ANOVA - Three way

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Introduction to the Problem

A company that manufactures large industrial fans recently acquired a smaller competitor manufacturing fans with stronger blades. The companies used different manufacturing methods to attach the fan blades (spyders) to the fan hubs, which give the assembly its strength. In an attempt to determine the best manufacturing process, an experiment was designed to investigate the better levels of:

1. Two types of hole in the spyder

2. Two assembly methods, and

3. Two hub (or barrel) shapes.

The full factorial design resulted in eight treatments.

Destructive testing was used to break the spyder from the hub and the Torque required to break the part was measured in footpounds. The levels of the three factors are denoted by plus(+) or minus(-) one. Here, we analyse the data to determine the optimal levels of the 3 factors resulting in the strongest spyders.

NOTE : The strongest Spyders are the ones which require the highest Torque that needs to be applied to break it. Essentially, we are seeking a combination of the 3 factors (Hub, Assembly, Hole) that will provide us with an indication of the highest Torque values.

Possible Questions to Answer

1. Does the Fan's Torque differ between the two differnt types of Holes?
2. Does the Fan's Torque differ between the two Assembly methods?
3. Does the Fan's Torque differ between the two Hub shapes?
4. Is there any interaction between the above metioned variables?

Data Analysis

```
inp.data <- read.table("C:\\Users\\Lenovo\\Desktop\\spyder_strength.data", header = TRUE)
inp.data$Hole <- as.factor(inp.data$Hole)
inp.data$Assembly <- as.factor(inp.data$Assembly)
inp.data$Hub <- as.factor(inp.data$Hub)
```

```
##Convert factors to readable formats
levels(inp.data$Hole)[levels(inp.data$Hole)=="-1"] <- "Hole1"
levels(inp.data$Hole)[levels(inp.data$Hole)=="1"] <- "Hole2"
levels(inp.data$Assembly)[levels(inp.data$Assembly)=="-1"] <- "Assembly1"
levels(inp.data$Assembly)[levels(inp.data$Assembly)=="1"] <- "Assembly2"
levels(inp.data$Hub)[levels(inp.data$Hub)=="-1"] <- "Hub1"
levels(inp.data$Hub)[levels(inp.data$Hub)=="1"] <- "Hub2"

##Creating Treatment Column (For comparison purposes)

for(i in 1:64){
  if (inp.data$Hole[i] == "Hole1" & inp.data$Assembly[i] == "Assembly1" & inp.data$Hub[i]=="Hub1")  inp.data$treatment[i] <- "H1A1H1"
  if (inp.data$Hole[i] == "Hole1" & inp.data$Assembly[i] == "Assembly1" & inp.data$Hub[i]=="Hub2")  inp.data$treatment[i] <- "H1A1H2"
  if (inp.data$Hole[i] == "Hole1" & inp.data$Assembly[i] == "Assembly2" & inp.data$Hub[i]=="Hub1")  inp.data$treatment[i] <- "H1A2H1"
  if (inp.data$Hole[i] == "Hole1" & inp.data$Assembly[i] == "Assembly2" & inp.data$Hub[i]=="Hub2")  inp.data$treatment[i] <- "H1A2H2"
  if (inp.data$Hole[i] == "Hole2" & inp.data$Assembly[i] == "Assembly1" & inp.data$Hub[i]=="Hub1")  inp.data$treatment[i] <- "H2A1H1"
  if (inp.data$Hole[i] == "Hole2" & inp.data$Assembly[i] == "Assembly1" & inp.data$Hub[i]=="Hub2")  inp.data$treatment[i] <- "H2A1H2"
  if (inp.data$Hole[i] == "Hole2" & inp.data$Assembly[i] == "Assembly2" & inp.data$Hub[i]=="Hub1")  inp.data$treatment[i] <- "H2A2H1"
  if (inp.data$Hole[i] == "Hole2" & inp.data$Assembly[i] == "Assembly2" & inp.data$Hub[i]=="Hub2")  inp.data$treatment[i] <- "H2A2H2"
}

inp.data$treatment <- as.factor(inp.data$treatment)
```

First we plot the Torque values for each of the 8 Treatment groups and visually inspect if there are any differences in the Mean Torque Values across the different groups.

```
bymedian <- with(inp.data, reorder(inp.data$treatment, inp.data$Torque, median))
boxplot(Torque~bymedian, data = inp.data, main = "Torque values for different Treatment Group", xlab = "Treatment Group", ylab ="Torque", cex.axis = 0.75)
```

## Torque values for different Treatment Group
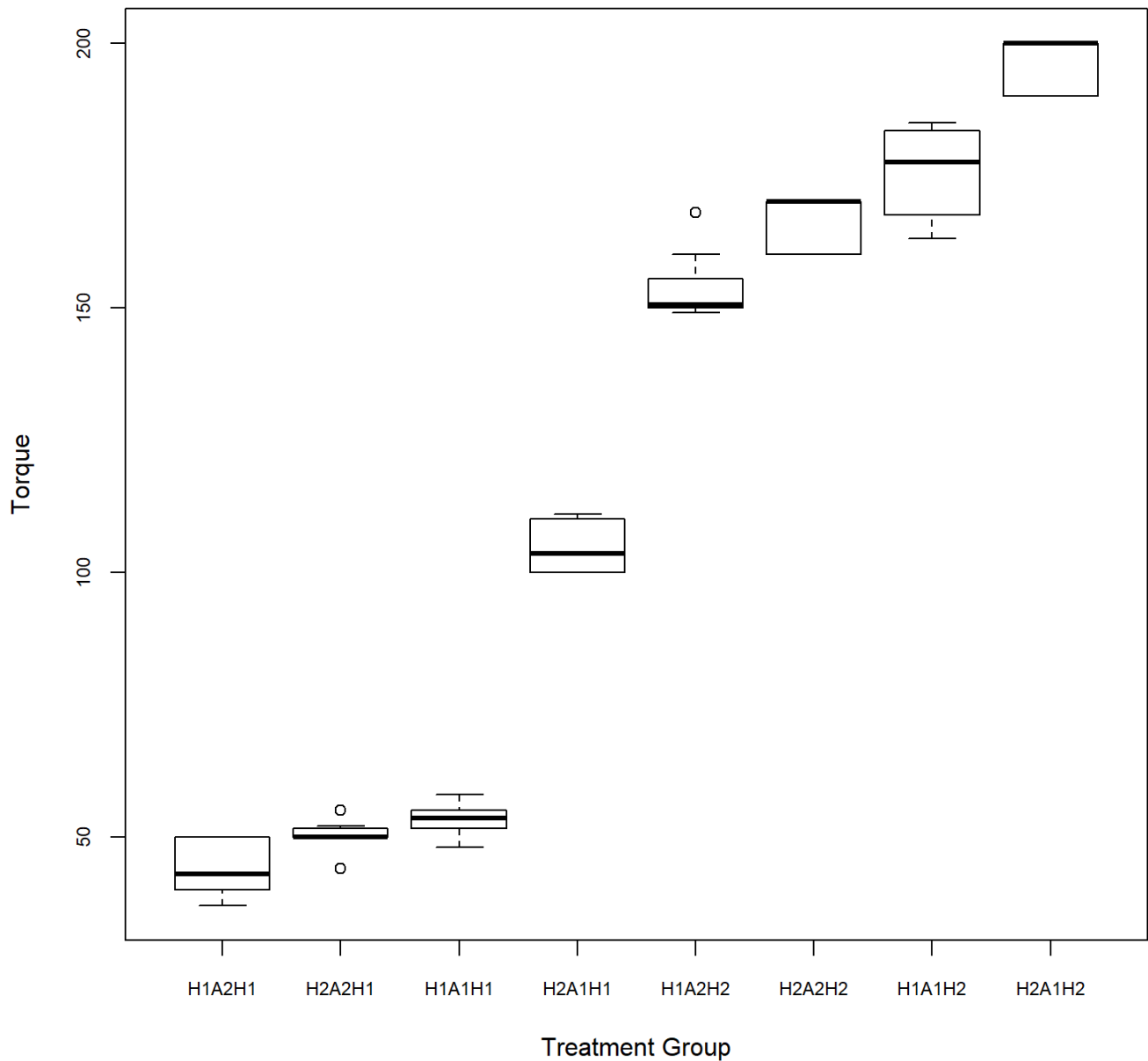
As can be seen from the boxplot above for Torque values for different Treatment groups, there seems to be a significant effect of various combinations of Hole, Assembly, and Hub factor levels on Torque.

We would next graphically explore how the mean Torque value changes given specific levels of each of the given Factors (Hub, Assembly, Hole) considered individually.

```
plot.design(Torque ~ Hole*Assembly*Hub,data=inp.data,xlab="Factors",main = "Main Effects Mode
l")
```

Main Effects Model
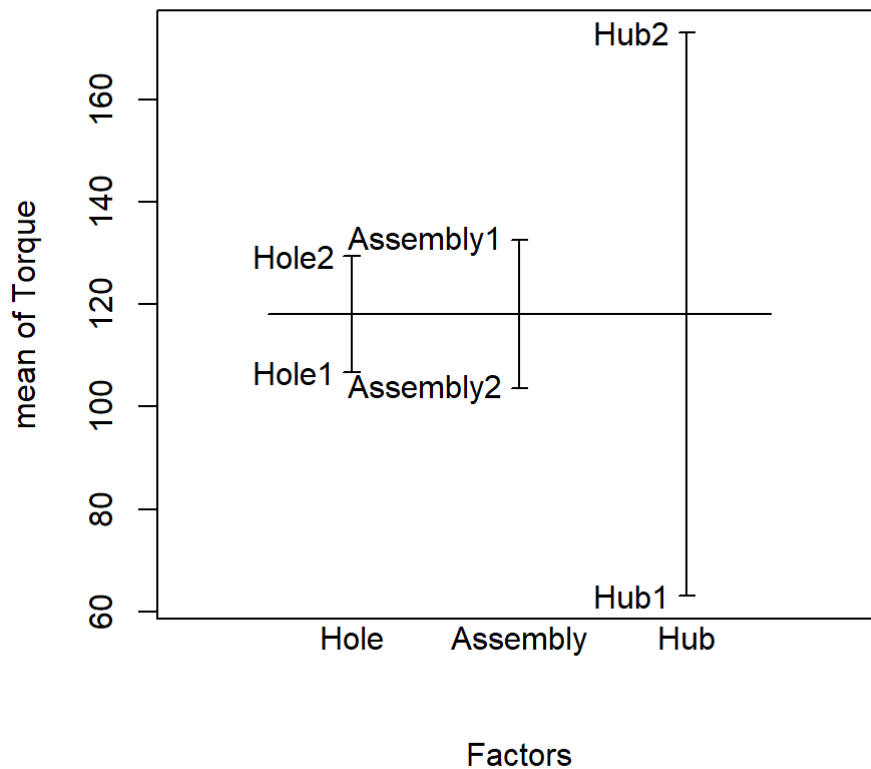
Factors

As can be seen from the plot, the mean value of Torque seems to change the most based on the level of Hub (Hub1 or Hub2) that is chosen.

We now proceed to see whether different combinations of levels of factors differently affect the Mean Torque value.

We can test for the statistical significance of "Treatment group affects Torque" by proceeding with a One-Way ANOVA Model for Treatment and Torque.

H_0 : There is no different in Mean values of Torque across the different Treatment Groups.

$\mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5 = \mu_6 = \mu_7 = \mu_8$

H_1: There is a significant difference in Mean values of Torque across different Treatment Groups.

$\mu_l \neq \mu_m$ for $l \neq m$. $l = 1..8$, $m = 1..8$

```
anovaModel1 <- anova(aov(Torque~treatment, data= inp.data))
anovaModel1
```

```
## Analysis of Variance Table
##
## Response: Torque
##            Df Sum Sq Mean Sq F value    Pr(>F)
## treatment   7 219653   31379  1013.3 < 2.2e-16 ***
## Residuals  56   1734      31
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The high F-value obtained above allows us to reject the Null Hypothesis that Mean values for Torques are equal across Treatment groups.

Now that we have confirmed that Mean values of Torque are different across different Treatment Groups, we can proceed with building an ANOVA model that helps us see the Main Effects and the Interaction Effects between Assembly Method, Hub Shape and Hole Type in the given data.

ANOVA Model

$SS_T = SS_{Treatments} + SS_E$

Assumptions for ANOVA Model

1. The dependent variable should be measured at the continuous level (i.e., it is an interval or ratio variable).

2. The three independent variables should each consist of two or more categorical, independent groups.

3. You should have independence of observations, which means that there is no relationship between the observations in each group or between the groups themselves.

4. There should be no significant outliers.

5. Your dependent variable should be approximately normally distributed for each combination of the groups of the three independent variables.

6. There needs to be homogeneity of variances for each combination of the groups of the three independent variables.

Assumptions 1, 2 and 3 are usually satisfied by the Design of the Experiment itself.

Assumption 4 can be tested as follows:

```
boxplot(inp.data$Torque, ylab = "Torque", main = "Boxplot of Torque values")
```
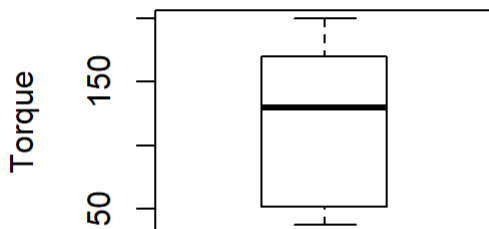

The boxplot indicates that there are No visible Outliers in the given data.

Normality Testing for each Treatment Group

```
## P-Values for Shapiro Wilk Test for Normality for different Treatment Groups
##   -----------------------------------------------------------------------
```

```
## Treatment Group  H1A1H1  :  0.9731535
## Treatment Group  H1A1H2  :  0.278501
## Treatment Group  H1A2H1  :  0.09648861
## Treatment Group  H1A2H2  :  0.001685335
## Treatment Group  H2A1H1  :  0.03940426
## Treatment Group  H2A1H2  :  0.0004790566
## Treatment Group  H2A2H1  :  0.09619312
## Treatment Group  H2A2H2  :  0.0004790566
```

Analysis of the obtained p-values shows that barring 3 samples, the rest of the samples hold up to Assumption 5.

Bartlett Test for Variance across Treatment Groups

H_0 : Variances are equal across Treatment Groups.

H_1 : Variances are not equal across Treatment Groups.

```
##Bartlett Test
bartlett.test(Torque ~ treatment, data=inp.data)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Torque by treatment
## Bartlett's K-squared = 11.553, df = 7, p-value = 0.1162
```

The p-value obtained above indicates that we cannot reject the Null Hypothesis that Variance is the same for all the Treatment Groups. Therefore Assumption 6 also holds.

Since we have completed checking the Assumptions we have made regarding the given data, we can proceed with ANOVA Model building.

ANOVA Model - Three Way Analysis of Variance

```
anovaModel3 <- anova(aov(Torque ~ Hole*Hub*Assembly , data = inp.data))
anovaModel3
```

```
## Analysis of Variance Table
##
## Response: Torque
##                  Df Sum Sq Mean Sq   F value    Pr(>F)
## Hole              1   8258    8258  266.6837 < 2.2e-16 ***
## Hub               1 193050  193050 6234.1653 < 2.2e-16 ***
## Assembly          1  13369   13369  431.7289 < 2.2e-16 ***
## Hole:Hub          1    594     594   19.1865 5.250e-05 ***
## Hole:Assembly     1   2849    2849   91.9991 2.026e-13 ***
## Hub:Assembly      1    135     135    4.3641   0.04126 *
## Hole:Hub:Assembly 1   1397    1397   45.1097 1.017e-08 ***
## Residuals        56   1734      31
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The F-values and the corresponding p-values for each of the above term indicates the following :

1. There are significant Main Effects of the 3 Factors (Hub, Assembly, Hole) on mean Torque values.

2. There are significant 2-way Interactions between any 2 of the given Factors.

3. There is a significant 3-way Interaction Effect in the Model between Hub, Assembly, and Hole.

The 3-way Interaction Effect can be visualized as follows:

3 Way Interaction
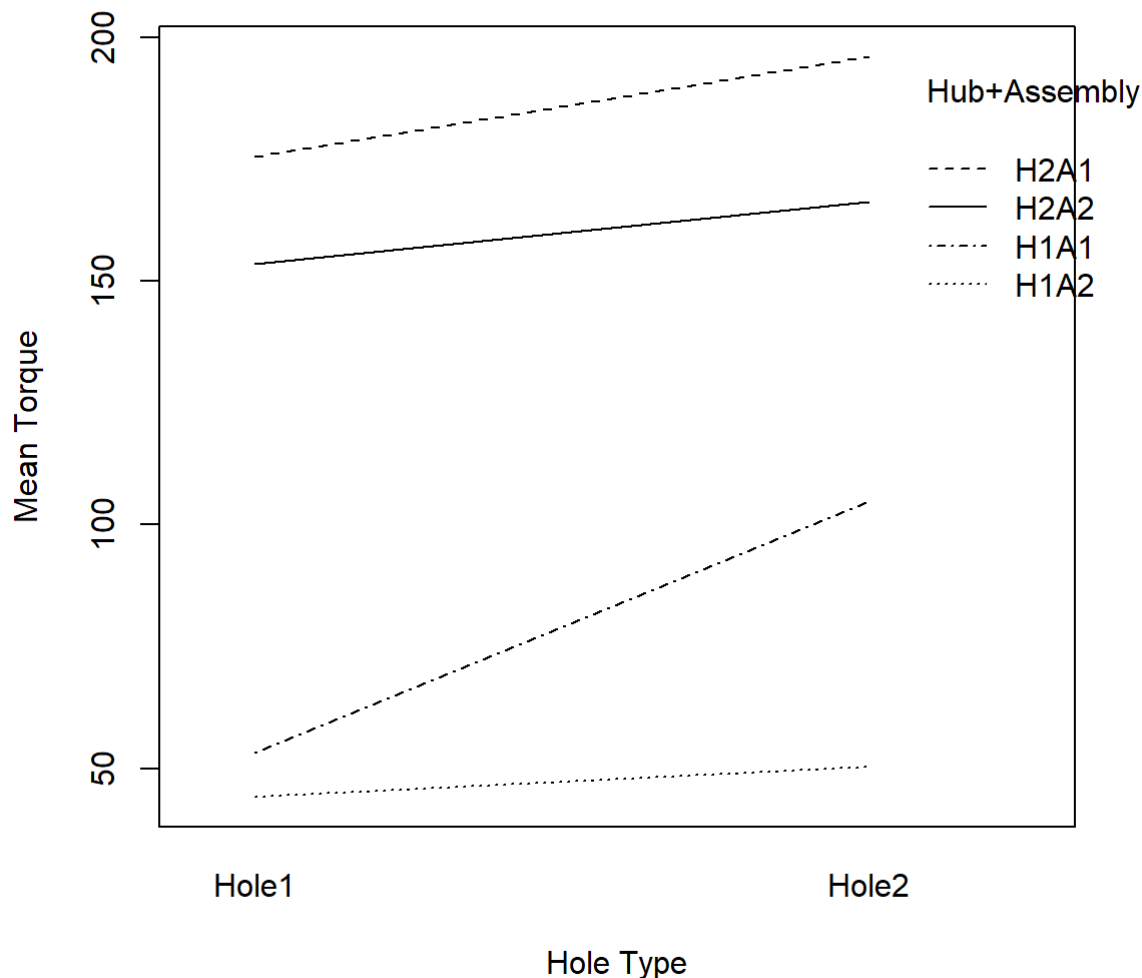
NOTE : The 3 way Interaction plot is built for Hole Type and Mean Torque values, after varying the levels for Hub shape and Assembly Method.

The statistical significance of the 3-way Interaction term and the plot above allows us to infer the following :

1. Choice of Hole Type affects the Mean Torque values differently based on the different combinations of Hub Shape and Assembly Method that is selected.

2. Choice of Hub Shape affects the Mean Torque values differently based on the different combinations of Assembly Method and Hole Type that is selected.

3. Choice of Assembly Method affects the Mean Torque values differently based on the different combinations of Hole Type and Hub Shape that is selected.

Another way of interpreting the 3 way Interaction in the above plot would be - The effect of interaction between Assembly Method and Hub shape, depends on the level of Hole Type.

For example, from the above plot, choice of Hole 2 produces a greater Mean Torque compared to Hole 1 when Hub 1 and Assembly 1 have been selected. Changing either Hub/Assembly levels changes the way Hole Type affects Torque values(Changing Hole Type from 1 to 2 doesn't seem to produce any significant difference in Mean Torque values when Hub 1 and Assembly 2 are selected).

Basically, a three-way interaction means that one, or more, two-way interactions differ across the levels of a third variable.

We can recursively observe the 3-way Interactions by keeping Hole Type fixed at Hole 1 and Hole 2 and checking the Interactions between Hub Shape and Assembly Method. Then we can fix Hub Shape at 1 or 2 and observe how Assembly Method affects Mean Torque Values.

```
df1 <- subset(inp.data, inp.data$Hole=="Hole1", select = -Hole)
interaction.plot(df1$Hub,df1$Assembly,df1$Torque,main="2 Way Interaction for Hole 1", xlab =
"Hub Type", ylab = "Mean Torque", legend =TRUE, trace.label = "Assembly Method")
```

2 Way Interaction for Hole 1
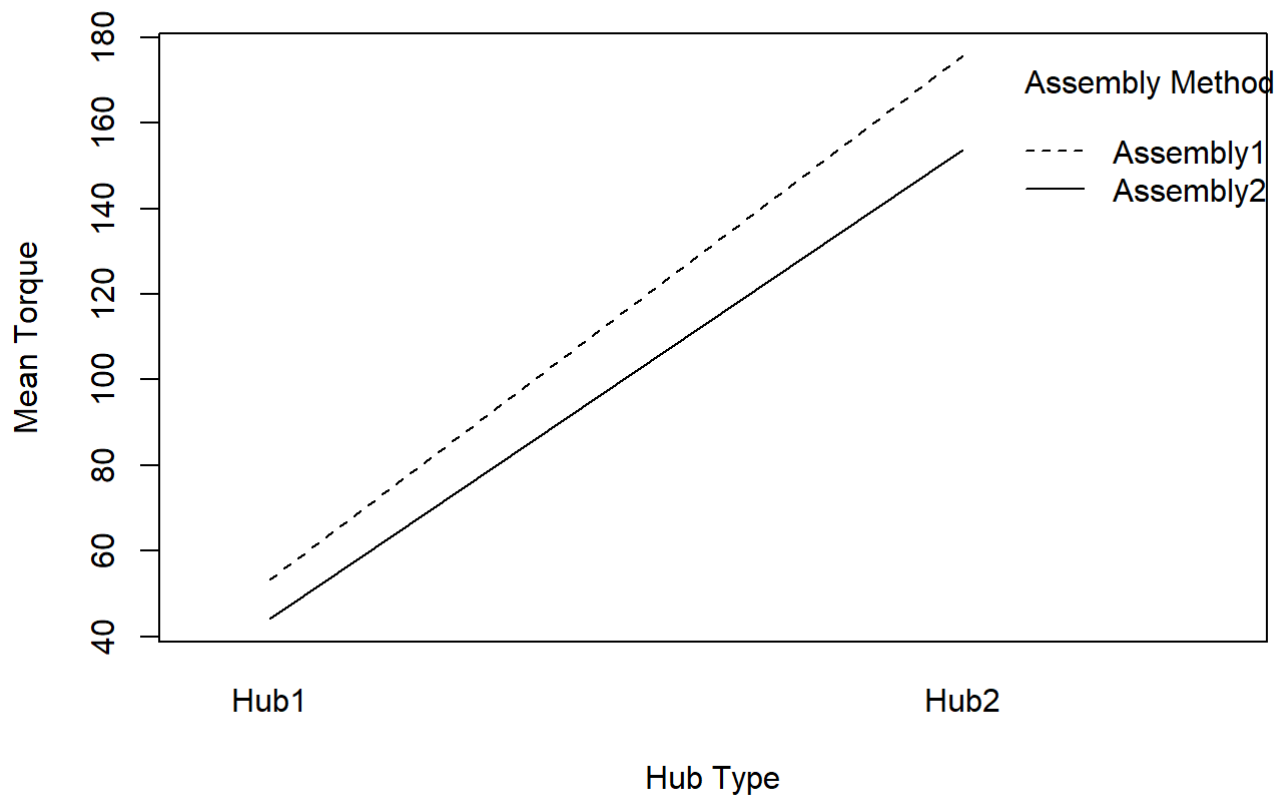

```
df2 <- subset(inp.data, inp.data$Hole=="Hole2", select = -Hole)
interaction.plot(df2$Hub,df2$Assembly,df2$Torque,main="2 Way Interaction for Hole 2", xlab =
"Hub Type", ylab = "Mean Torque", legend =TRUE, trace.label = "Assembly Method")
```
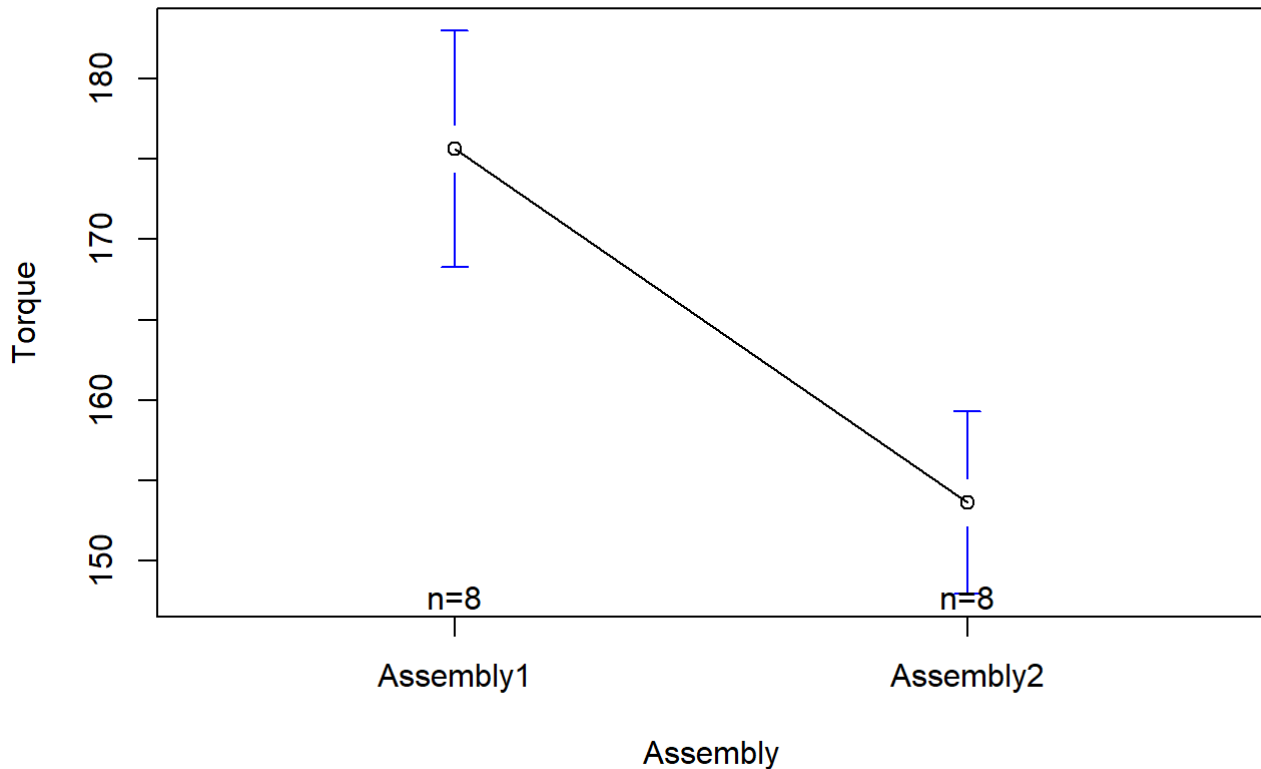
2 Way Interaction for Hole 2
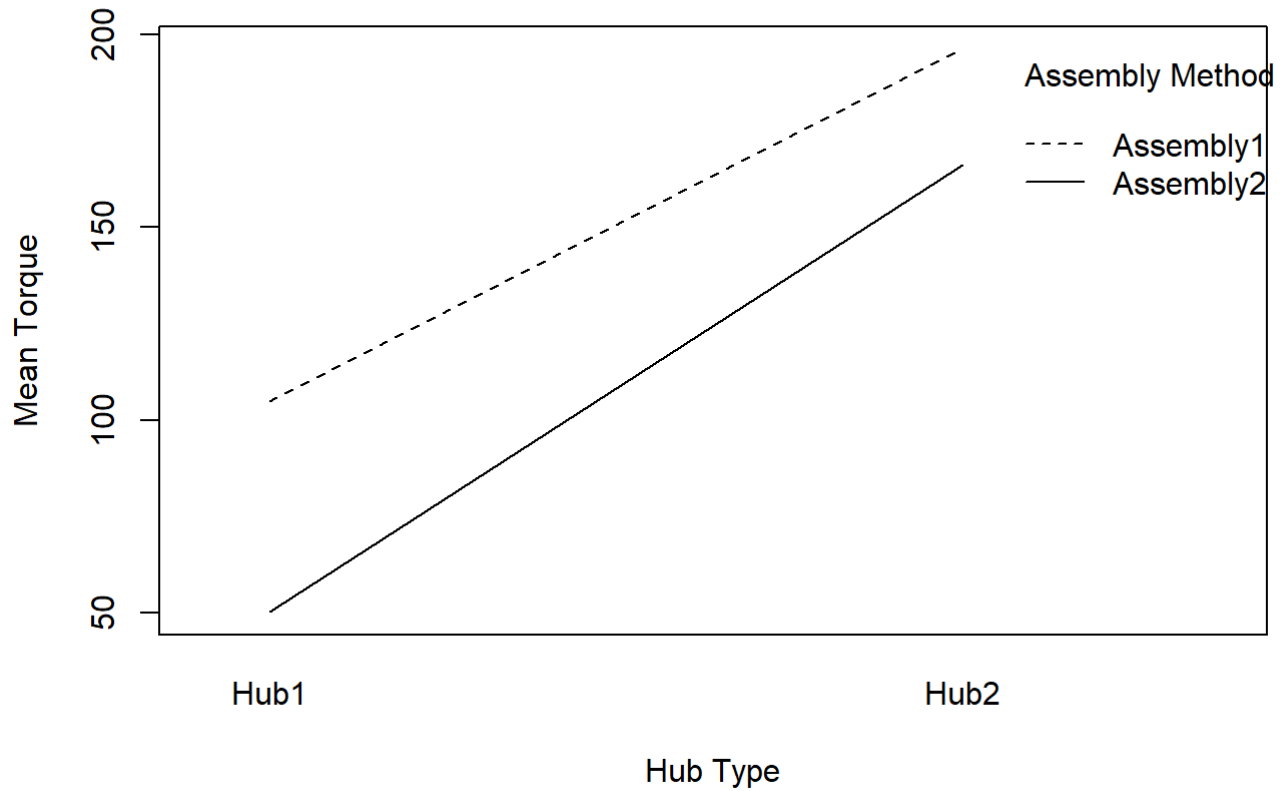

```
df3 <- subset(df1, df1$Hub=="Hub1", select = -Hub)
plotmeans(Torque~ Assembly,xlab="Assembly",ylab="Torque",main="For Hole 1 and Hub 1",data = d
f3)
```

For Hole 1 and Hub 1
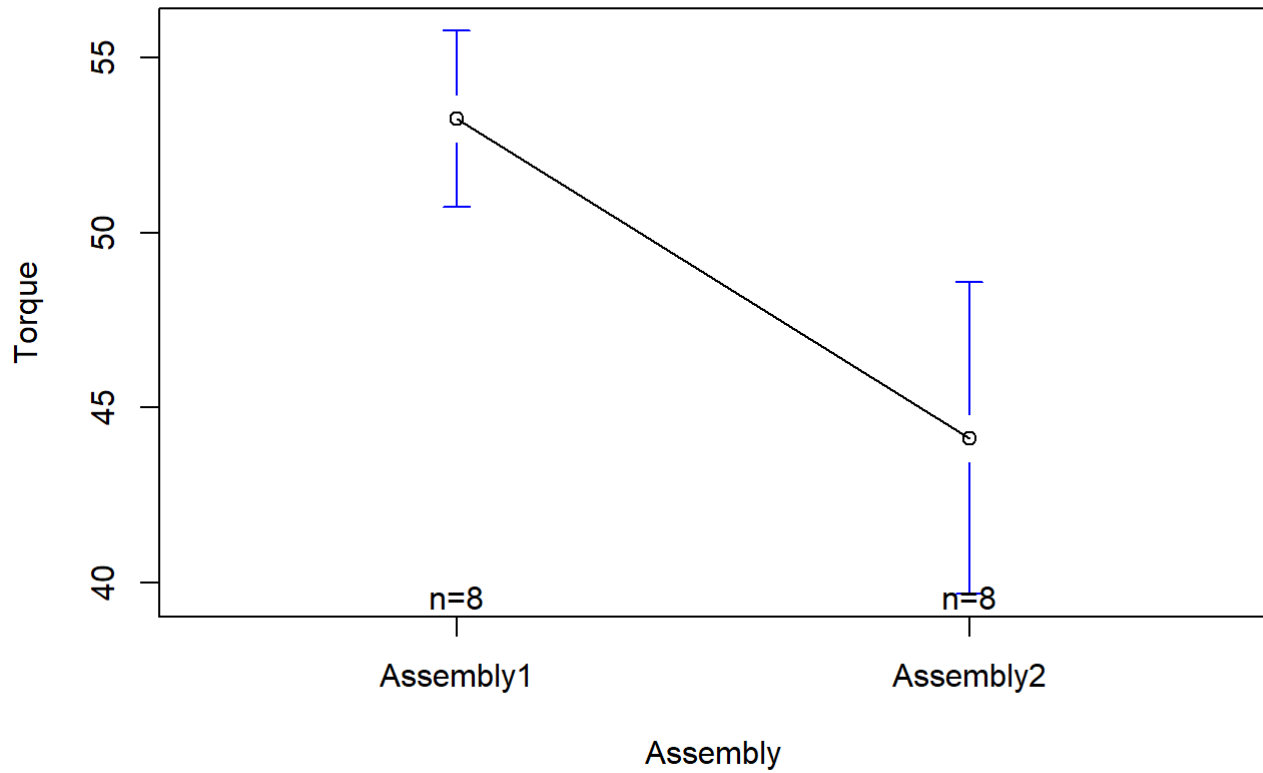

```
df4 <- subset(df1, df1$Hub=="Hub2", select = -Hub)
plotmeans(Torque~ Assembly,xlab="Assembly",ylab="Torque",main="For Hole 1 and Hub 2",data = d
f4)
```

For Hole 1 and Hub 2

Above, we have plotted Interactions for :

1. Keeping Hole Type fixed at 1 and checking Interactions for Hub and Assembly.

2. Keeping Hole Type fixed at 2 and checking Interactions for Hub and Assembly.

The Interaction between Hub and Assembly seems to change for the two levels of Hole Type.

Next we plotted :

1. Hole Type = 1 and Hub Shape = 1 (fixed) to give Effect of Assembly on Mean Torque.

2. Hole Type = 1 and Hub Shape = 2 (fixed) to give Effect of Assembly on Mean Torque.

We can observe how fixing the levels of Hole and Hub factors impacts the choice of Assembly Method on Mean Torques.

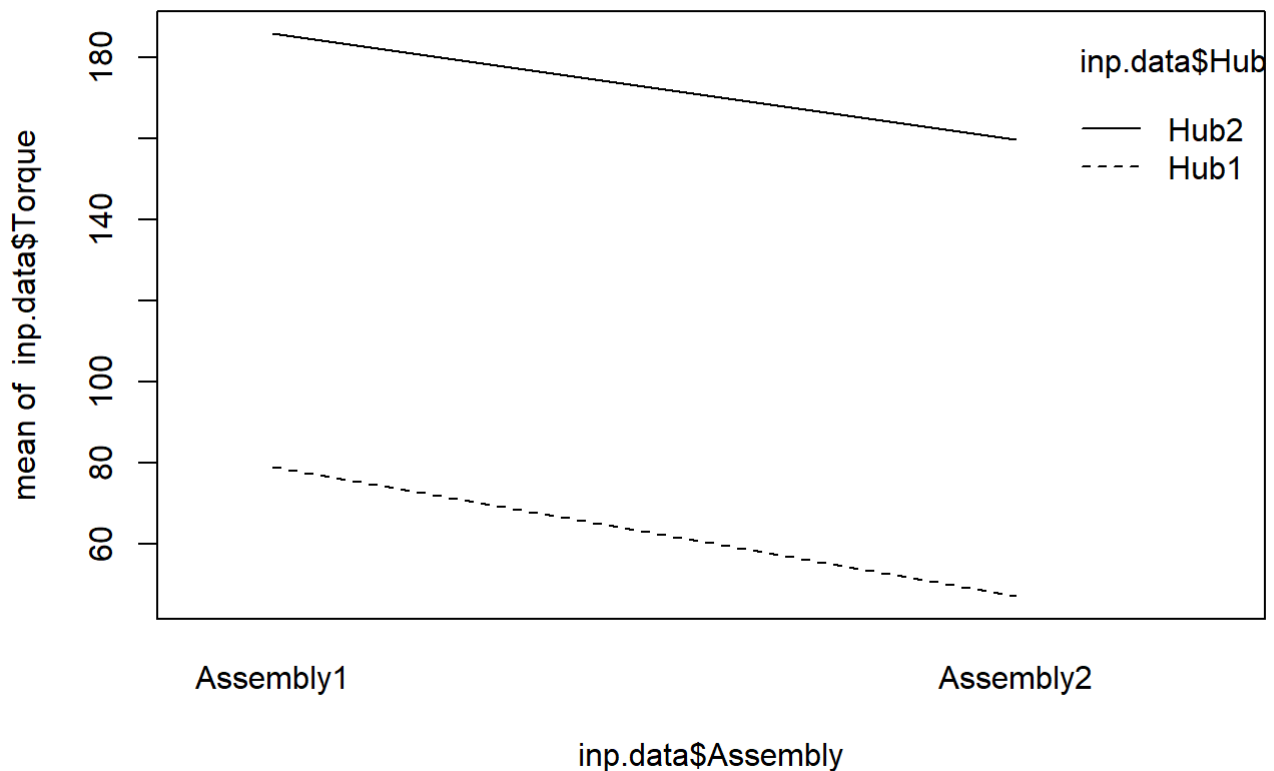The 2-way Interaction Effects can be visualized as follows:

```
interaction.plot(inp.data$Hole,inp.data$Assembly,inp.data$Torque,main="2 Way Interaction - Ho
le vs Assembly")
```
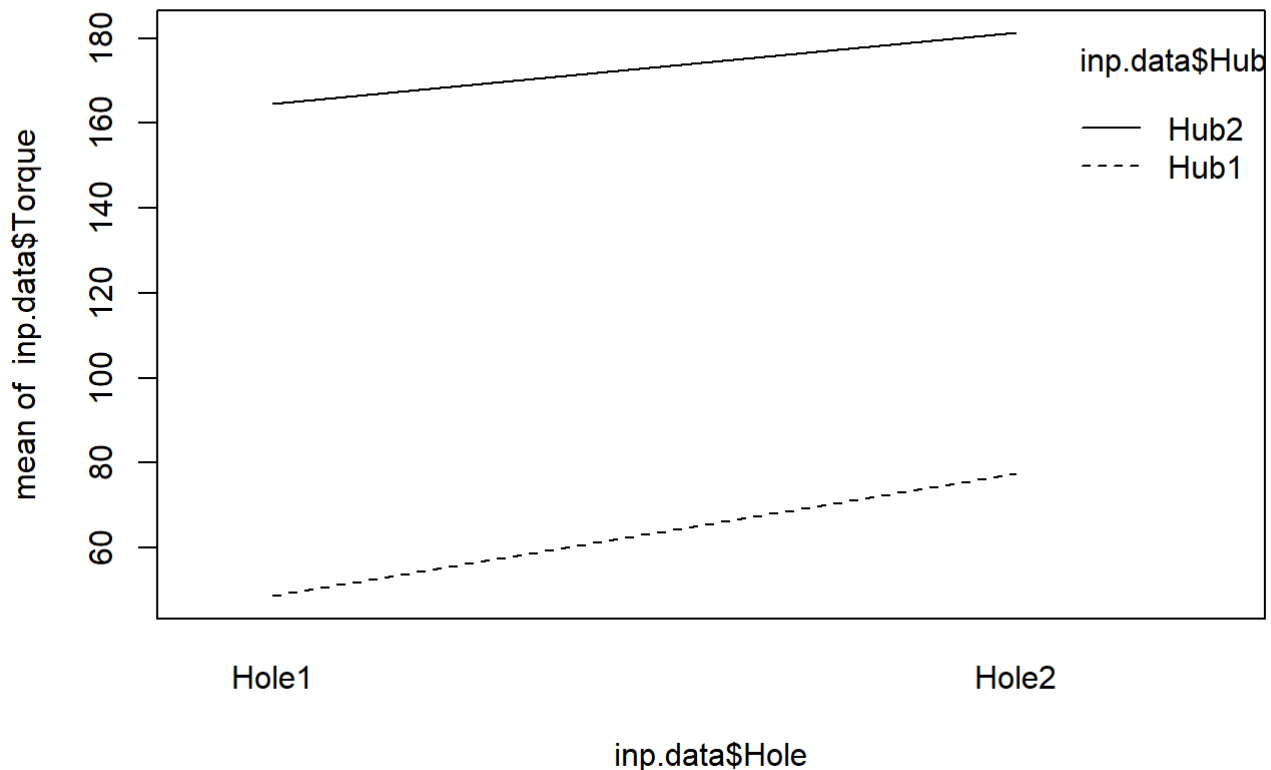
2 Way Interaction - Hole vs Assembly
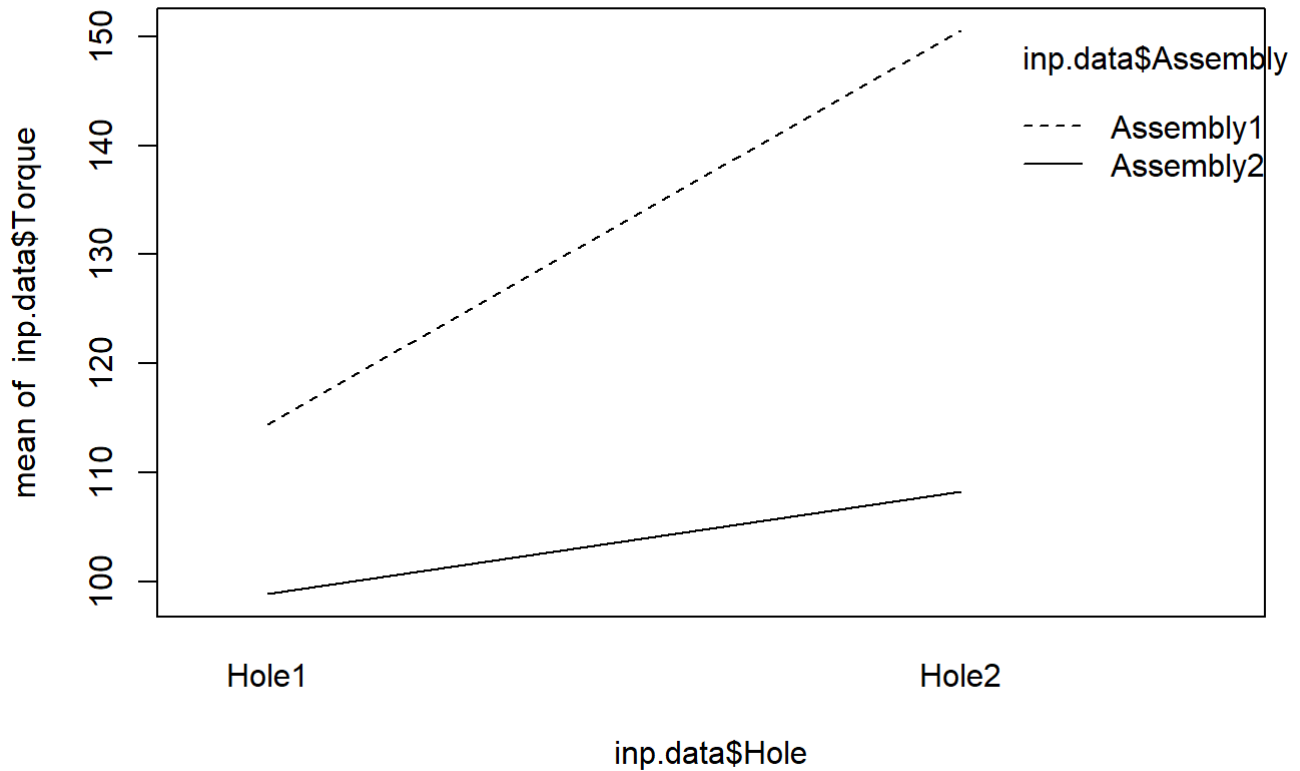

```
interaction.plot(inp.data$Assembly,inp.data$Hub,inp.data$Torque,main="2 Way Interaction - Ass
embly vs Hub")
```

2 Way Interaction - Assembly vs Hub

```
interaction.plot(inp.data$Hole,inp.data$Hub,inp.data$Torque,main="2 Way Interaction - Hole vs
Hub")
```

2 Way Interaction - Hole vs Hub

Each of the above plots indicates that there are 2-way Interactions between each of the Factors. While the plots don't show "explicit" Interactions (indicated by intersection of lines), the non-parallel nature of the plot indicates Ordinal Interactions. We can infer the following from the ANOVA table and the above plots (keeping in mind the 3-way Interaction):

1. The relationship between Hole Type and Torque values depends on the value of Assembly Method. Similarly, the relationship between Assembly Method and Torque values depends on the value of Hole type.

2. The relationship between Assembly Method and Torque values depends on the value of Hub shape. Similarly, the relationship between Hub shape and Torque values depends on the value of Assembly Method.

3. The relationship between Hole Type and Torque values depends on the value of Hub shape. Similarly, the relationship between Hub Shape and Torque values depends on the value of Hole Type.

NOTE : All of the above inferences can be made keeping in mind the significance of the F-values obtained for 3-way and 2-way Interactions in the ANOVA table.

The Main Effects (keeping in mind the 2-way and 3-way Interaction Effects) can be visualized as follows:

```
plotmeans(Torque~ Hole,xlab="Hole",ylab="Torque",main="Mean Torque for Hole Levels",data = in
p.data)
```
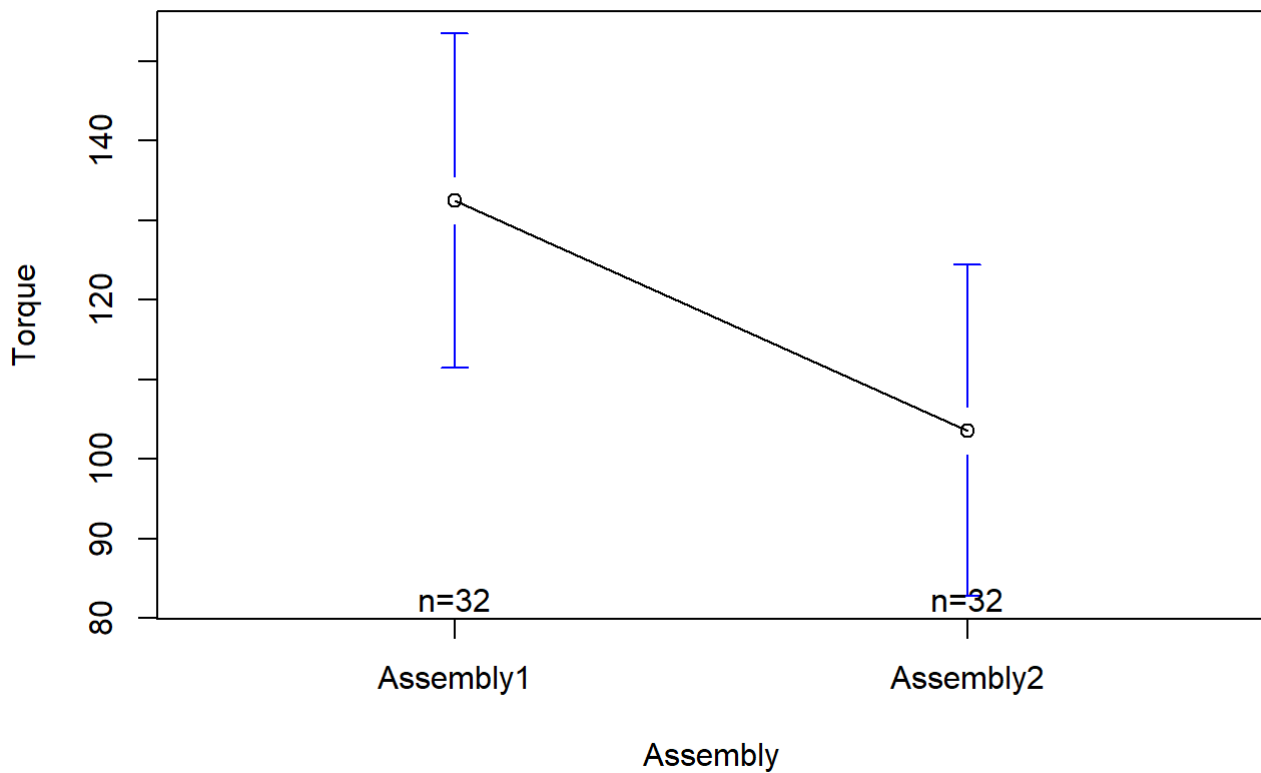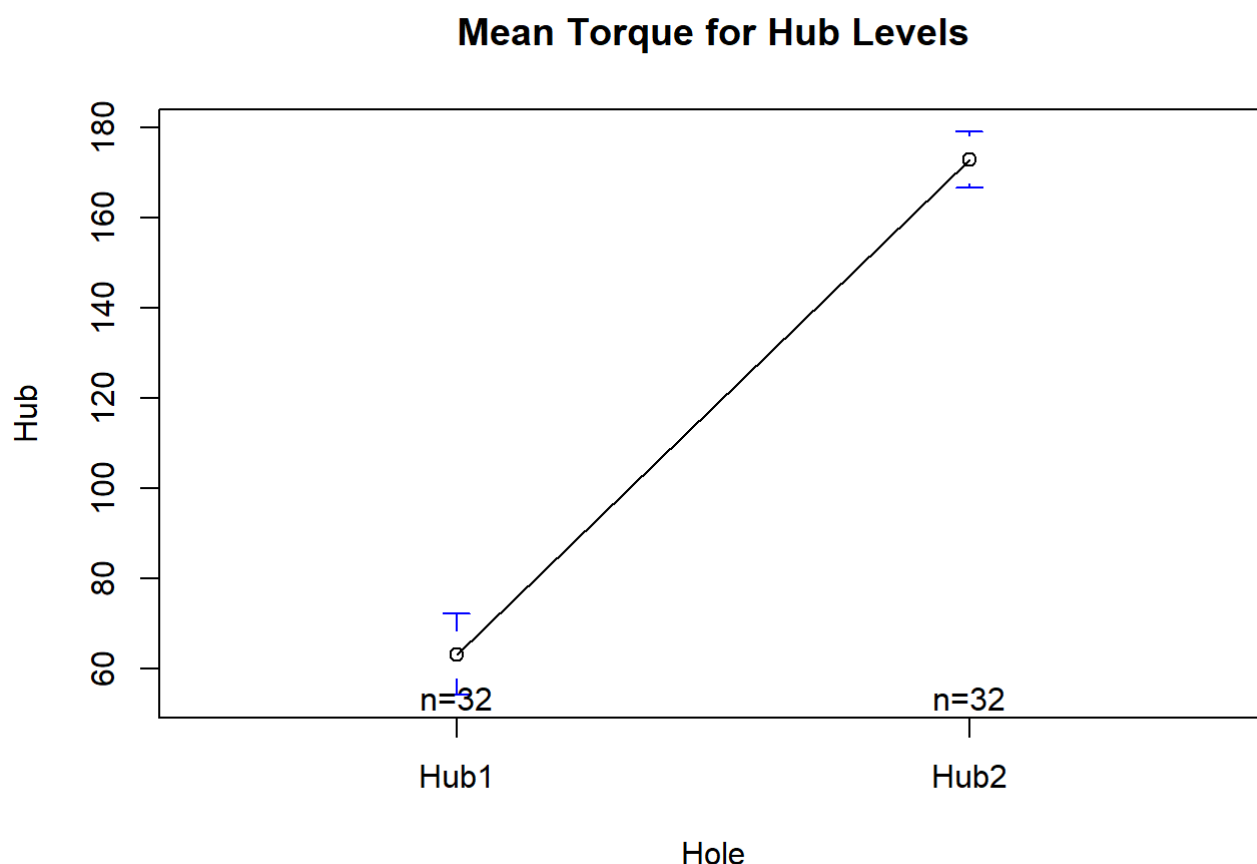
Mean Torque for Hole Levels
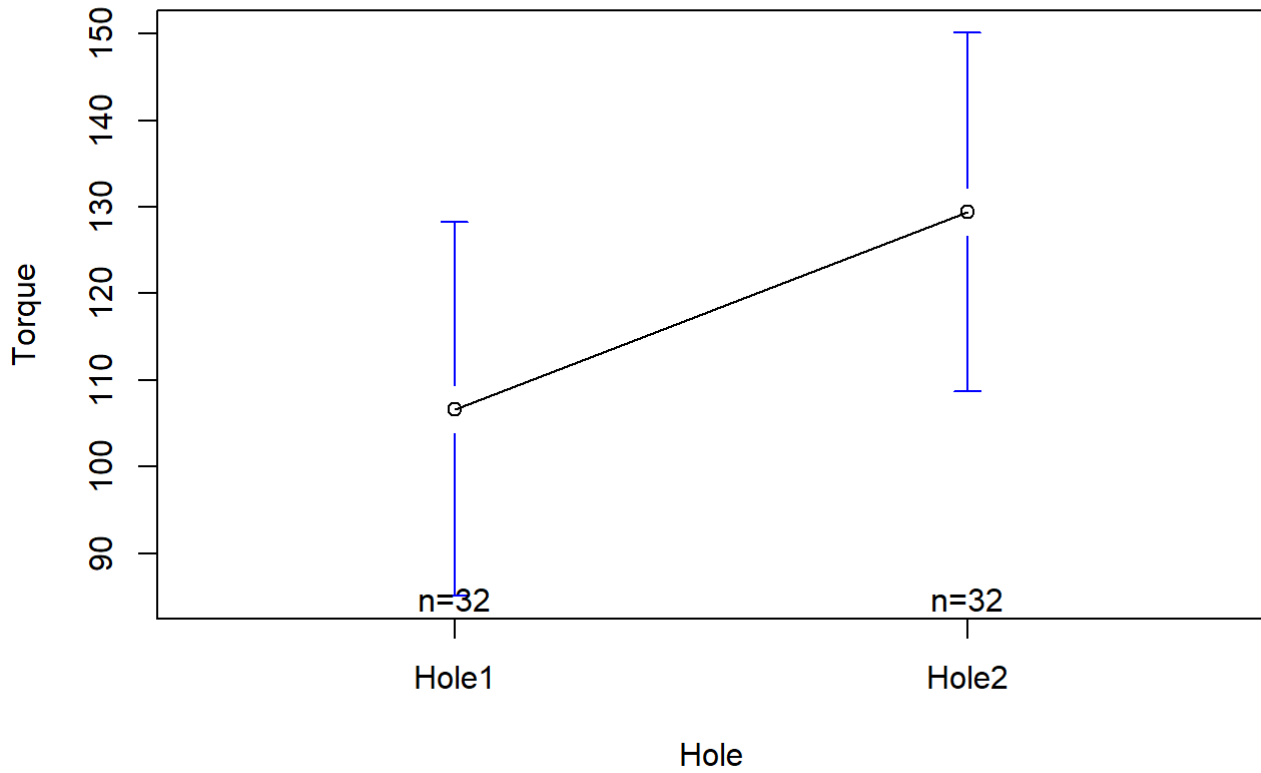

```
plotmeans(Torque~ Assembly,xlab="Assembly",ylab="Torque",main="Mean Torque for Assembly Level
s",data = inp.data)
```

Mean Torque for Assembly Levels

```
plotmeans(Torque~ Hub,xlab="Hole",ylab="Hub",main="Mean Torque for Hub Levels",data = inp.dat
a )
```

Mean Torque for Hub Levels

A visual inspection indicates the following:

1. Mean Torque for Hole 2 is greater than Mean Torque for Hole 1.

2. Mean Torque for Assembly 1 is greater than Mean Torque for Assembly 2.

3. Mean Torque for Hub 2 is greater than Mean Torque for Hub 1.

We can infer statistical significance of the differences in Mean Torque values for each of the above case only after performing a Tukey Honest Significant Difference (HSD) Test.

A Table containing the Mean Torque Values for each Combination of the given factors as well as the Grand Mean is as shown below :

```
fm <- aov(Torque ~ Hole*Hub*Assembly , data = inp.data)
model.tables(fm, data = inp.data, type = "means")
```
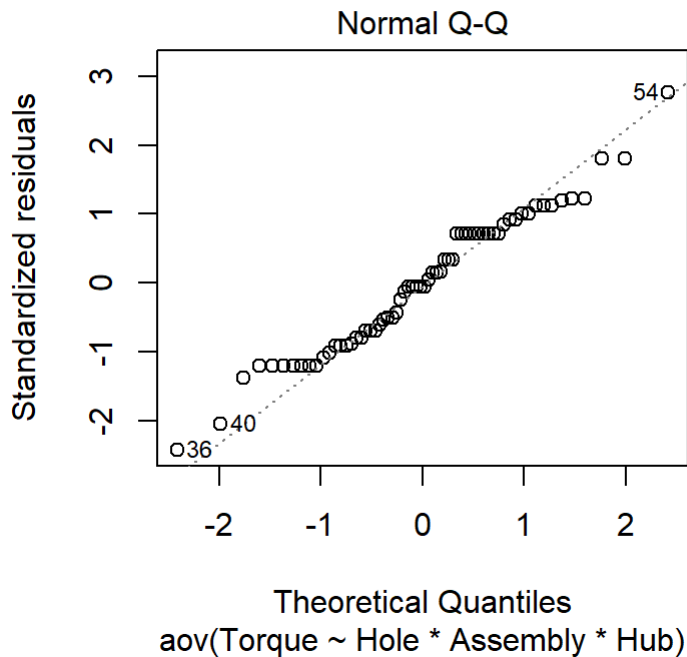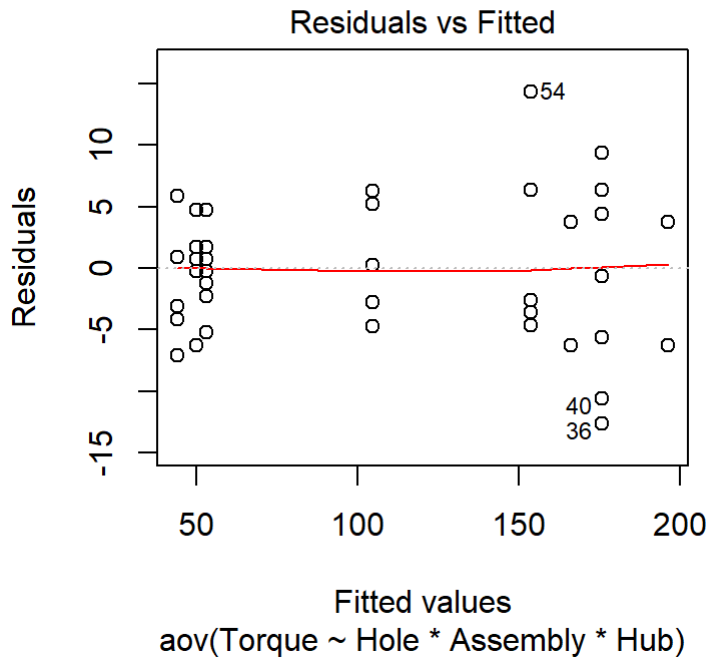
```
## Tables of means
## Grand mean
##
## 118.0156
##
##  Hole
## Hole
##  Hole1  Hole2
## 106.66 129.38
##
##  Hub
## Hub
##    Hub1    Hub2
##  63.09 172.94
##
##  Assembly
## Assembly
## Assembly1 Assembly2
##    132.47    103.56
##
##  Hole:Hub
##        Hub
## Hole    Hub1    Hub2
##    Hole1  48.69 164.62
##    Hole2  77.50 181.25
##
##  Hole:Assembly
##        Assembly
## Hole    Assembly1 Assembly2
##    Hole1 114.44      98.88
##    Hole2 150.50     108.25
##
##  Hub:Assembly
##        Assembly
## Hub      Assembly1 Assembly2
##    Hub1  79.00      47.19
##    Hub2 185.94     159.94
##
##  Hole:Hub:Assembly
## , , Assembly = Assembly1
##
##          Hub
## Hole    Hub1    Hub2
##    Hole1  53.25 175.62
##    Hole2 104.75 196.25
##
## , , Assembly = Assembly2
##
##          Hub
## Hole    Hub1    Hub2
##    Hole1  44.12 153.62
##    Hole2  50.25 166.25
```

Before we proceed with Tukey HSD Test, we need to test if the ANOVA Model we have fitted is adequate i.e. it holds up to Residual Analysis.

Residual Analysis

```
model <- aov(Torque~Hole*Assembly*Hub ,data =inp.data )
res<-resid(model)
plot(model,which=c(1,2))
```


Residuals vs Fitted
Fitted values
aov(Torque ~ Hole * Assembly * Hub)

Normal Q-Q
Theoretical Quantiles
aov(Torque ~ Hole * Assembly * Hub)

From the above NQQ plot, it would appear the the Residuals are Normal. We can test this formally as follows:

H_0 : The given data follows a Normal Distribution.

H_1 : The given data doesn't follow a Normal Distribution.

```
normtest(res)
```

```
## Warning: package 'nortest' was built under R version 3.4.1
```

```
##                                          Method     P.Value
## 1                   Shapiro-Wilk normality test 0.172357678
## 2                 Anderson-Darling normality test 0.043735579
## 3                 Cramer-von Mises normality test 0.051058803
## 4 Lilliefors (Kolmogorov-Smirnov) normality test 0.004193211
## 5                 Shapiro-Francia normality test 0.121477563
```
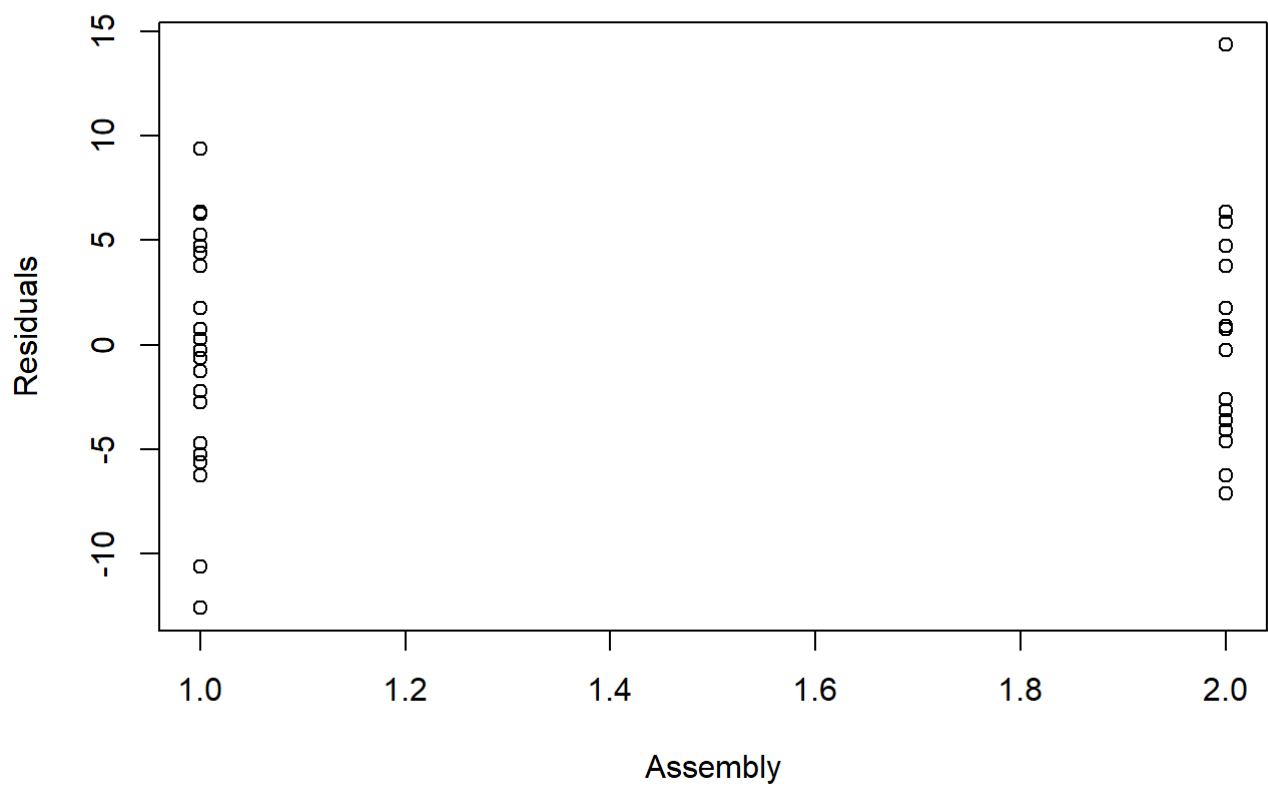
The p-value indicates the Residuals obtained follow a Normal Distribution.
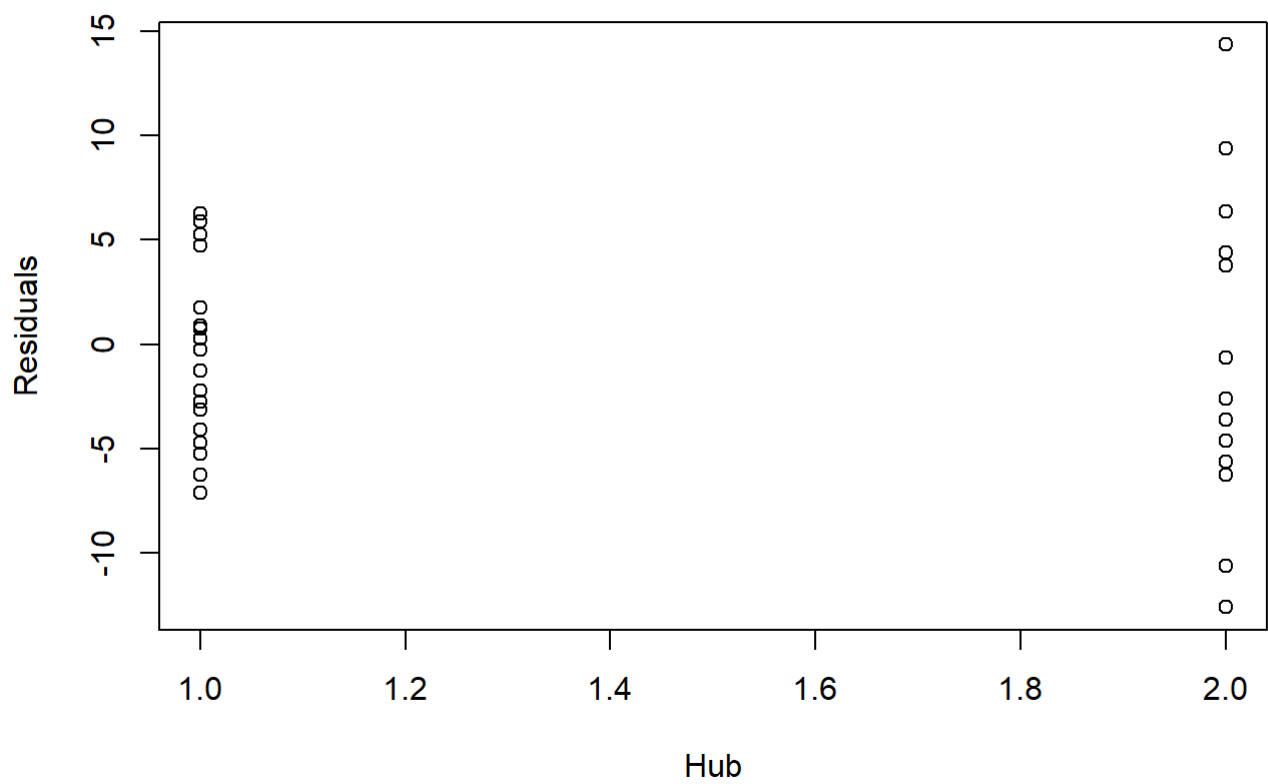
Plotting the Residuals against various Factors :

```
plot(as.numeric(inp.data$Hole),res,xlab="Hole",ylab="Residuals")
```
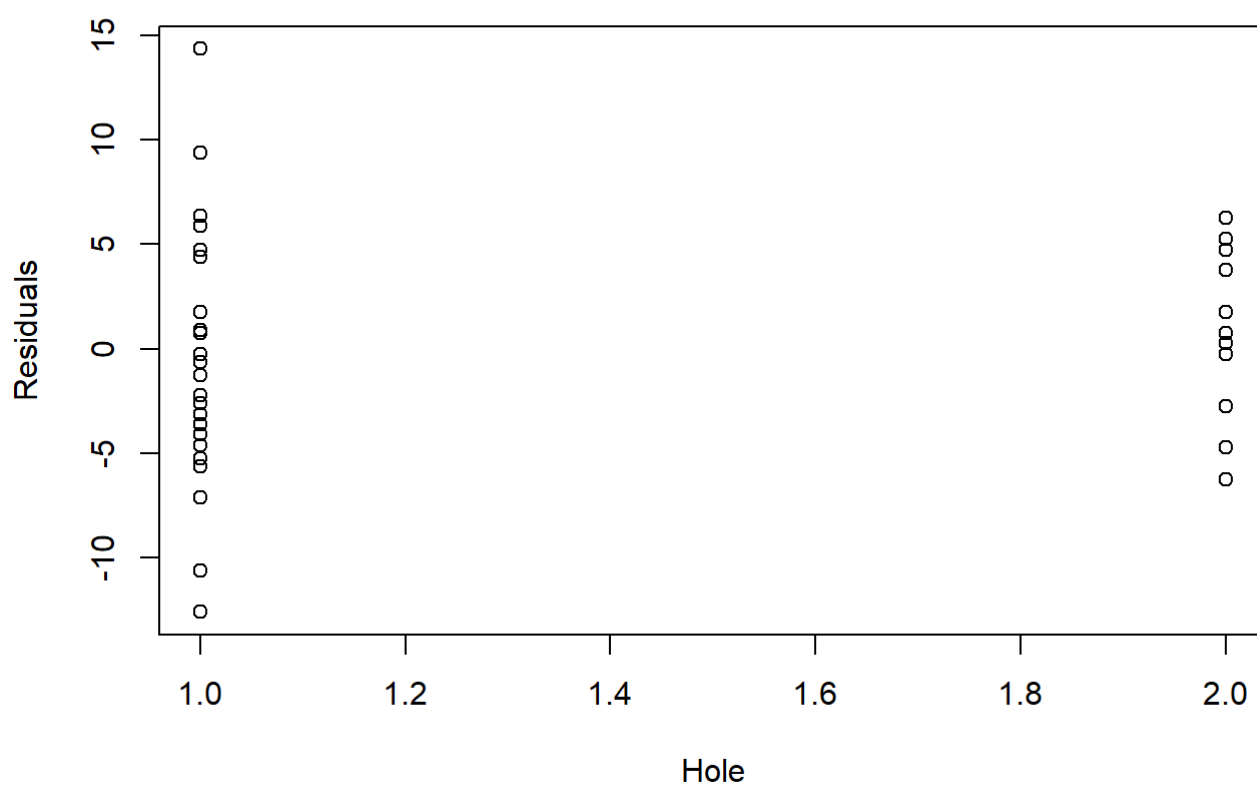


```
plot(as.numeric(inp.data$Assembly),res,xlab="Assembly",ylab="Residuals")
```

```
plot(as.numeric(inp.data$Hub),res,xlab="Hub",ylab="Residuals")
```

While variance seems to be equal across the different groups, we can formally Test it as follows:

H_0 : The variance is equal across the groups.

H_1 : The variance is unequal across the groups.

Bartlett's Test

```
bartlett.test(res~inp.data$Hole)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  res by inp.data$Hole
## Bartlett's K-squared = 2.8068, df = 1, p-value = 0.09386
```

```
bartlett.test(res~inp.data$Assembly)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  res by inp.data$Assembly
## Bartlett's K-squared = 0.3554, df = 1, p-value = 0.5511
```

```
bartlett.test(res~inp.data$Hub)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  res by inp.data$Hub
## Bartlett's K-squared = 6.121, df = 1, p-value = 0.01336
```

Based on the p-values obtained for the 3 factors above, we can conclude that variance in Residuals across each of the different factor groups is equal.

Also, the Residuals plotted against Subjects gives no visible pattern so we can conclude that the ANOVA Model we have fitted is adequate.

Finally, we can check for statistical significance of differences in Mean Torque Values across different Treatment Groups using a Tukey HSD Test.

Significance of difference in Mean Torque values across Treatment groups

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Torque ~ Hole * Assembly * Hub, data = inp.data)
##
## $Hole
##           diff      lwr      upr p adj
## H2-H1 22.71875 19.93186 25.50564     0
##
## $Assembly
##            diff       lwr       upr p adj
## A2-A1 -28.90625 -31.69314 -26.11936     0
##
## $Hub
##             diff      lwr      upr p adj
## Hu2-Hu1 109.8437 107.0569 112.6306     0
##
## $`Hole:Assembly`
##                 diff        lwr        upr     p adj
## H2:A1-H1:A1  36.0625  30.852944  41.2720558 0.0000000
## H1:A2-H1:A1 -15.5625 -20.772056 -10.3529442 0.0000000
## H2:A2-H1:A1  -6.1875 -11.397056  -0.9779442 0.0137571
## H1:A2-H2:A1 -51.6250 -56.834556 -46.4154442 0.0000000
## H2:A2-H2:A1 -42.2500 -47.459556 -37.0404442 0.0000000
## H2:A2-H1:A2   9.3750   4.165444  14.5845558 0.0000799
##
## $`Hole:Hub`
##                   diff       lwr       upr p adj
## H2:Hu1-H1:Hu1  28.8125  23.60294  34.02206     0
## H1:Hu2-H1:Hu1 115.9375 110.72794 121.14706     0
## H2:Hu2-H1:Hu1 132.5625 127.35294 137.77206     0
## H1:Hu2-H2:Hu1  87.1250  81.91544  92.33456     0
## H2:Hu2-H2:Hu1 103.7500  98.54044 108.95956     0
## H2:Hu2-H1:Hu2  16.6250  11.41544  21.83456     0
##
## $`Assembly:Hub`
##                   diff       lwr       upr p adj
## A2:Hu1-A1:Hu1 -31.8125 -37.02206 -26.60294     0
## A1:Hu2-A1:Hu1 106.9375 101.72794 112.14706     0
## A2:Hu2-A1:Hu1  80.9375  75.72794  86.14706     0
## A1:Hu2-A2:Hu1 138.7500 133.54044 143.95956     0
## A2:Hu2-A2:Hu1 112.7500 107.54044 117.95956     0
## A2:Hu2-A1:Hu2 -26.0000 -31.20956 -20.79044     0
##
## $`Hole:Assembly:Hub`
##                         diff        lwr        upr     p adj
## H2:A1:Hu1-H1:A1:Hu1   51.500  42.740286  60.2597138 0.0000000
## H1:A2:Hu1-H1:A1:Hu1   -9.125 -17.884714  -0.3652862 0.0354797
## H2:A2:Hu1-H1:A1:Hu1   -3.000 -11.759714   5.7597138 0.9587675
## H1:A1:Hu2-H1:A1:Hu1  122.375 113.615286 131.1347138 0.0000000
## H2:A1:Hu2-H1:A1:Hu1  143.000 134.240286 151.7597138 0.0000000
## H1:A2:Hu2-H1:A1:Hu1  100.375  91.615286 109.1347138 0.0000000
## H2:A2:Hu2-H1:A1:Hu1  113.000 104.240286 121.7597138 0.0000000
## H1:A2:Hu1-H2:A1:Hu1  -60.625 -69.384714 -51.8652862 0.0000000
## H2:A2:Hu1-H2:A1:Hu1  -54.500 -63.259714 -45.7402862 0.0000000
## H1:A1:Hu2-H2:A1:Hu1   70.875  62.115286  79.6347138 0.0000000
## H2:A1:Hu2-H2:A1:Hu1   91.500  82.740286 100.2597138 0.0000000
```

```
## H1:A2:Hu2-H2:A1:Hu1  48.875  40.115286  57.6347138 0.0000000
## H2:A2:Hu2-H2:A1:Hu1  61.500  52.740286  70.2597138 0.0000000
## H2:A2:Hu1-H1:A2:Hu1   6.125  -2.634714  14.8847138 0.3667120
## H1:A1:Hu2-H1:A2:Hu1 131.500 122.740286 140.2597138 0.0000000
## H2:A1:Hu2-H1:A2:Hu1 152.125 143.365286 160.8847138 0.0000000
## H1:A2:Hu2-H1:A2:Hu1 109.500 100.740286 118.2597138 0.0000000
## H2:A2:Hu2-H1:A2:Hu1 122.125 113.365286 130.8847138 0.0000000
## H1:A1:Hu2-H2:A2:Hu1 125.375 116.615286 134.1347138 0.0000000
## H2:A1:Hu2-H2:A2:Hu1 146.000 137.240286 154.7597138 0.0000000
## H1:A2:Hu2-H2:A2:Hu1 103.375  94.615286 112.1347138 0.0000000
## H2:A2:Hu2-H2:A2:Hu1 116.000 107.240286 124.7597138 0.0000000
## H2:A1:Hu2-H1:A1:Hu2  20.625  11.865286  29.3847138 0.0000000
## H1:A2:Hu2-H1:A1:Hu2 -22.000 -30.759714 -13.2402862 0.0000000
## H2:A2:Hu2-H1:A1:Hu2  -9.375 -18.134714  -0.6152862 0.0278403
## H1:A2:Hu2-H2:A1:Hu2 -42.625 -51.384714 -33.8652862 0.0000000
## H2:A2:Hu2-H2:A1:Hu2 -30.000 -38.759714 -21.2402862 0.0000000
## H2:A2:Hu2-H1:A2:Hu2  12.625   3.865286  21.3847138 0.0007601
```
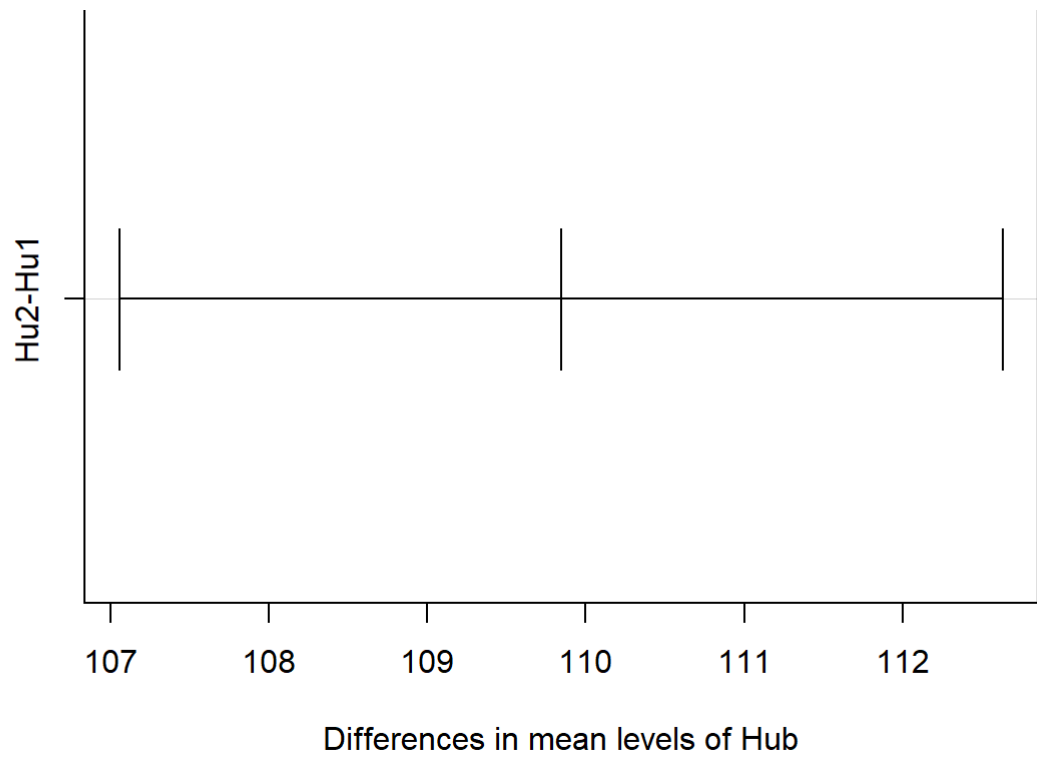
95% family-wise confidence level
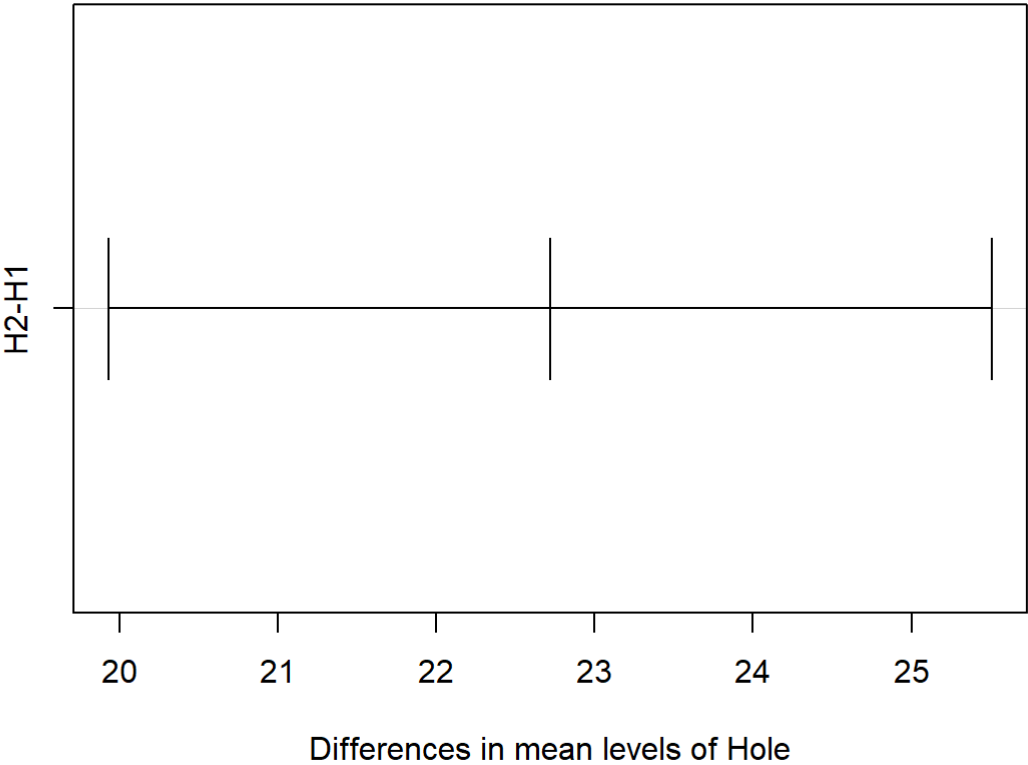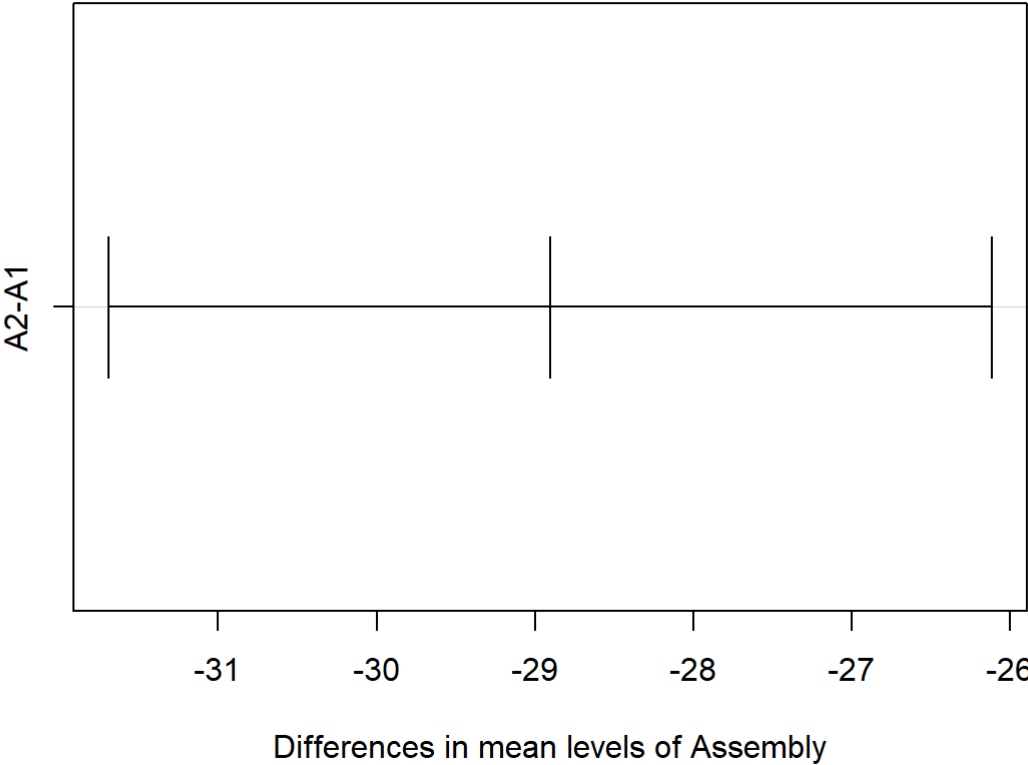
Differences in mean levels of Hole
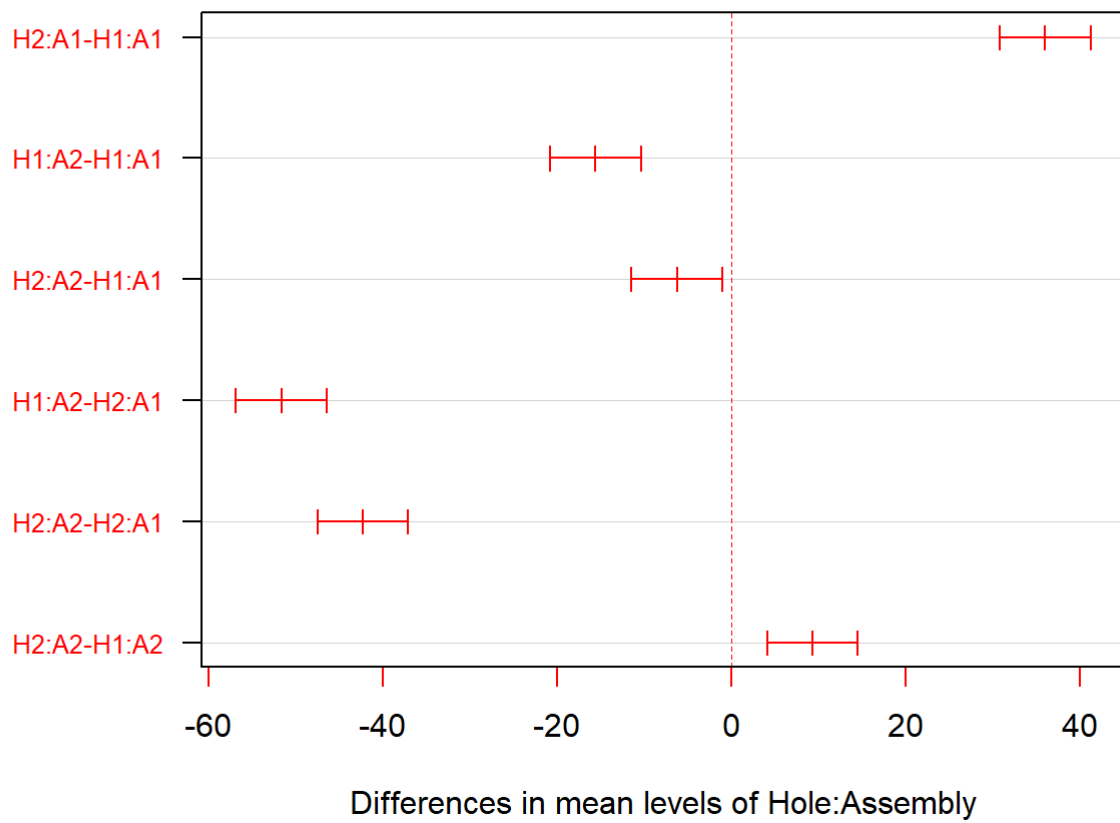
95% family-wise confidence level

Differences in mean levels of Assembly

95% family-wise confidence level

Differences in mean levels of Hub

95% family-wise confidence level
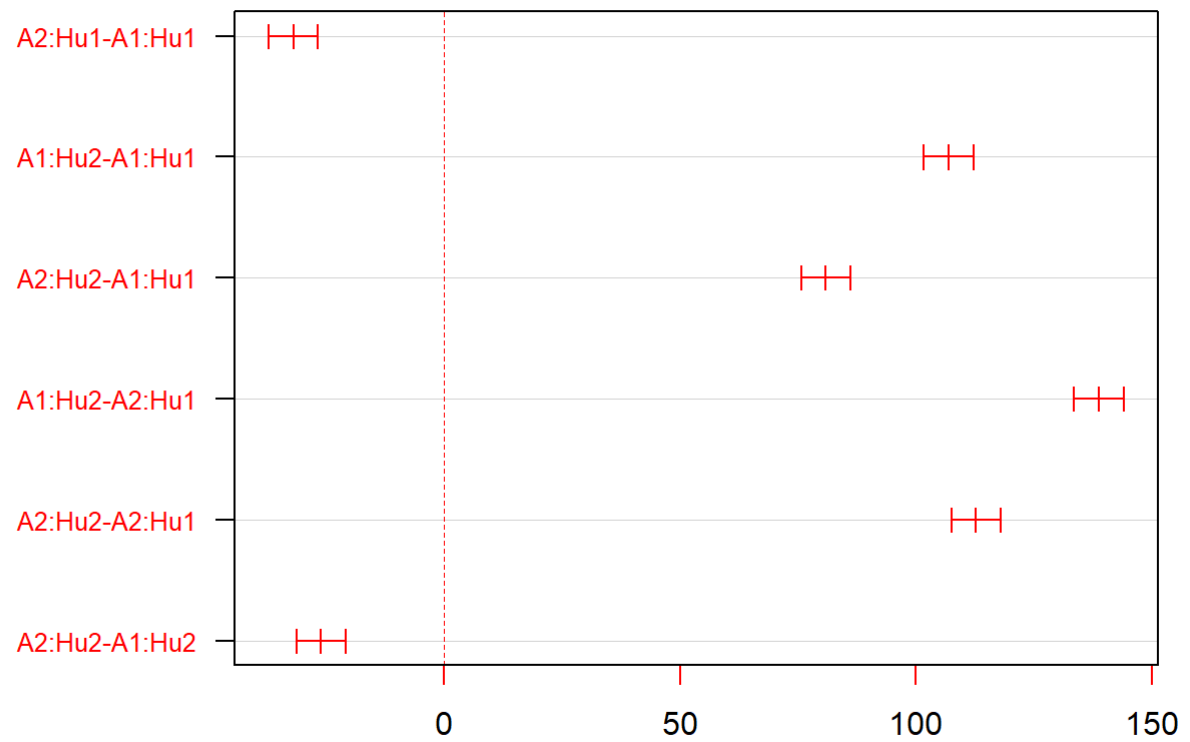

Differences in mean levels of Hole:Assembly
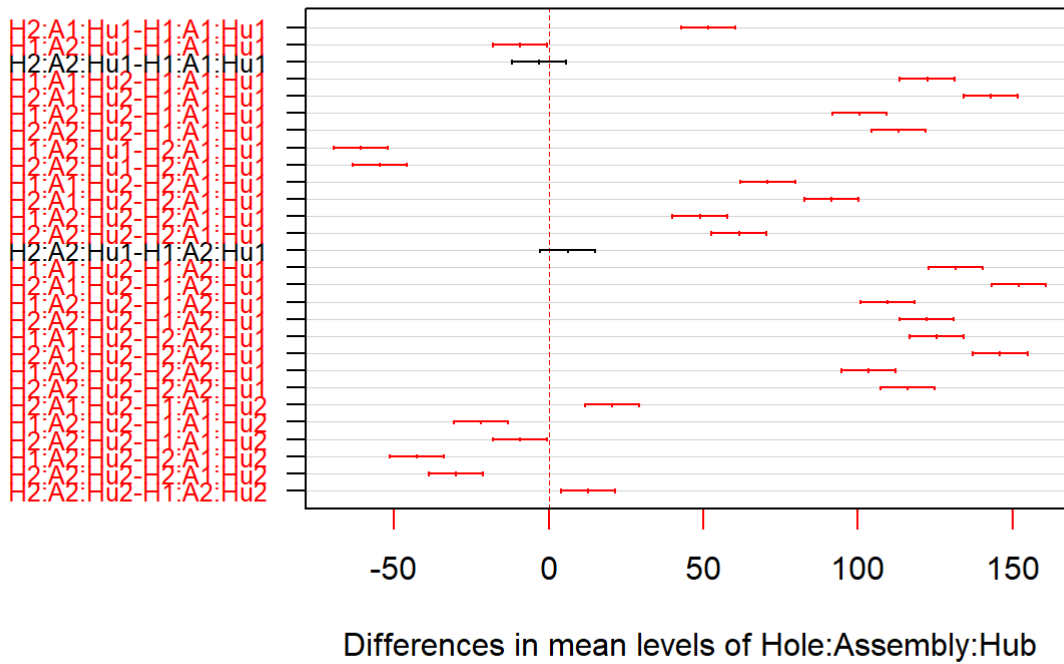
95% family-wise confidence level
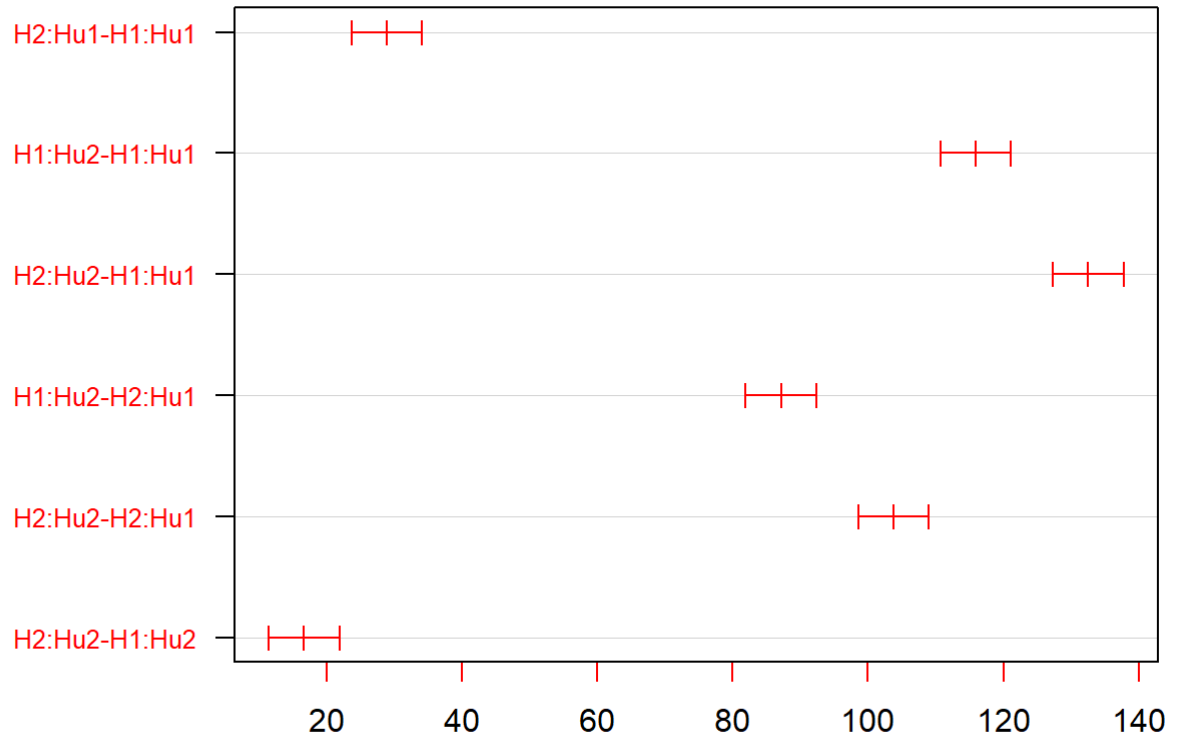
Differences in mean levels of Hole:Hub

95% family-wise confidence level

Differences in mean levels of Assembly:Hub

95% family-wise confidence level

Differences in mean levels of Hole:Assembly:Hub

In the above Plot, the Values marked in Black indicate those configurations of Factor Variables that have no Significant Difference in Mean Torque Values namely :

1. Hole Type 2, Assembly Method 2, Hub Shape 1 and Hole Type 1, Assembly Method 1, Hub Shape 1 have no significant difference in the Mean Torque Values.

2. Hole Type 2, Assembly Method 2, Hub Shape 1 and Hole Type 1, Assembly Method 2, Hub Shape 1 have no significant difference in the Mean Torque Values.

For the remaining 26 combinations of Factor levels, it can be seen that there are significant differences in the mean values for Torques produced.

Conclusion

We would recommend proceeding with **Hole Type 2, Assembly Method 1 and Hub Shape 2** for obtaining Spyders that are the most resistant to destructive testing (high Torque values).

One of the main goals of ANOVA is establishing the order of importance between various Factors and their Interactions. Based on our Analysis, the following list has been created that ranks the various factors in descending order of Importance :

1.Hub

2.Assembly

3.Hole

4.Hole : Assembly

5.Hole : Assembly : Hub

6.Hole : Hub

7.Hub : Assembly