Data Screening

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Dataset:

600 employees participated in a company-wide experiment to test if an educational program would be effective at increasing employee satisfaction. Half of the employees were assigned to be in the control group, while the other half were assigned to be in the experimental group. The experimental group was the only group that received the educational intervention. All groups were given an employee satisfaction scale at time one to measure their initial levels of satisfaction. The same scale was then used half way through the program and at the end of the program. The goal of the experiment was to assess satisfaction to see if it increased across the measurements during the program as compared to a control group.

Variables:

```
a) Gender (1 = male, 2 = female)
b) Group (1 = control group, 2 = experimental group)
c) 3 satisfaction scores, ranging from 2-100 points. Decimals are possible!
The control group was measured at the same three time points, but did not
take part in the educational program.
    i) Before the program
    ii) Half way through the program
    iii) After the program
```

```
eduResearchData <- read.csv('06_data.csv')
summary(eduResearchData)
```

```
##      Gender          Group           Begin            Middle
##  Min.   :1.000   Min.   :1.000   Min.   : 61.15   Min.   :37.35
##  1st Qu.:1.000   1st Qu.:1.000   1st Qu.: 94.72   1st Qu.:59.88
##  Median :2.000   Median :2.000   Median :102.26   Median :64.12
##  Mean   :1.505   Mean   :1.508   Mean   :102.17   Mean   :63.86
##  3rd Qu.:2.000   3rd Qu.:2.000   3rd Qu.:110.04   3rd Qu.:68.18
##  Max.   :2.000   Max.   :2.000   Max.   :148.25   Max.   :83.79
##  NA's   :8       NA's   :8       NA's   :8        NA's   :8
##      After
##  Min.   : 48.15
##  1st Qu.: 89.99
##  Median : 97.42
##  Mean   : 95.83
##  3rd Qu.:103.73
```

```
##  Max.   :120.41
##  NA's   :8
```

Data screening:

Accuracy:

```
a)  Include output and indicate how the data are not accurate.
b)  Include output to show how you fixed the accuracy errors, and describe
what you did.

eduResearchData$Gender = factor(eduResearchData$Gender, levels = c(1,2),
labels = c("male", "female"))

eduResearchData$Group = factor(eduResearchData$Group, levels = c(1,2), labels
= c("control", "experimental"))

table(eduResearchData$Gender)

##
##   male female
##    194    198

table((eduResearchData$Group))

##
##      control experimental
##          193          199
```

Missing data:

```
a)  Include output that shows you have missing data.
b)  Include output and a description that shows what you did with the missing
data.
    i)  Replace all participant data if they have less than or equal to 20%
of missing data by row.
    ii) You can leave out the other participants (i.e. you do not have to
create allrows).


summary(eduResearchData)

##     Gender             Group         Begin             Middle
##  male  :194   control     :193   Min.   : 61.15   Min.   :37.35
##  female:198   experimental:199   1st Qu.: 94.72   1st Qu.:59.88
##  NA's  :  8   NA's        :  8   Median :102.26   Median :64.12
##                                  Mean   :102.17   Mean   :63.86
##                                  3rd Qu.:110.04   3rd Qu.:68.18
##                                  Max.   :148.25   Max.   :83.79
##                                  NA's   :8        NA's   :8
##      After
```

```
##  Min.   : 48.15
##  1st Qu.: 89.99
##  Median : 97.42
##  Mean   : 95.83
##  3rd Qu.:103.73
##  Max.   :120.41
##  NA's   :8
```

```
percentageMissingData = function(x){sum(is.na(x))/length(x)*100}
missingData = apply(eduResearchData, 1, percentageMissingData)
table(missingData)
```

```
## missingData
##   0  20  40  60
## 363  35   1   1
```

```
replcacedData = subset(eduResearchData, missingData <= 20)
notReplcedData = subset(eduResearchData, missingData > 20)
missingDataLessThanTwenty = apply(replcacedData, 1, percentageMissingData)
table(missingDataLessThanTwenty)
```

```
## missingDataLessThanTwenty
##   0  20
## 363  35
```

```
library('mice')
```

```
##
## Attaching package: 'mice'
```

```
## The following objects are masked from 'package:base':
##
##     cbind, rbind
```

```
noMissingDataTemp = mice(replcacedData)
```

```
##
##  iter imp variable
##   1   1  Gender  Group  Begin  Middle  After
##   1   2  Gender  Group  Begin  Middle  After
##   1   3  Gender  Group  Begin  Middle  After
##   1   4  Gender  Group  Begin  Middle  After
##   1   5  Gender  Group  Begin  Middle  After
##   2   1  Gender  Group  Begin  Middle  After
##   2   2  Gender  Group  Begin  Middle  After
##   2   3  Gender  Group  Begin  Middle  After
##   2   4  Gender  Group  Begin  Middle  After
##   2   5  Gender  Group  Begin  Middle  After
##   3   1  Gender  Group  Begin  Middle  After
##   3   2  Gender  Group  Begin  Middle  After
##   3   3  Gender  Group  Begin  Middle  After
##   3   4  Gender  Group  Begin  Middle  After
```

```
##   3   5  Gender  Group  Begin  Middle  After
##   4   1  Gender  Group  Begin  Middle  After
##   4   2  Gender  Group  Begin  Middle  After
##   4   3  Gender  Group  Begin  Middle  After
##   4   4  Gender  Group  Begin  Middle  After
##   4   5  Gender  Group  Begin  Middle  After
##   5   1  Gender  Group  Begin  Middle  After
##   5   2  Gender  Group  Begin  Middle  After
##   5   3  Gender  Group  Begin  Middle  After
##   5   4  Gender  Group  Begin  Middle  After
##   5   5  Gender  Group  Begin  Middle  After
```

```
noMissingData = complete(noMissingDataTemp, 1)
summary(noMissingData)
```

```
##     Gender             Group         Begin            Middle
##  male  :198   control     :197   Min.   : 61.15   Min.   :37.35
##  female:200   experimental:201   1st Qu.: 94.65   1st Qu.:59.92
##                                  Median :102.26   Median :64.12
##                                  Mean   :102.14   Mean   :63.87
##                                  3rd Qu.:110.10   3rd Qu.:68.14
##                                  Max.   :148.25   Max.   :83.79
##      After
##  Min.   : 48.15
##  1st Qu.: 90.08
##  Median : 97.42
##  Mean   : 95.78
##  3rd Qu.:103.64
##  Max.   :120.41
```

```
allRow = rbind(notReplcedData, noMissingData)
summary(allRow)
```

```
##     Gender             Group         Begin            Middle
##  male  :198   control     :197   Min.   : 61.15   Min.   :37.35
##  female:201   experimental:201   1st Qu.: 94.72   1st Qu.:59.87
##  NA's  :  1   NA's        :  2   Median :102.22   Median :64.12
##                                  Mean   :102.12   Mean   :63.85
##                                  3rd Qu.:110.04   3rd Qu.:68.12
##                                  Max.   :148.25   Max.   :83.79
##                                                   NA's   :1
##      After
##  Min.   : 48.15
##  1st Qu.: 89.92
##  Median : 97.40
##  Mean   : 95.75
##  3rd Qu.:103.63
##  Max.   :120.41
##  NA's   :1
```

Outliers:

a) Include a summary of your mahal scores that are greater than the cutoff.
b) What are the df for your Mahalanobis cutoff?
c) What is the cut off score for your Mahalanobis measure?

```r
cutoffScore = qchisq(0.999, ncol(allRow[,c(3,4,5)]))
cutoffScore
```

```
## [1] 16.26624
```

d) How many outliers did you have?
Solution: 1 outliers in Gender and 2 Outliers in Group

e) Delete all outliers.

```r
noMissData1 = noMissingData[,c(3,4,5)]
cutoff = qchisq(1-.001,ncol(noMissData1))
mahal = mahalanobis(noMissData1, colMeans(noMissData1, na.rm = TRUE),
cov(noMissData1, use = "pairwise.complete.obs"))
summary(mahal>cutoff)
```

```
##    Mode   FALSE    TRUE
## logical     396       2
```

```r
output = subset(noMissingData, mahal<cutoff)
str(output)
```

```
## 'data.frame':    396 obs. of  5 variables:
##  $ Gender: Factor w/ 2 levels "male","female": 2 2 2 2 2 2 2 2 2 2 ...
##  $ Group : Factor w/ 2 levels "control","experimental": 2 2 2 2 2 2 2 2 2
2 ...
##  $ Begin : num  104.3 69.8 87.3 94.8 98.6 ...
##  $ Middle: num  64 63.8 56.2 63.5 71 ...
##  $ After : num  105.3 98.4 93 106.9 112.7 ...
```

Assumptions:

Additivity:

a) Include the symnum bivariate correlation table of your continuous measures.
b) Do you meet the assumption for additivity?

Solution: Yes, I have met the assumption of aditivity.

```
symnum(cor(output[, c(3,4,5)]))
```

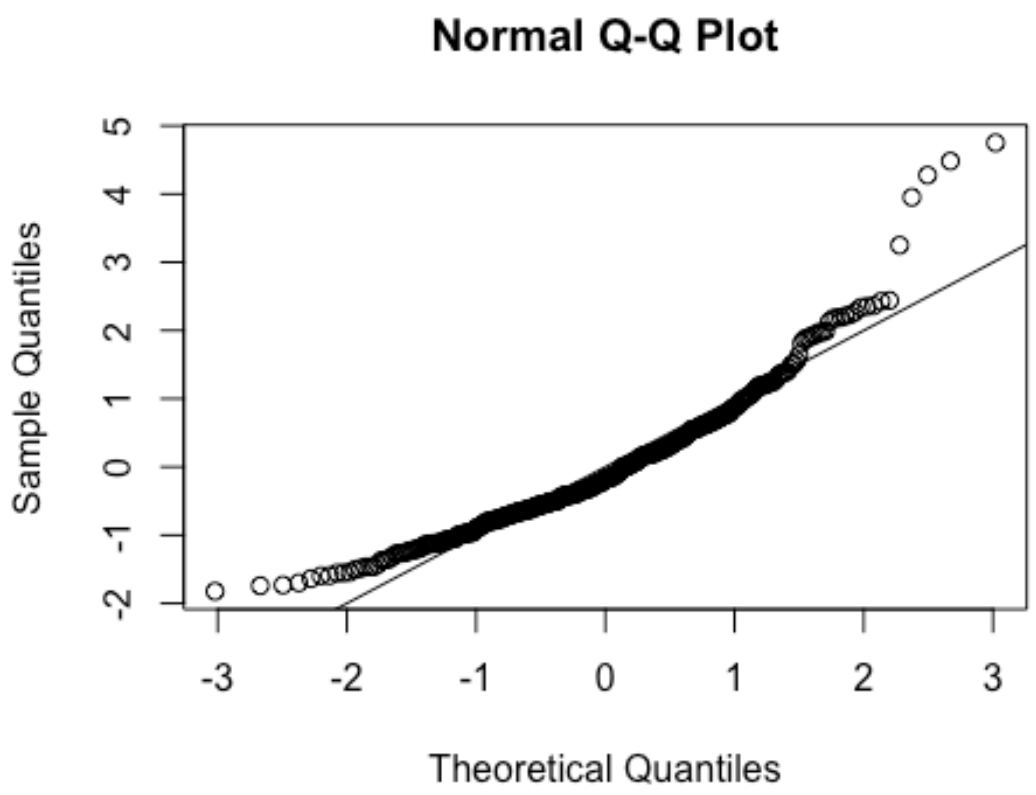
```
##        B M A
## Begin  1
## Middle   1
## After      1
## attr(,"legend")
## [1] 0 ' ' 0.3 '.' 0.6 ',' 0.8 '+' 0.9 '*' 0.95 'B' 1
```

Linearity:

```
a)  Include a picture that shows how you might assess multivariate linearity.
b)  Do you think you've met the assumption for linearity?

      Solution: Yes, it seems I have reached the linearity.
```

```
linearityOutput = rchisq(nrow(output), 7)
plot1 = lm(linearityOutput~., data = output)
standardizedPlot = rstudent(plot1)
as.numeric(unlist(qqnorm(standardizedPlot))) + abline(0,1)
```



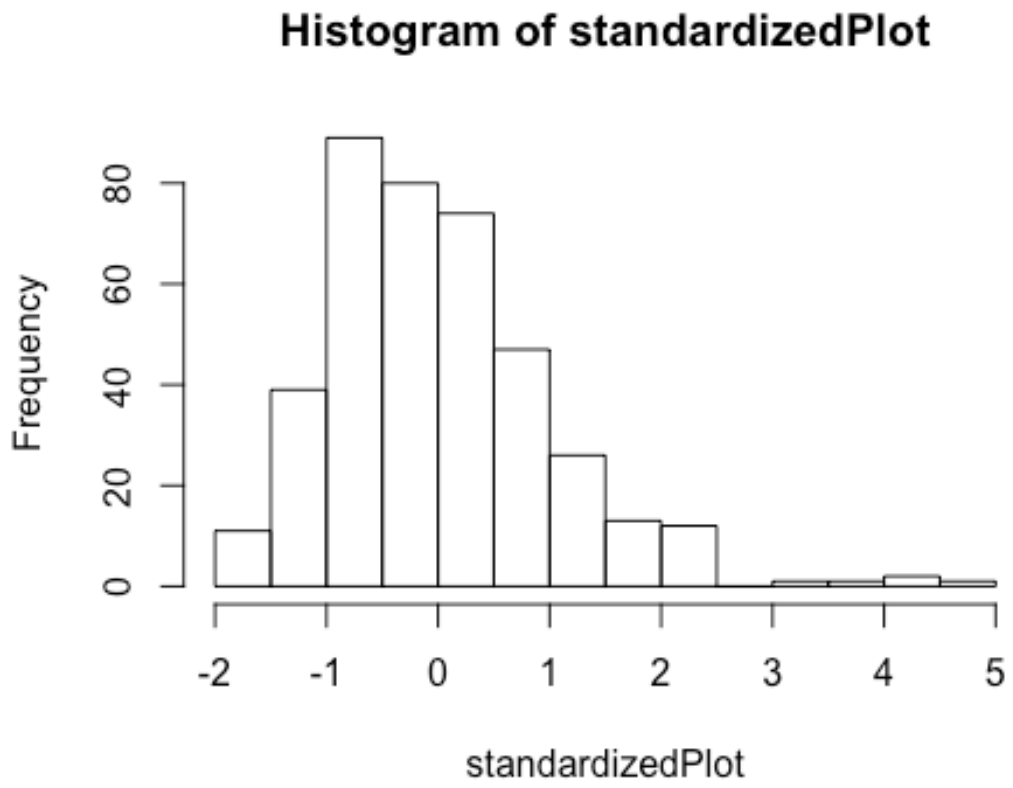

```
## numeric(0)
```

Normality:

```
a)  Include a picture that shows how you might assess multivariate normality.
b)  Do you think you've met the assumption for normality?

      Solution: From the above picture it is clearly seen that data is skewed
to the left
```

```
hist(standardizedPlot, breaks = 15)
```

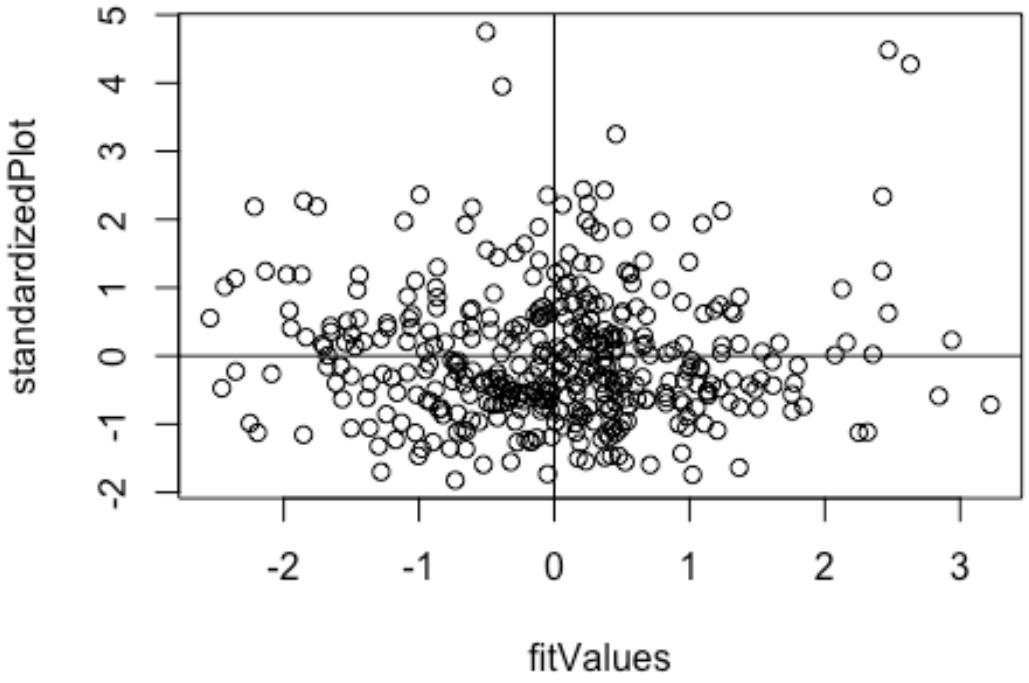


##

Homogeneity/Homoscedasticity:

```
a)  Include a picture that shows how you might assess multivariate
homogeneity.
b)  Do you think you've met the assumption for homogeneity?
    Solution: No, I dont think I met the homogeneity. left to right is met,
but no the top to bottom.
c)  Do you think you've met the assumption for homoscedasticity?
    Solution: Yes, suumption of homoscedasticity is met.
```

```
fitValues = scale(plot1$fitted.values)
{plot(fitValues, standardizedPlot)+abline(0,0)+abline(v =0)}
```




```
## integer(0)
```