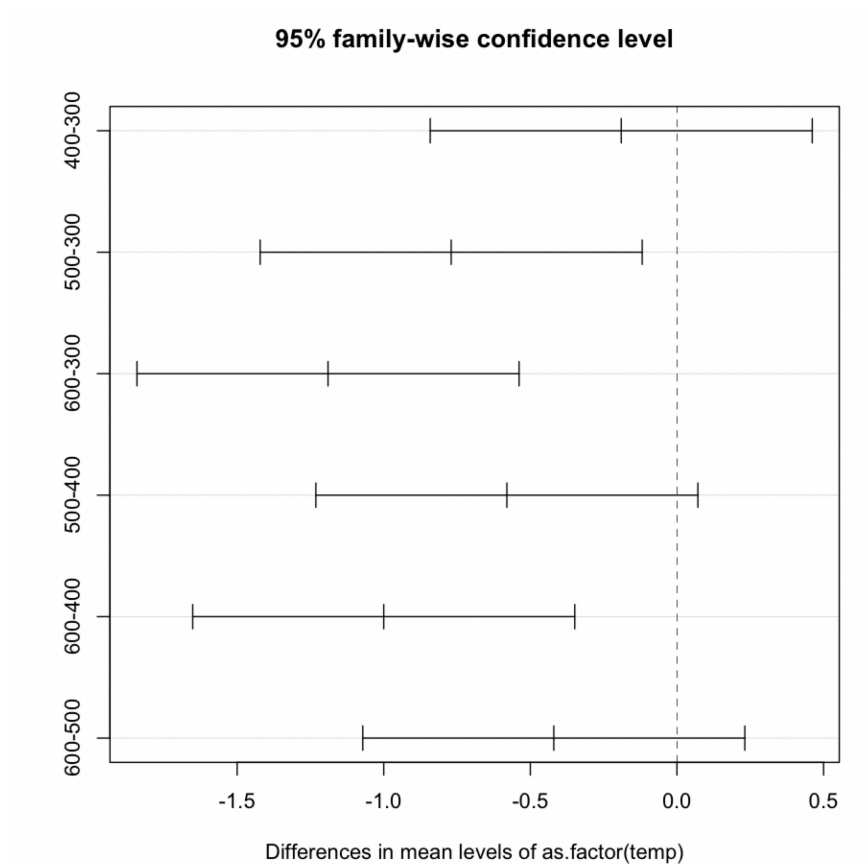
We can arrange the means in increasing order :

6.24	6.66	7.24	7.43
600	500	400	300

from the table in the first part we can see that the first two means corresponding to temps 600 and 500 are not significantly different from each other and the same goes for the means corresponding to temps 400 and 300 as well as the middle two values . This can be seen in the plot directly above.

2.) With a level of significance of .01 we want to test if there is some interaction between the variables S and C. To do that we need to look at the analysis of variance table and check the F value. Ultimately we can reject $H_0 : \gamma_{ij} = 0$ if $F_{SC} \geq F_{(S-1)(C-1),ab(n-1):0.01}$. We can see from the table below that even before we need to check the F table we can see that the p value associated with this value is higher than 0.01 meaning we cannot reject the null hypothesis and there may be some interaction between the variables .

```
PROBLEMS  45    OUTPUT    DEBUG CONSOLE    TERMINAL

> anova(fitcell)
Analysis of Variance Table

Response: y
                            Df  Sum Sq Mean Sq  F value    Pr(>F)
as.factor(S)                 2 2.42453 1.21227 146.1735 < 2.2e-16 ***
as.factor(C)                 4 0.76724 0.19181  23.1282 1.345e-11 ***
as.factor(S):as.factor(C)    8 0.12070 0.01509   1.8192   0.09103 .
Residuals                   60 0.49760 0.00829
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> []
```

B.) we can see from the output below that the phone types that are different from each other with a significance of 0.01 are all except for B5-B1, B4-b2, B4-B3, and B5-B3. As for each of the levels all appear to be significantly different from each other.

```
PROBLEMS  46    OUTPUT    DEBUG CONSOLE    TERMINAL

> tukcell = TukeyHSD(fitcell)
> tukcell
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = y ~ as.factor(S) * as.factor(C), data = celldata)

$`as.factor(S)`
        diff        lwr        upr p adj
L-H -0.4388 -0.5007017 -0.3768983     0
M-H -0.2520 -0.3139017 -0.1900983     0
M-L  0.1868  0.1248983  0.2487017     0

$`as.factor(C)`
            diff          lwr          upr      p adj
B2-B1  0.27533333  0.181809954  0.36885671 0.0000000
B3-B1  0.15800000  0.064476621  0.25152338 0.0001238
B4-B1  0.24533333  0.151809954  0.33885671 0.0000000
B5-B1  0.08800000 -0.005523379  0.18152338 0.0746708
B3-B2 -0.11733333 -0.210856713 -0.02380995 0.0069794
B4-B2 -0.03000000 -0.123523379  0.06352338 0.8949578
B5-B2 -0.18733333 -0.280856713 -0.09380995 0.0000049
B4-B3  0.08733333 -0.006190046  0.18085671 0.0782490
B5-B3 -0.07000000 -0.163523379  0.02352338 0.2314578
B5-B4 -0.15733333 -0.250856713 -0.06380995 0.0001330
```
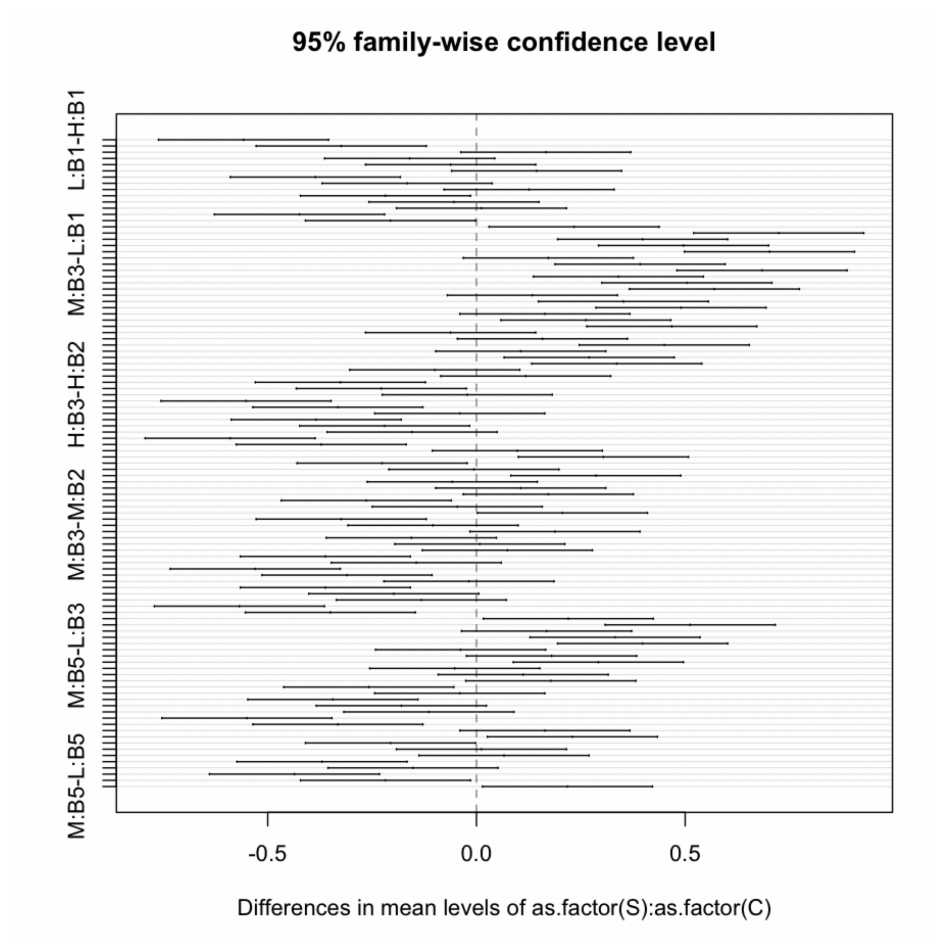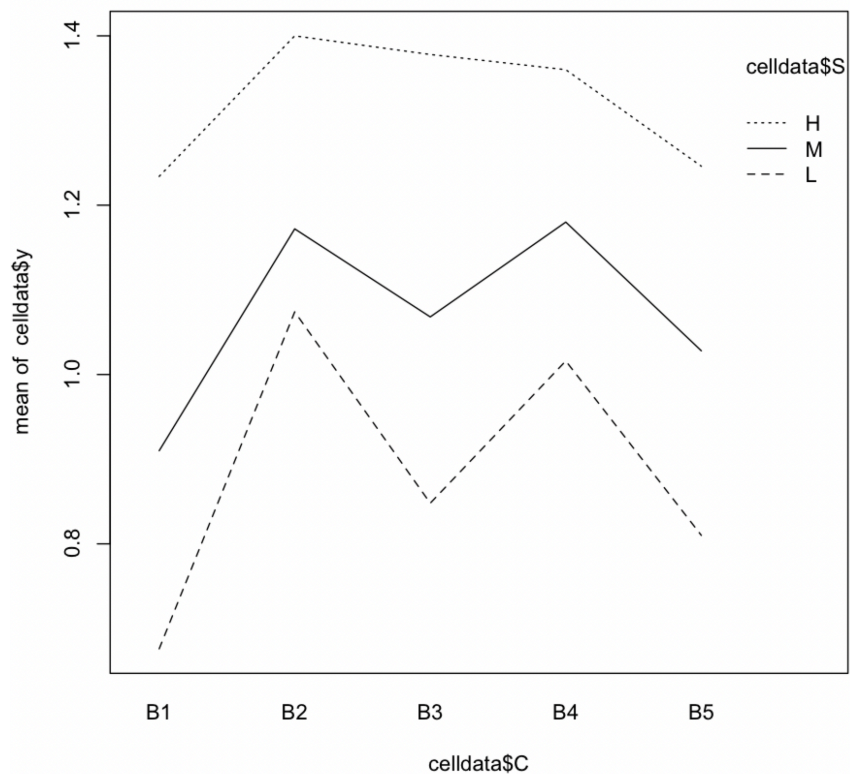
For fun here is the plot:

95% family-wise confidence level

Differences in mean levels of as.factor(S):as.factor(C)

Here we can see that the line are not parallel at every point meaning there is some slight interaction between variable which is backed up by our conclusions on the null hypothesis earlier . As for checking the normality assumptions we can see from the residuals plot below that the distribution of the residuals is quite random fitting in with our error term assumption.

Residuals vs Fitted

aov(y ~ as.factor(S) * as.factor(C))
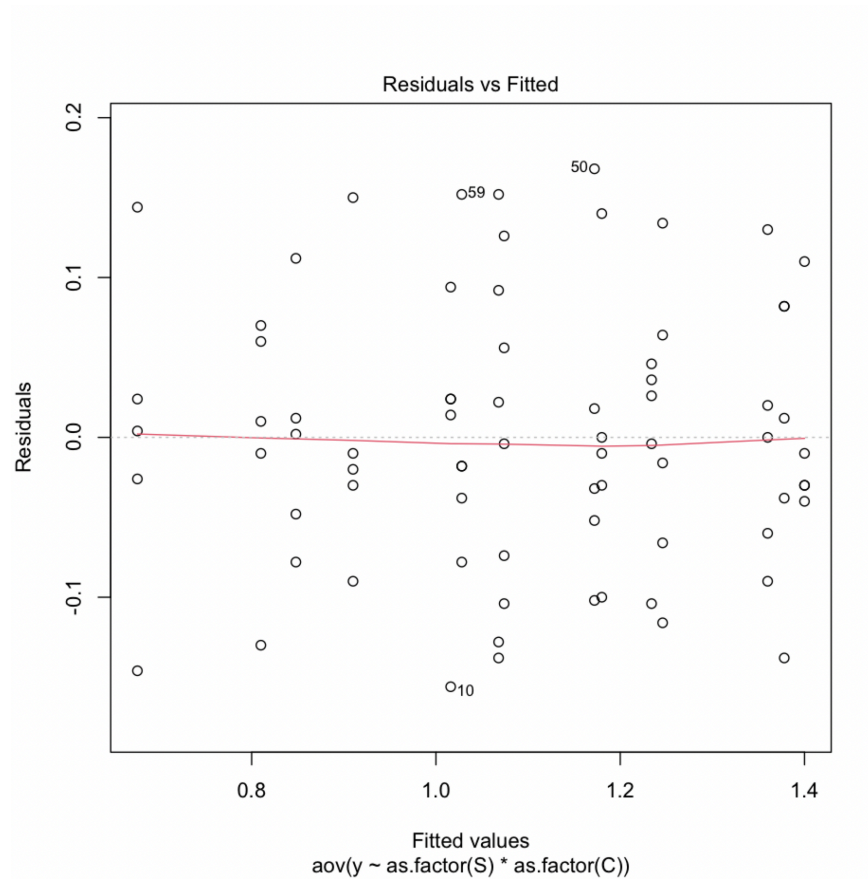
We can look at the QQ plot below and see that our values closely fall on the line , thus confirming our normality assumptions.:

Normal Q-Q

Standardized residuals

Theoretical Quantiles
aov(y ~ as.factor(S) * as.factor(C))