

stat 453 project analysis

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```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'  
  
## The following objects are masked from 'package:stats':  
##  
##   filter, lag  
  
## The following objects are masked from 'package:base':  
##  
##   intersect, setdiff, setequal, union
```

```
library(ggplot2)
```

```
library(dplyr)  
library(ggplot2)  
df <- read.csv("combined_data.csv")  
head(df)
```

```
##   Person Score  Treatment Gender List  
## 1      1      5 Audiovisual Female   1  
## 2      1      5      Visual Female   2  
## 3      1      4      Audio Female   3  
## 4      2      4 Audiovisual   Male   2  
## 5      2      4      Visual   Male   3  
## 6      2      4      Audio    Male   1
```

```
df$Treatment <- as.factor(df$Treatment)  
df$Person <- as.factor(df$Person)  
df$Score <- as.numeric(df$Score)  
levels(df$Treatment)
```

```
## [1] "Audio"      "Audiovisual" "Visual"
```

```
levels(df$Person)
```

```
## [1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10"
```

```
df %>%
  group_by(Treatment) %>%
  summarise(
    count = n(),
    mean = mean(Score, na.rm = TRUE),
    sd = sd(Score, na.rm = TRUE)
  )
```

```
## # A tibble: 3 x 4
##   Treatment    count  mean    sd
##   <fct>      <int> <dbl> <dbl>
## 1 Audio         30  4.97  1.43
## 2 Audiovisual   30  5.63  1.54
## 3 Visual        30  5.87  1.66
```

```
df %>%
  group_by(Person) %>%
  summarise(
    count = n(),
    mean = mean(Score, na.rm = TRUE),
    sd = sd(Score, na.rm = TRUE)
  )
```

```
## # A tibble: 10 x 4
##   Person count  mean    sd
##   <fct>  <int> <dbl> <dbl>
## 1 1         9  5.22  0.667
## 2 2         9  5.56  1.59
## 3 3         9   6    1.32
## 4 4         9  5.33  0.707
## 5 5         9  5.33  1.66
## 6 6         9  5.22  1.09
## 7 7         9  5.67  2.69
## 8 8         9  5.78  2.33
## 9 9         9  5.44  1.42
## 10 10        9  5.33  1.73
```

Hypothesis Testing Null Hypothesis (H_0): There is no significant difference between treatment means.

Alternative Hypothesis (H_1): At least one treatment has a different mean.

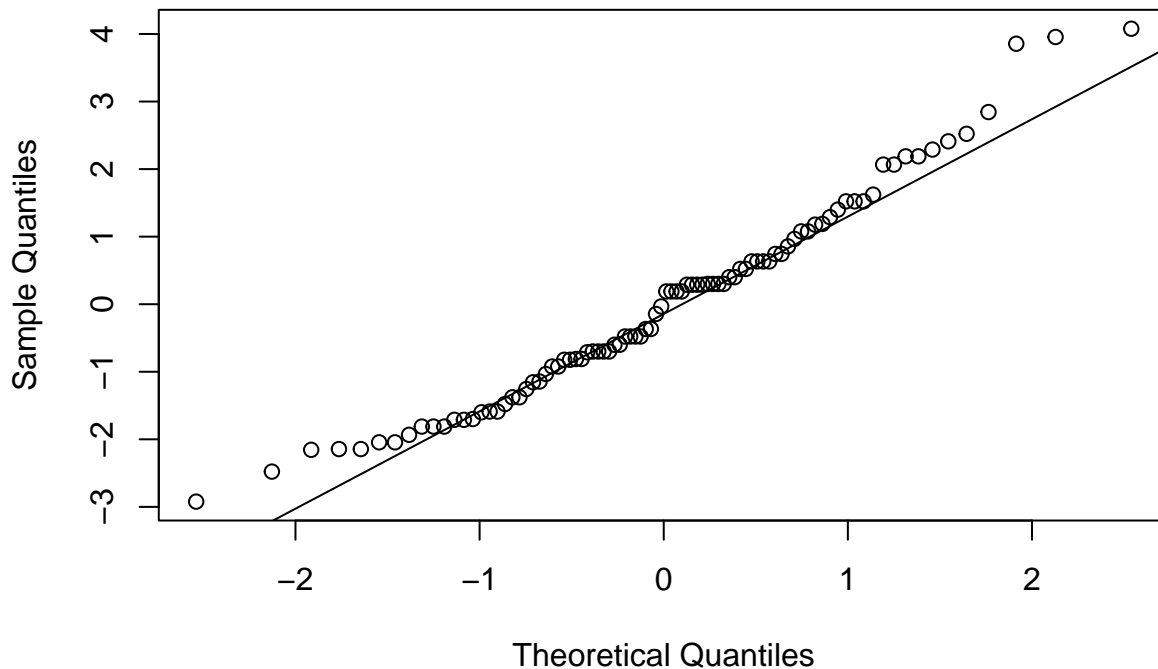
```
res.aov <- aov(Score ~ Treatment + Person, data = df)
summary(res.aov)
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## Treatment  2  13.09   6.544    2.527 0.0864 .
## Person     9   5.38   0.598    0.231 0.9891
## Residuals 78 202.02   2.590
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The p-value > 0.05 , we have no significant evidence against H_0 to reject H_0 , meaning there is no significant difference between treatment means.

```
residuals <- residuals(res.aov)
qqnorm(residuals)
qqline(residuals)
```

Normal Q-Q Plot



It can be seen from the qq-plot that the residuals of the datapoints are not normally distributed towards the end. they are kind of skewed. Therefore dataset has possible skewness or heavy tails

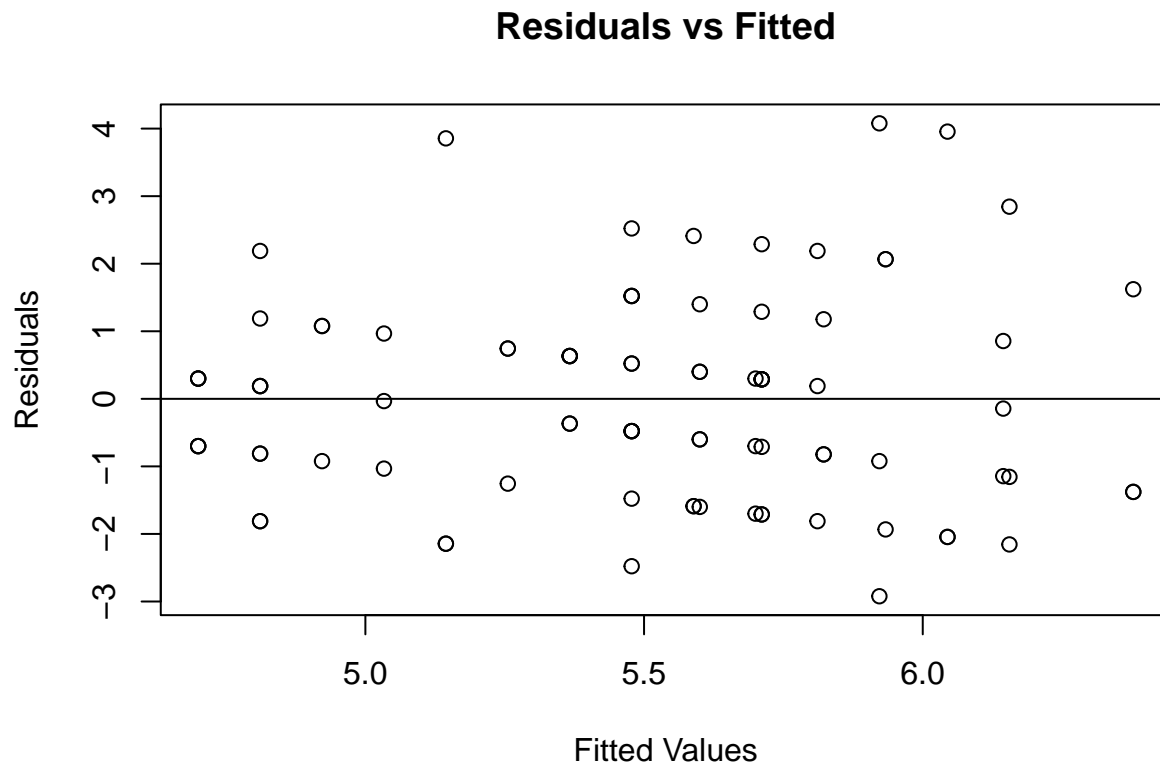
```
shapiro.test(residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals
## W = 0.97084, p-value = 0.04052
```

To check the normality of the residues, we can do the shapiro test. After doing the test it can be interpreted with the help of the p-value of the test statistic that residuals are not normally distributed.

Now we will check for homoscedasticity.

```
fitted_values <- fitted(res.aov)
plot(fitted_values, residuals,
     ylab="Residuals", xlab="Fitted Values", main="Residuals vs Fitted")
abline(h=0)
```

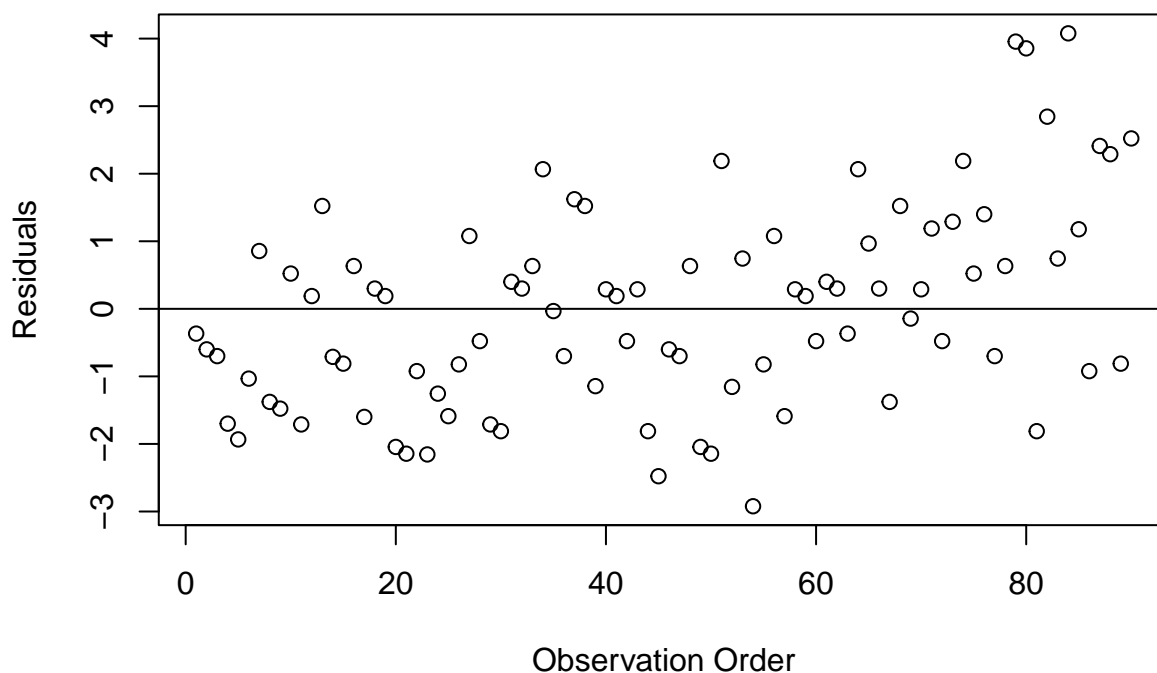


From the graph it can be interpreted that residuals are randomly scattered around the horizontal line with constant spread. No clear pattern is visible on the graph. therefore it can be said that the data has homoscedasticity.

Now we will check for autocorrelation

```
plot(1:length(fitted_values), residuals,  
     ylab="Residuals", xlab="Observation Order", main="Residuals vs Order")  
abline(h=0)
```

Residuals vs Order



It can be seen that residuals appear randomly scattered around zero, with no visible patterns or trends. No clustering, cycles, or trends over time are visible in the graph. Therefore it can be said that there is no autocorrelation present in the data set.

```
TukeyHSD(res.aov, "Treatment", conf.level=0.95)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Score ~ Treatment + Person, data = df)
##
## $Treatment
##          diff          lwr          upr          p adj
## Audiovisual-Audio 0.6666667 -0.32615260 1.659486 0.2498819
## Visual-Audio      0.9000000 -0.09281926 1.892819 0.0835432
## Visual-Audiovisual 0.2333333 -0.75948593 1.226153 0.8408542
```

From the Tukey test, it can be interpreted that the difference between the three treatments is not significant as the p-values are all greater 0.05. To confirm our hypothesis, we can see that confidence interval also includes Zero in it which means that the difference among the treatment is not significant.

```
df$Gender <- as.factor(df$Gender)
```

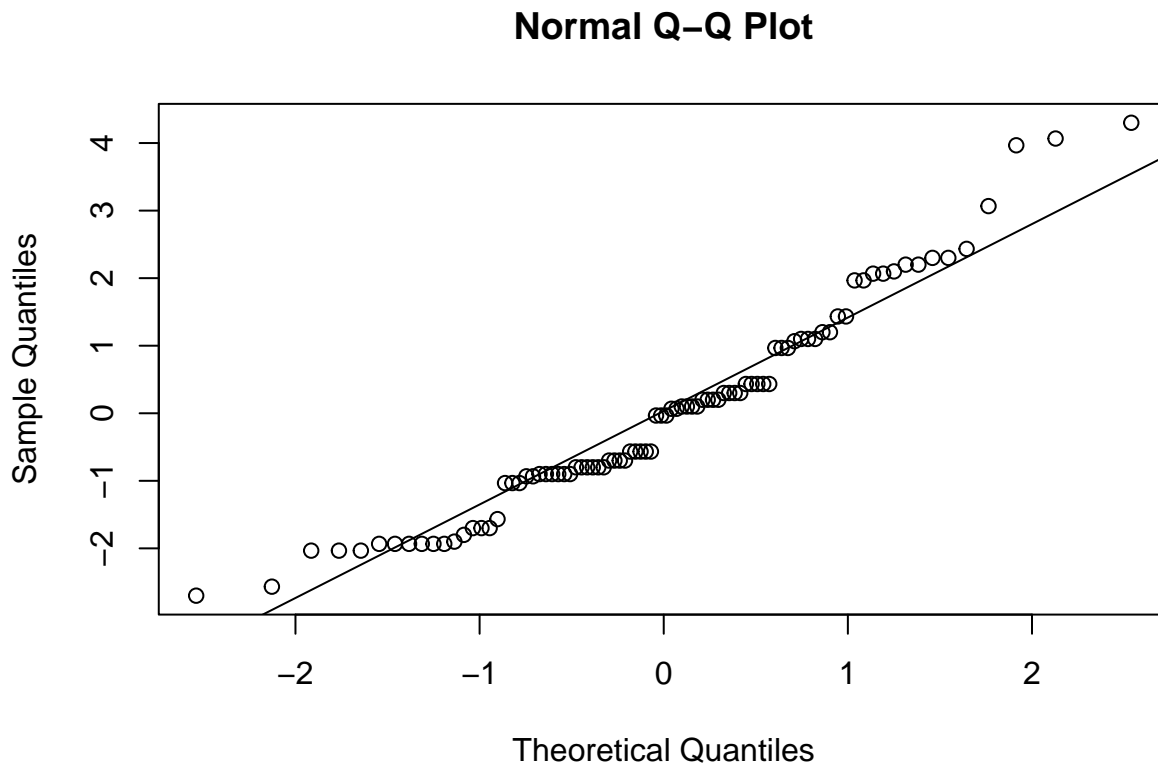
```
res.aov2 <- aov(Score ~ Treatment + Gender, data = df)
summary(res.aov2)
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## Treatment  2  13.09   6.544   2.719 0.0716 .
```

```
## Gender      1    0.40    0.400    0.166 0.6845
## Residuals   86 207.00    2.407
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The p-value > 0.05 , we do not have enough evidence to reject H_0 , meaning that there is no significant difference between treatment means.

```
residuals2 <- residuals(res.aov2)
qqnorm(residuals2)
qqline(residuals2)
```



It can be seen from the qq-plot that the residuals of the datapoints are approximately normal.

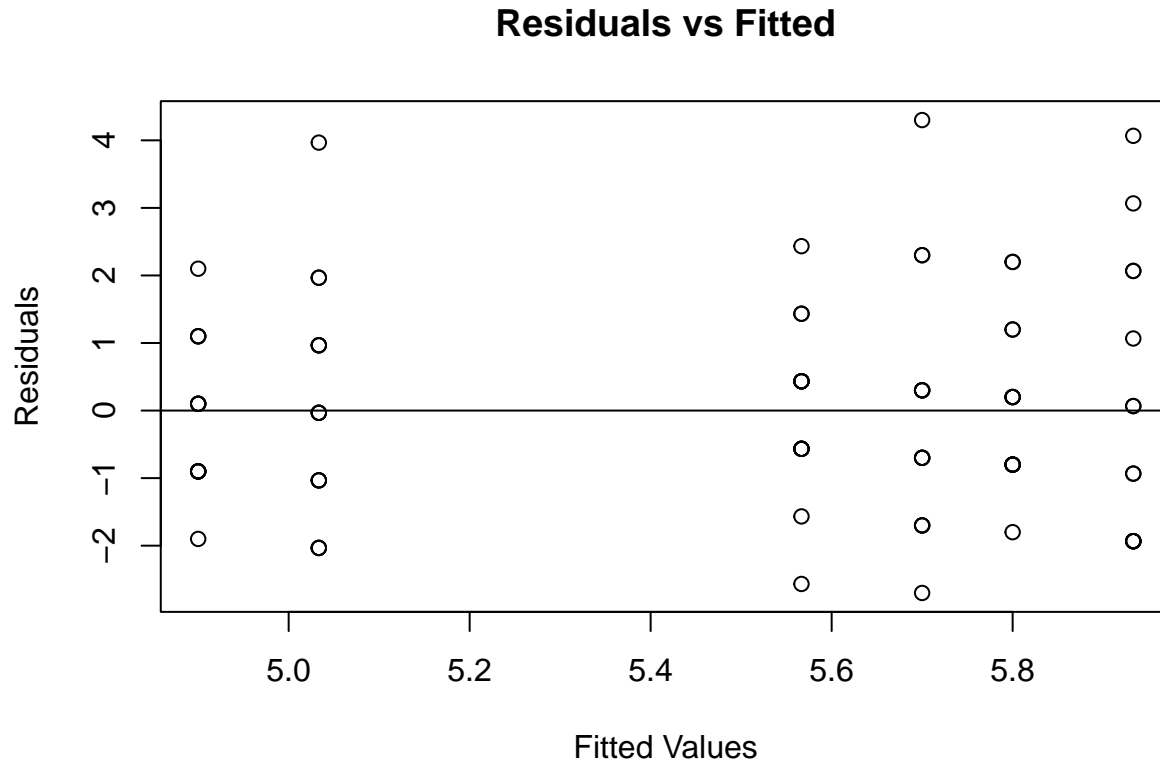
```
shapiro.test(residuals2)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  residuals2
## W = 0.95402, p-value = 0.002987
```

To check the normality of the residues, we can do the shapiro test. After doing the test it can be interpreted with the help of the p-value of the test statistic that there is enough evidence against the null hypothesis meaning that residuals are not normally distributed.

Now we will check for homoscedasticity.

```
fitted_values2 <- fitted(res.aov2)
plot(fitted_values2, residuals2,
     ylab="Residuals", xlab="Fitted Values", main="Residuals vs Fitted")
abline(h=0)
```

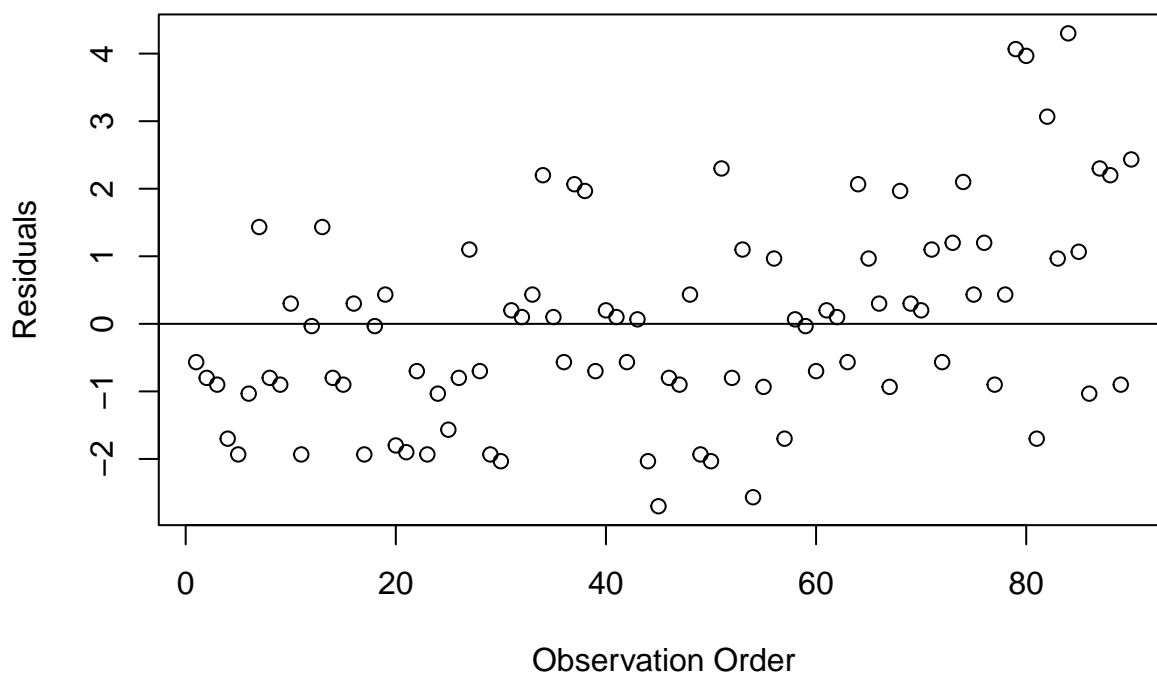


From the graph it can be interpreted that residuals are randomly scattered around the horizontal line with constant spread. No clear pattern is visible on the graph. therefore it can be said that the data has homoscedasticity.

Now we will check for autocorrelation

```
plot(1:length(fitted_values2), residuals2,
     ylab="Residuals", xlab="Observation Order", main="Residuals vs Order")
abline(h=0)
```

Residuals vs Order



It can be seen that residuals appear randomly scattered around zero, with no visible patterns or trends. No clustering, cycles, or trends over time are visible in the graph. Therefore it can be said that there is no autocorrelation present in the dataset.

```
TukeyHSD(res.aov2, "Treatment", conf.level=0.95)
```

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = Score ~ Treatment + Gender, data = df)
##
## $Treatment
##          diff          lwr          upr      p adj
## Audiovisual-Audio 0.6666667 -0.28870321 1.622037 0.2248525
## Visual-Audio      0.9000000 -0.05536988 1.855370 0.0691461
## Visual-Audiovisual 0.2333333 -0.72203654 1.188703 0.8298420
```

From the Tukey test, it can be interpreted that the difference between the three treatments is not significant as the p-values are all greater 0.05. To confirm our hypothesis, we can see that confidence interval also includes Zero in it which means that the difference among the treatment is not significant.