Exam 2 - Question 1

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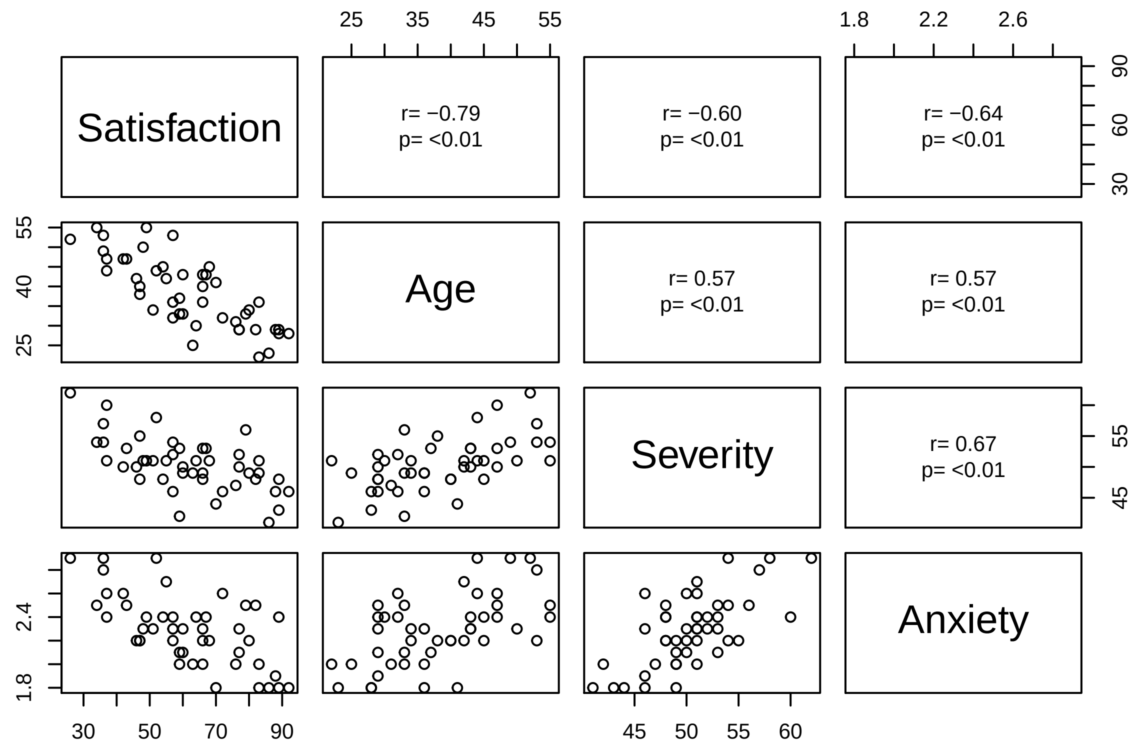
Problem 1 - Do problem 6.15 on page 250.

- Do not do part (a)
- Do parts (b-g)
- Extra - Conduct Brown-Forsythe test or Levene test. Group them based on median of predicted value of Y.

B. Scatter plot matrix and correlation matrix with interpretation.

```
panel.cor <- function(x, y, digits = 2, cex.cor, ...){
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  # correlation coefficient
  r <- cor(x, y)
  txt <- format(c(r, 0.123456789), digits = digits)[1]
  txt <- paste("r= ", txt, sep = "")
  text(0.5, 0.6, txt)

  # p-value calculation
  p <- cor.test(x, y)$p.value
  txt2 <- format(c(p, 0.123456789), digits = digits)[1]
  txt2 <- paste("p= ", txt2, sep = "")
  if(p<0.01) txt2 <- paste("p= ", "<0.01", sep = "")
  text(0.5, 0.4, txt2)
}
df <- read.csv("data/6.15-6.16.csv")
names(df) = c("Satisfaction","Age", "Severity", "Anxiety")
pairs(df, upper.panel = panel.cor)
```



The matrix plot shows that all three predictor varaibles are all at least moderately correlated and linear to the outcome varaible of satisfaction.

Part C. Create a regression model for all three predictors and state the predicted regression function. How is β_2 interpreted?

```
result <- lm(Satisfaction ~ Age + Severity + Anxiety, data=df)
result_smry <- summary(result)
F_stat <- round(as.numeric(result_smry$fstatistic["value"]),1)
F_crit <- round(qf(0.95, df1=3, df2=result_smry$df[2]),1)
result_smry
```

```
##
## Call:
## lm(formula = Satisfaction ~ Age + Severity + Anxiety, data = df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.3524  -6.4230   0.5196   8.3715  17.1601
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 158.4913    18.1259   8.744 5.26e-11 ***
## Age          -1.1416     0.2148  -5.315 3.81e-06 ***
```

```
## Severity     -0.4420     0.4920  -0.898   0.3741
## Anxiety     -13.4702     7.0997  -1.897   0.0647 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.06 on 42 degrees of freedom
## Multiple R-squared:  0.6822, Adjusted R-squared:  0.6595
## F-statistic: 30.05 on 3 and 42 DF,  p-value: 1.542e-10
```

Regression Model: Satisfaction = 158.49 - 1.14 x Age - 0.44 x Severity - 13.47 x Anxiety

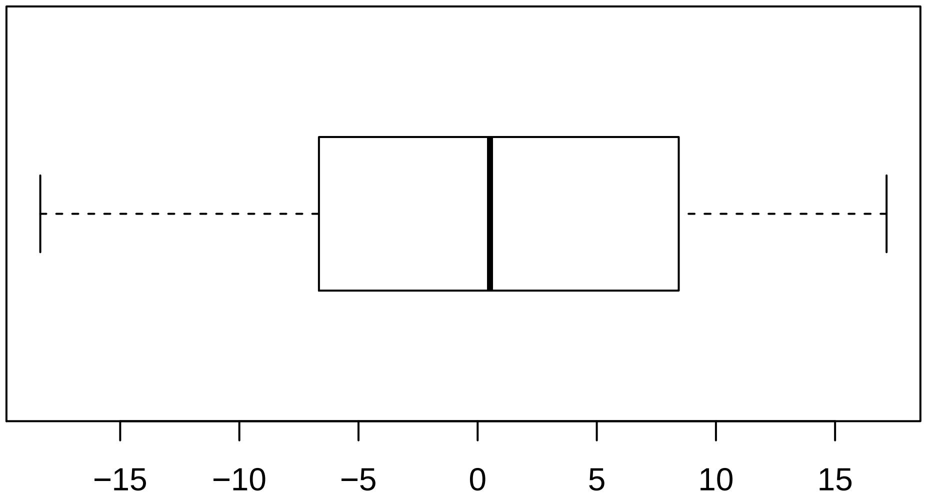
β_2 (Severity) has a coefficient of -0.44 which means that as severity increases 1 unit satisfaction drops 0.44 units where the other parameters are held constant.

D. Obtain the residuals and prepare a boxplot. Are there any outliers.

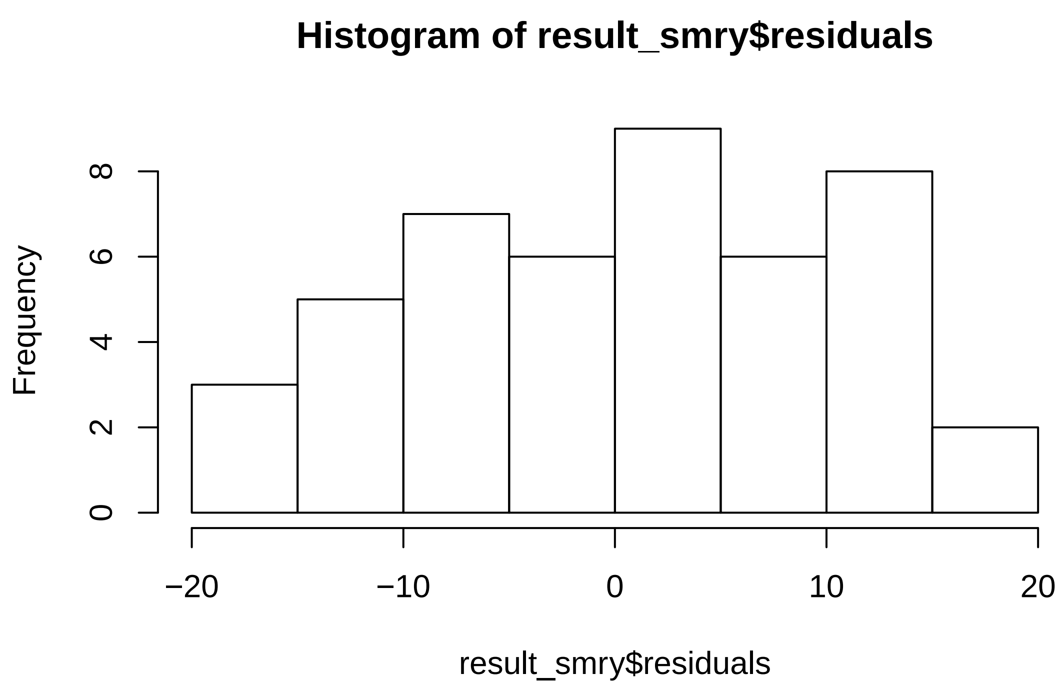
```r
library(knitr)
iqr <- IQR(result$residuals)
smry <- summary(result$residuals)
smry <- t(as.matrix(smry, nrow=1))
smry <- data.frame(smry)
names(smry) = c("Min", "FirstQtr", "Median", "Mean", "ThirdQtr", "Max")
smry <- cbind(smry,
             Low1.5xIQR=(smry$FirstQtr - (1.5 * iqr)),
             Uppr1.5xIQR=(smry$ThirdQtr + (1.5 * iqr)),
             Low3xIQR=(smry$FirstQtr - (3 * iqr)),
             Uppr3xIQR=(smry$ThirdQtr + (3 * iqr)))
smry <- round(smry, 3)
kable(smry)
```

Min	FirstQtr	Median	Mean	ThirdQtr	Max	Low1.5xIQR	Uppr1.5xIQR	Low3xIQR	Uppr3xIQR
-18.35	-6.423	0.52	0	8.372	17.16	-28.615	30.564	-50.807	52.756

```r
boxplot(result_smry$residuals, horizontal=T)
```




```r
hist(result_smry$residuals, breaks=12)
```



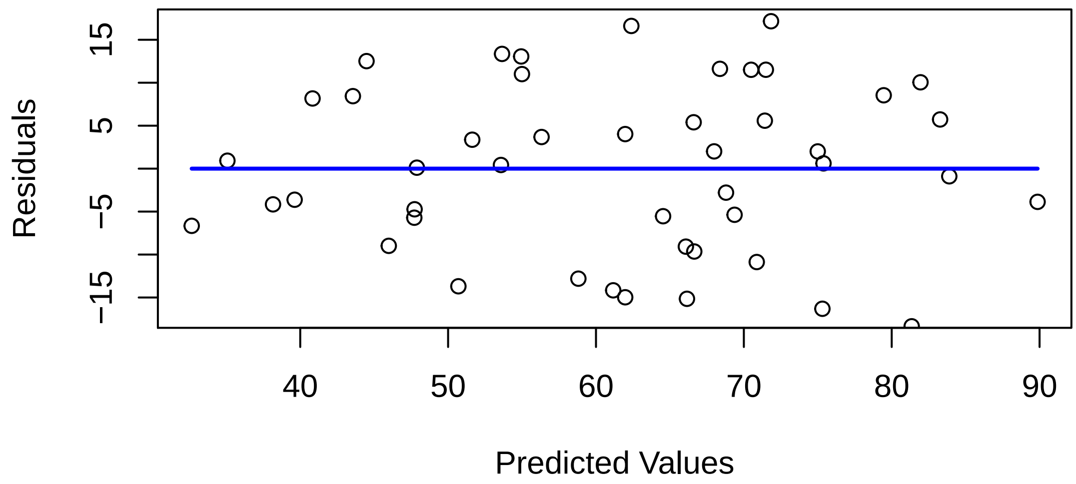
Outlier	Definition
Lower Mild	1st Qtr - 1.5 x IQR
Upper Mild	3rd Qtr + 1.5 x IQR
Lower Extreme	1st Qtr - 3 x IQR
Upper Extreme	3rd Qtr + 3 x IQR

There does not appear to be outliers in the box plot but the histogram shows a non normal distribution of residuals.

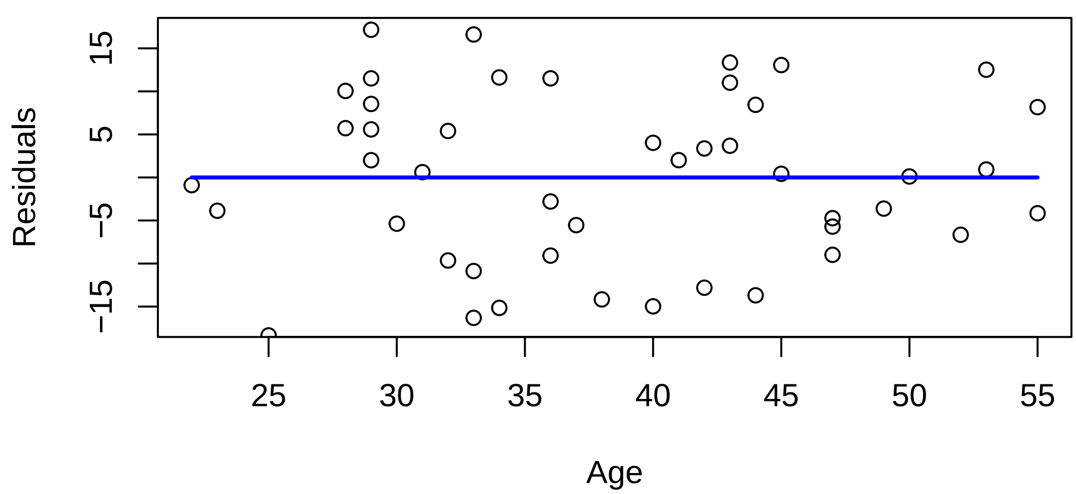
E. Plot the residuals against predicted values and two factor interactions. Prepare a normal probability plot. Interpret.

```
df_model <- result$model[, 1:4]
df_model$Residuals <- result_smry$residuals
df_model$PredictedVals <- result$fitted.values
df_model$AgeSeverity<- df_model$Age * df_model$Severity
df_model$AgeAnxiety <- df_model$Age * df_model$Anxiety
df_model$SeverityAnxiety <- df_model$Severity * df_model$Anxiety
```

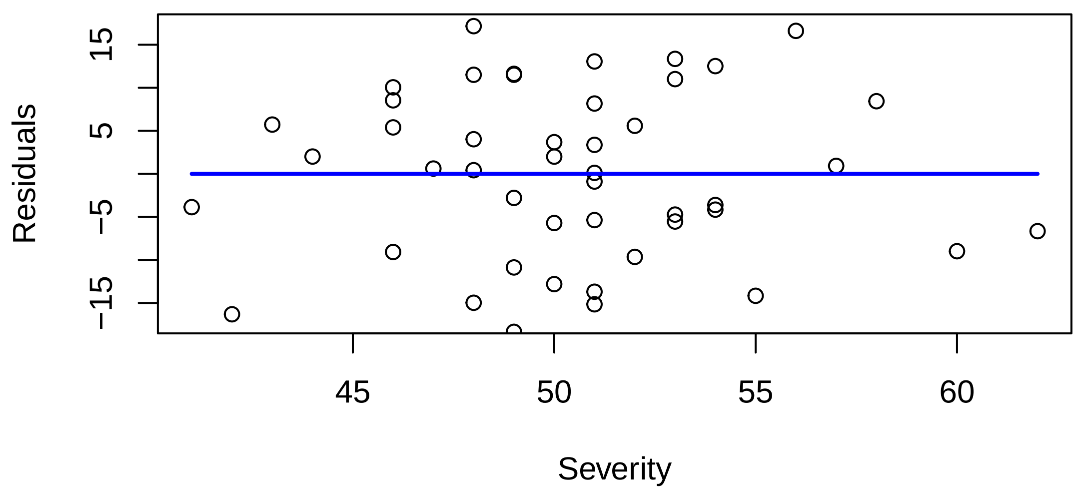
```
with(df_model, {
     plot(x=PredictedVals, y=Residuals,
          ylim=c(-max(Residuals), max(Residuals)),
          xlab="Predicted Values", ylab="Residuals", main="")
     points(c(min(PredictedVals), max(PredictedVals)),
            c(0,0), type="l", lwd="2", col="blue")
     })
```



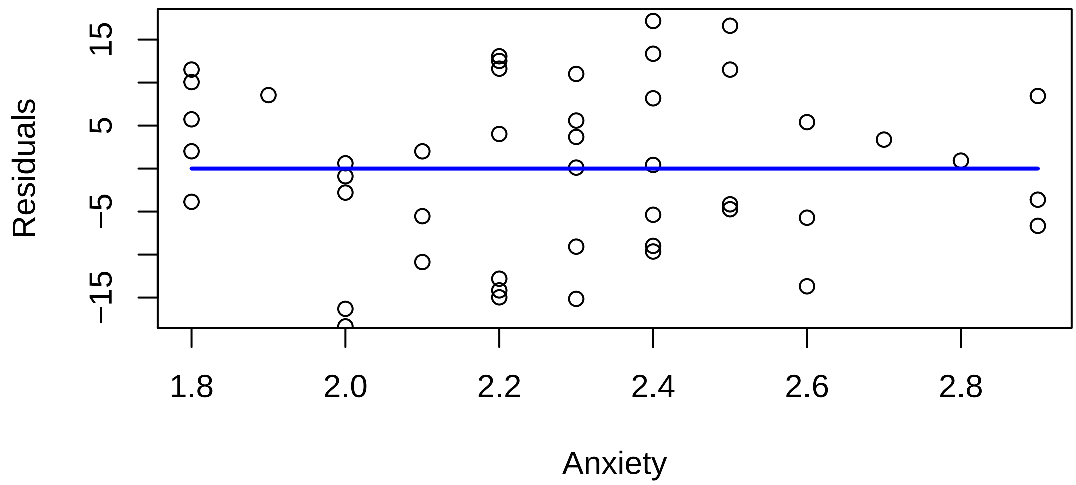

```
with(df_model, {
     plot(x=Age, y=Residuals,
          ylim=c(-max(Residuals), max(Residuals)),
          xlab="Age", ylab="Residuals", main="")
     points(c(min(Age), max(Age)),
              c(0,0), type="l", lwd="2", col="blue")
     })
```



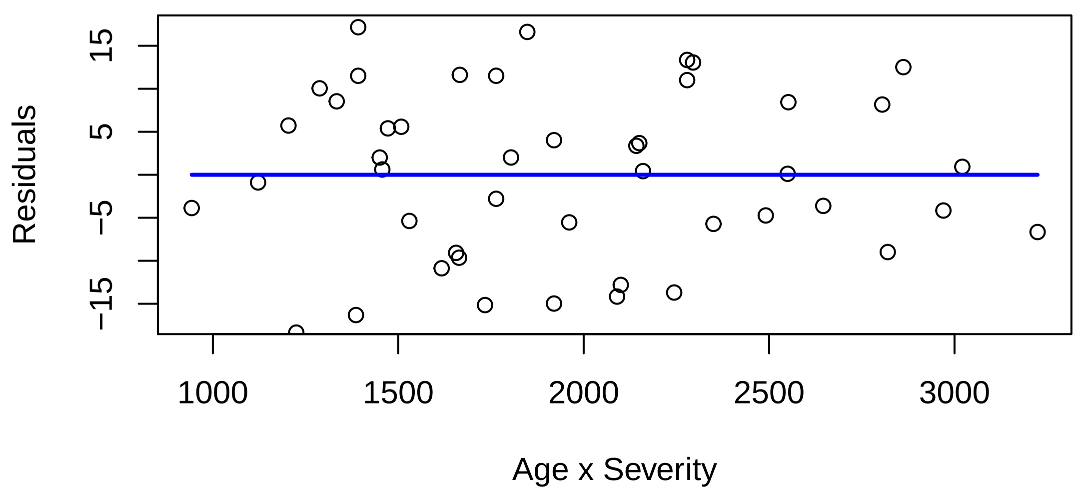
```r
with(df_model, {
     plot(x=Severity, y=Residuals,
          ylim=c(-max(Residuals), max(Residuals)),
          xlab="Severity", ylab="Residuals", main="")
     points(c(min(Severity), max(Severity)),
            c(0,0), type="l", lwd="2", col="blue")
     })
```



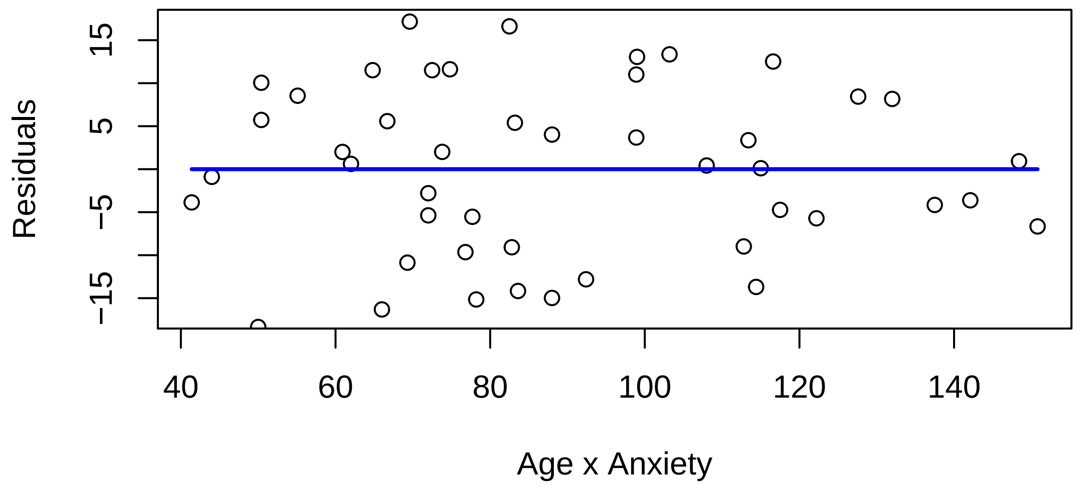

```r
with(df_model, {
     plot(x=Anxiety, y=Residuals,
          ylim=c(-max(Residuals), max(Residuals)),
          xlab="Anxiety", ylab="Residuals", main="")
     points(c(min(Anxiety), max(Anxiety)),
            c(0,0), type="l", lwd="2", col="blue")
     })
```



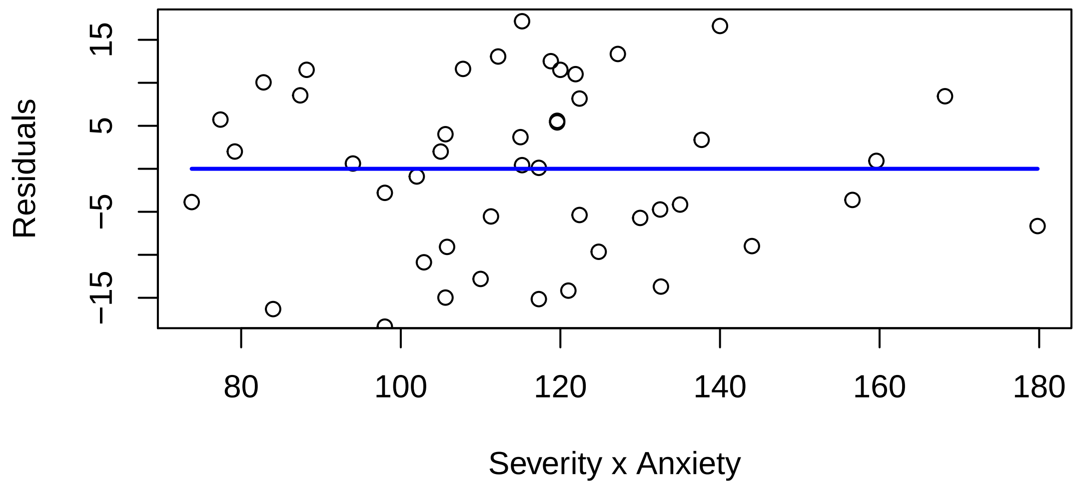

```r
with(df_model, {
     plot(x=AgeSeverity, y=Residuals,
          ylim=c(-max(Residuals), max(Residuals)),
          xlab="Age x Severity", ylab="Residuals", main="")
     points(c(min(AgeSeverity), max(AgeSeverity)),
              c(0,0), type="l", lwd="2", col="blue")
     })
```



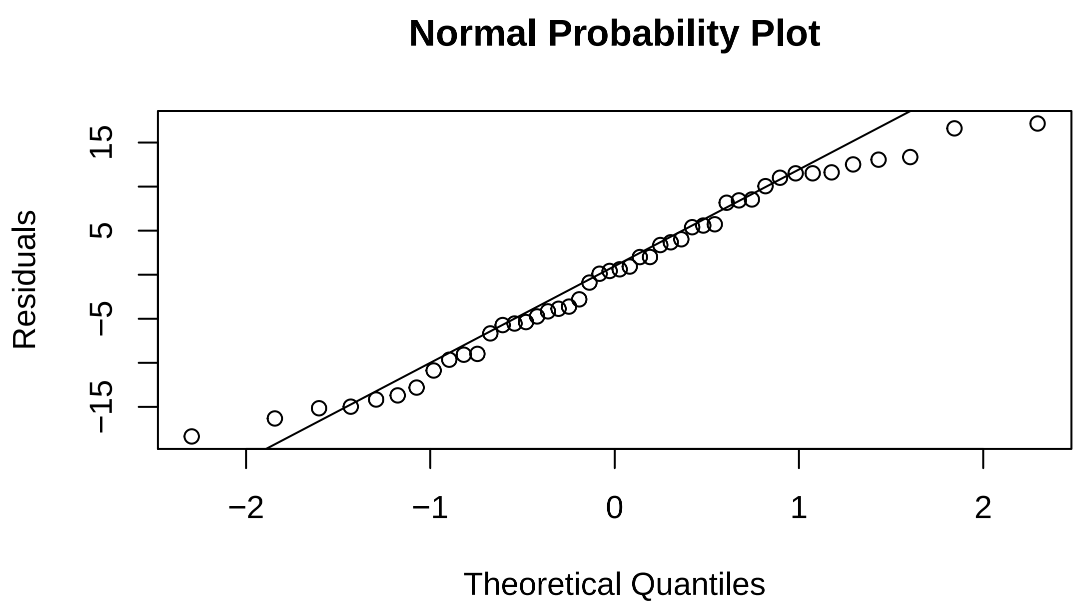
```
with(df_model, {
     plot(x=AgeAnxiety, y=Residuals,
          ylim=c(-max(Residuals), max(Residuals)),
          xlab="Age x Anxiety", ylab="Residuals", main="")
     points(c(min(AgeAnxiety), max(AgeAnxiety)),
              c(0,0), type="l", lwd="2", col="blue")
     })
```




```
with(df_model, {
     plot(x=SeverityAnxiety, y=Residuals,
          ylim=c(-max(Residuals), max(Residuals)),
          xlab="Severity x Anxiety", ylab="Residuals", main="")
     points(c(min(SeverityAnxiety), max(SeverityAnxiety)),
              c(0,0), type="l", lwd="2", col="blue")
     })
```




```
qqnorm(result$residuals, ylab="Residuals", main="Normal Probability Plot")
qqline(result$residuals)
```



The residual scatter plots do not show any major or systematic pattern or non-normal variance of the error terms against any of the predictor variables or predicted varaibles as well as the two-factor interactions of them. The normal probability plot however does suggest there is a deviation from normality with values greater than the 3rd quartile of the predictors.

Part F. Conduct a formal test for lack of fit.

First check for repeating groups of predictor combinations to assess whether artificial repeating groups are needed.

```
df$CommonPredictors <- with(df,paste(
  as.character(Age),
  as.character(Severity),
  as.character(Anxiety),
  sep="-"))

library(dplyr)
library(knitr)
df_tbl <- tbl_df(df)
df_tbl_levels <- group_by(df_tbl, CommonPredictors) %>% summarize(LevelRepeats=n()) %>% arrange(LevelRep
df_levels <- as.data.frame(df_tbl_levels)
kable(df_levels)
```

CommonPredictors	LevelRepeats
22-51-2	1
23-41-1.8	1
25-49-2	1
28-43-1.8	1
28-46-1.8	1
29-46-1.9	1
29-48-2.4	1
29-48-2.5	1
29-50-2.1	1
29-52-2.3	1
30-51-2.4	1
31-47-2	1
32-46-2.6	1
32-52-2.4	1
33-42-2	1
33-49-2.1	1
33-56-2.5	1
34-49-2.2	1
34-51-2.3	1
36-46-2.3	1
36-49-1.8	1
36-49-2	1
37-53-2.1	1
38-55-2.2	1

CommonPredictors	LevelRepeats
41-44-1.8	1
42-50-2.2	1
42-51-2.7	1
43-50-2.3	1
43-53-2.3	1
43-53-2.4	1
44-51-2.6	1
44-58-2.9	1
45-48-2.4	1
45-51-2.2	1
47-50-2.6	1
47-53-2.5	1
47-60-2.4	1
49-54-2.9	1
50-51-2.3	1
52-62-2.9	1
53-54-2.2	1
53-57-2.8	1
55-51-2.4	1
55-54-2.5	1
40-48-2.2	2

There is one repeating set of rows for values Age-Severity-Anxiety of 40-48-2.2 so yes you can do a lack of fit test.

```r
reduced <- lm(Satisfaction ~ Age + Severity + Anxiety, data=df)
full <- lm(Satisfaction ~ factor(Age) + factor(Severity) + factor(Anxiety), data=df)
anova(reduced, full)
```

```
## Analysis of Variance Table
##
## Model 1: Satisfaction ~ Age + Severity + Anxiety
## Model 2: Satisfaction ~ factor(Age) + factor(Severity) + factor(Anxiety)
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1     42 4248.8
## 2      1  180.5 41    4068.3 0.5497 0.8152
```

The anova of the reduced verse full model is used to assess the appropriateness (fittness) of the model:

$H_o : E\{Y\} = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 x_3$ * Concludes that the regression function is linear where p-value > 0.05

$H_a : E\{Y\} \neq \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 x_3$ * Concludes that there is a lack of linear fit where p-value <= 0.05

Since p-value > 0.05 we do not reject the null hypothesis, the model appears adequate

Part G. Conduct Breusch-Pagan test for constancy of error variance of the models.

```
library(lmtest)
bptest(result)
```

```
##
##  studentized Breusch-Pagan test
##
## data:  result
## BP = 2.5583, df = 3, p-value = 0.4648
```

H_o: the error terms have constant variance

H_a: at least one parameter has errors with non-constanct variance

Since the p-value is > 0.05 we do not reject the H_o and conclude there is constant variance (no-heterskedacity).

Extra: Conduct Leven test with grouping by the median of predicted Y

```
library(lawstat)
median_yhat <- median(df_model$PredictedVals)
df_model$LeveneGrps <- ifelse(df_model$PredictedVals <= median_yhat, "A","B")
with(df_model, levene.test(Residuals, as.factor(LeveneGrps),location="mean"))
```

```
##
##  classical Levene's test based on the absolute deviations from the
##  mean ( none not applied because the location is not set to median
##  )
##
## data:  Residuals
## Test Statistic = 0.0213, p-value = 0.8847
```

The Leven test assumes the two population's variances are equal

H_o: no difference in population variances

H_o: there are differences in the populations variances

Since p-value > 0.05 we do not reject the null hypothsis and conclude equal variance of the error terms.