AMOD-5210H: Foundations of Modelling

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PART 1: EFFECT SIZES

The following questions requires the use of **"healthdata.xlsx"**.

Firstly, loading the required packages and then reading the excel file.

```
health_dataset <- read_excel("health-data.xlsx")
```

Now, let's performing data extraction.

```
set.seed(0758054)
index <- sample(1:nrow(health_dataset),200)
AMOD5210_Part1 <- health_dataset[index, ]
```

Part 1: Question 1

Using an appropriate inferential statistic and effect size, determine whether there is a significant difference between students and non-students on "Health" and "Depress".

For the variable "Health":

Step 1 : Hypothesis & Assumptions

The H_0 is Null hypothesis and H_A is Alternative hypothesis.

$$H_0 : \text{There is no difference in "health" variable for students and non-students.}$$
$$\text{vs.}$$
$$H_A : \text{There is a difference in "health" variable for students and non-students.}$$

Let's check the head of Health dataset

```
head(AMOD5210_Part1, 3)
```

```
## # A tibble: 3 x 10
##      ID Gender Student Honesty Leader Persevere Regulat~1 Health Depress Dstatus
##   <dbl> <chr>  <chr>     <dbl>  <dbl>     <dbl>     <dbl>  <dbl>   <dbl> <chr>
## 1    48 Female No           20     19        19        10     12       1 No
## 2   576 Female Yes          21     11        17         8     25      10 No
## 3   525 Female No           21     18        19        19     15       4 No
## # ... with abbreviated variable name 1: Regulation
```

Now, let's grouping with students and checking the summary.

```r
grouping_student <- group_by(AMOD5210_Part1, Student)
get_summary_stats(grouping_student, Health, type="mean_sd")
```

```
## # A tibble: 2 x 5
##   Student variable     n  mean    sd
##   <chr>   <fct>    <dbl> <dbl> <dbl>
## 1 No      Health     161  16.1  5.02
## 2 Yes     Health      39  18.5  5.09
```

Now, we need to test some **assumptions** about our data.

```r
identify_outliers(grouping_student, Health)
```

```
## # A tibble: 1 x 12
##   Student    ID Gender Honesty Leader Persevere Regulat~1 Health Depress Dstatus
##   <chr>   <dbl> <chr>    <dbl>  <dbl>     <dbl>     <dbl>  <dbl>   <dbl> <chr>
## 1 No        354 Female      23     17        18        10      3       0 No
## # ... with 2 more variables: is.outlier <lgl>, is.extreme <lgl>, and
## #   abbreviated variable name 1: Regulation
```

Here, We get no outliers. We will now test for **normality** from the health-data. For that, we will use the **Shapiro-Wilks Test**. If $p > 0.05$, the data is normal.

```r
shapiro_test(grouping_student, Health)
```

```
## # A tibble: 2 x 4
##   Student variable statistic     p
##   <chr>   <chr>        <dbl> <dbl>
## 1 No      Health       0.987 0.158
## 2 Yes     Health       0.969 0.347
```

Now, we need to test for **homogeneity of variance**. We can use the **Levene's Test** for this. If $p > 0.05$, variances are homogeneous.

```r
levene_test(AMOD5210_Part1, Health ~ Student)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## # A tibble: 1 x 4
##     df1   df2 statistic     p
##   <int> <int>     <dbl> <dbl>
## 1     1   198     0.347 0.557
```

Step 2 : Testing

Now, we will run **Independent t-test**. Since, the homogeneity of variance assumption was not violated, we will set var.equal to TRUE.

```
t_test(AMOD5210_Part1, Health ~ Student, var.equal=TRUE)
```

```
## # A tibble: 1 x 8
##   .y.    group1 group2    n1    n2 statistic    df       p
## * <chr>  <chr>  <chr>  <int> <int>     <dbl> <dbl>   <dbl>
## 1 Health No     Yes      161    39     -2.62   198 0.00959
```

Since, $p < 0.05$, the test shows a significant difference. We have enough evidence to reject the null hypothesis, H_O.

Calculating Cohen's d

Also, the t-Test is significant, we need to calculate **Cohen's d** for our effect size. We need to specify "paired = FALSE" to indicate the groups are independent, and specify "pooled_sd = TRUE" to indicate the variances are equal.

```
cohens_d(Health ~ Student, data = AMOD5210_Part1, paired = FALSE, pooled_sd = TRUE)
```

```
## Cohen's d |         95% CI
## --------------------------
## -0.47     | [-0.82, -0.11]
##
## - Estimated using pooled SD.
```

Based on Cohen's (1988) conventions we have a small effect.

Step 3 : Conclusion

The current study sought to determine whether or not there is a significant difference between students and non-students on "Health". 200 study participants were randomly sampled from the general public (39 students, 161 non-students). The sample contained no extreme outliers. A Shapiro-Wilks test demonstrated normality by group, and Levene's test demonstrated homogeneity of variance. The mean "Health" variable of non-students in the sample was 16.112 (SD = 5.020) whereas the mean "Health" variable of the students in the sample was 18.462 (SD = 5.088). A Welch's independent t-test showed that the mean difference in "Health" variable between student and non-students in the sample was statistically significant, $t(198) = -2.615876$, $p < 0.05$, $d = -0.47$, with students tending to be more "Healthy" than non-students. According to Cohen's (1988) conventions, this is a small effect.

For the variable "Depress":

Step 1 : Hypothesis & Assumptions

The H_0 is Null hypothesis and H_A is Alternative hypothesis.

$$H_0 : \text{There is no difference in "depress" variable for students and non-students.}$$
$$\text{vs.}$$
$$H_A : \text{There is a difference in "depress" variable for students and non-students.}$$

```
get_summary_stats(grouping_student, Depress, type="mean_sd")
```

```
## # A tibble: 2 x 5
##   Student variable     n  mean    sd
##   <chr>   <fct>    <dbl> <dbl> <dbl>
## 1 No      Depress    161  4.83  4.44
## 2 Yes     Depress     39  6.97  5.06
```

Now, we need to test some **assumptions** about our data.

```
identify_outliers(grouping_student, Depress)
```

```
## # A tibble: 7 x 12
##   Student    ID Gender Honesty Leader Persevere Regulat~1 Health Depress Dstatus
##   <chr>   <dbl> <chr>    <dbl>  <dbl>     <dbl>     <dbl>  <dbl>   <dbl> <chr>
## 1 No        249 Female      13     22        10         9     21      20 Yes
## 2 No         96 Male        20     16        17        10     24      21 Yes
## 3 No         92 Female      19     18        21        12     18      17 Yes
## 4 Yes       760 Female      21     15        17        18     29      17 Yes
## 5 Yes       498 Female      24     16        10         6     21      18 Yes
## 6 Yes       557 Female      21     18        15        17     20      18 Yes
## 7 Yes       186 Female      19     13        12        15     26      18 Yes
## # ... with 2 more variables: is.outlier <lgl>, is.extreme <lgl>, and
## #   abbreviated variable name 1: Regulation
```

Here, We get no outliers. We will now test for **normality** from the health-data. For that, we will use the **Shapiro-Wilks Test**. If $p > 0.05$, the data is normal.

```
shapiro_test(grouping_student, Depress)
```

```
## # A tibble: 2 x 4
##   Student variable statistic             p
##   <chr>   <chr>        <dbl>         <dbl>
## 1 No      Depress      0.894 0.00000000241
## 2 Yes     Depress      0.884 0.000807
```

It can be seen that our data is not normal. We are still going to proceed with the test.

Now, we need to test for **homogeneity of variance**. We can use the **Levene's Test** for this. If $p > 0.05$, variances are homogeneous.

```
levene_test(AMOD5210_Part1, Depress ~ Student)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## # A tibble: 1 x 4
##     df1   df2 statistic     p
##   <int> <int>     <dbl> <dbl>
## 1     1   198     0.158 0.691
```

Step 2 : Testing

Now, we will run **Independent t-test**. Since, the homogeneity of variance assumption was not violated, we will set var.equal to TRUE.

```
t_test(AMOD5210_Part1, Depress ~ Student, var.equal=TRUE)
```

```
## # A tibble: 1 x 8
##   .y.     group1 group2    n1    n2 statistic    df       p
## * <chr>   <chr>  <chr>  <int> <int>     <dbl> <dbl>   <dbl>
## 1 Depress No     Yes      161    39     -2.63   198 0.00908
```

Since, $p < 0.05$, the test shows a significant difference. We have enough evidence to reject the null hypothesis, H_O.

Calculating Cohen's d

Also, the t-Test is significant, we need to calculate **Cohen's d** for our effect size. We need to specify "paired = FALSE" to indicate the groups are independent, and specify "pooled_sd = TRUE" to indicate the variances are equal.

```
cohens_d(Depress ~ Student, data = AMOD5210_Part1, paired = FALSE, pooled_sd = TRUE)
```

```
## Cohen's d |         95% CI
## --------------------------
## -0.47     | [-0.82, -0.12]
##
## - Estimated using pooled SD.
```

Based on Cohen's (1988) conventions we have a small effect.

Step 3 : Conclusion

The current study sought to determine whether or not there is a significant difference between students and non-students on variable "Depress". 200 study participants were randomly sampled from the general public (39 students, 161 non-students). The sample contained no extreme outliers. A Shapiro-Wilks test demonstrated normality by group, and Levene's test demonstrated homogeneity of variance. The mean "Depress" variable of non-students in the sample was 4.826 (SD = 4.445) whereas the mean "Depress" variable of the students in the sample was 6.974 (SD = 5.055). A Welch's independent t-test showed that the mean difference in "Depress" variable between student and non-students in the sample was statistically significant, $t(198) = -2.634914$, $p < 0.05$, $d = -0.47$, with students tending to be more "Depress" than non-students. According to Cohen's (1988) conventions, this is a small effect.

Part 1: Question 2

Using an appropriate inferential statistic and effect size, determine whether there is a significant difference in the proportion of men and women diagnosed with or without depression.

We are going to use a $\chi 2$ Test of Independence for this question.

Step 1 : Hypothesis & Assumptions

The H_0 is Null hypothesis and H_A is Alternative hypothesis.

H_0 : There is no difference in the proportion of men and women diagnosed with or without depression.

vs.

H_A : There is a significant difference in the proportion of men and women diagnosed with or without depression.

Below is the frequency table based on the continuous variable Gender and Dstatus:

```r
frequency_table <- table(AMOD5210_Part1$Gender, AMOD5210_Part1$Dstatus)
frequency_table
```

```
##
##           No Yes
##   Female 137  14
##   Male    47   2
```

Step 2 : Testing

Let us now perform the test, $\chi 2$ **Test of Independence**.

```r
chisq.test(x = frequency_table, correct = FALSE)
```

```
## Warning in chisq.test(x = frequency_table, correct = FALSE): Chi-squared
## approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  frequency_table
## X-squared = 1.3539, df = 1, p-value = 0.2446
```

```r
chisq.posthoc.test(frequency_table)
```

```
## Warning in chisq.test(x, ...): Chi-squared approximation may be incorrect
```

```
##   Dimension     Value        No       Yes
## 1    Female Residuals -1.163565  1.163565
## 2    Female  p values  0.978401  0.978401
## 3      Male Residuals  1.163565 -1.163565
## 4      Male  p values  0.978401  0.978401
```

Since $p > 0.05$ we fail to reject the null hypothesis, H_O.

Let's perform **Post-hoc Analysis** test:

```
chisq.posthoc.test(frequency_table)
```

```
## Warning in chisq.test(x, ...): Chi-squared approximation may be incorrect
```

```
##   Dimension     Value        No       Yes
## 1    Female Residuals -1.163565  1.163565
## 2    Female  p values  0.978401  0.978401
## 3      Male Residuals  1.163565 -1.163565
## 4      Male  p values  0.978401  0.978401
```

Calculating Cohen's d

Now, need to calculate the odds ratio as our **effect size**.

```
oddsratio(frequency_table)
```

```
## Odds ratio |       95% CI
## -------------------------
## 0.42       | [0.09, 1.90]
```

Based on Cohens (1988) conventions, we have less than the small category.

Step 3 : Conclusion

The present research seeks to determine whether there is a significant difference in the proportion of men and women diagnosed with or without depression. 200 people (49 Male, 151 Female) reported if they diagnosed with (16) or without depression (184). A Chi-square Test of Independence revealed that there is no difference in the proportion of men and women diagnosed with or without depression, Chi Squared(1, N = 200) = 1.3539, $p > 0.001$, OR = 0.42. According to Cohen's (1988) conventions, this effect was small.

Part 1: Question 3

Researchers are interested to determine whether character strengths are significant predictors of depression symptoms.

a) Using the Pearson's r correlation and r^2, determine whether there are significant correlations between depression symptoms and the four character strengths variables ("Honesty", "Leader", "Persevere", "Regulation"). Report the r and p-values for each correlation. Also, report r^2 for each correlation.

Fristly, let's see the summary statistics:

```
describe(AMOD5210_Part1, fast = TRUE)
```

```
## Warning in FUN(newX[, i], ...): no non-missing arguments to min; returning Inf

## Warning in FUN(newX[, i], ...): no non-missing arguments to min; returning Inf

## Warning in FUN(newX[, i], ...): no non-missing arguments to min; returning Inf

## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf

## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf

## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf
```

```
##            vars   n   mean     sd min  max range    se
## ID            1 200 468.48 268.94  13  944   931 19.02
## Gender        2 200    NaN     NA Inf -Inf  -Inf    NA
## Student       3 200    NaN     NA Inf -Inf  -Inf    NA
## Honesty       4 200  21.06   2.52  12   25    13  0.18
## Leader        5 200  18.18   3.22   8   25    17  0.23
## Persevere     6 200  19.06   3.40   8   25    17  0.24
## Regulation    7 200  16.59   3.60   6   25    19  0.25
## Health        8 200  16.57   5.11   3   29    26  0.36
## Depress       9 200   5.24   4.64   0   21    21  0.33
## Dstatus      10 200    NaN     NA Inf -Inf  -Inf    NA
```

Now, we need to test some assumptions about our data. Let's, check weather a sample contain any extreme outliers or not?

Let's first check the assumptions **"Honesty" variable**.

```
identify_outliers(AMOD5210_Part1, Honesty)
```

```
## # A tibble: 7 x 12
##      ID Gender Student Honesty Leader Persevere Regulat~1 Health Depress Dstatus
##   <dbl> <chr>  <chr>     <dbl>  <dbl>     <dbl>     <dbl>  <dbl>   <dbl> <chr>
## 1   249 Female No           13     22        10         9     21      20 Yes
## 2   935 Female No           13     18        20        21     16       2 No
## 3    23 Female No           13     20        14        12     22       8 No
## 4    47 Female Yes          15     13        10        14     25      14 No
```

```
## 5   666 Male   Yes          12     15         20         15     15       6 No
## 6   792 Female No           14     11         18         11      8       0 No
## 7   344 Female No           14     15         11         16      4       0 No
## # ... with 2 more variables: is.outlier <lgl>, is.extreme <lgl>, and
## #   abbreviated variable name 1: Regulation
```

Hence, there is no extreme outliers in *"Honesty" variable*.

Checking the **"Leader" variable**.

```
identify_outliers(AMOD5210_Part1, Leader)
```

```
## # A tibble: 1 x 12
##      ID Gender Student Honesty Leader Persevere Regulat~1 Health Depress Dstatus
##   <dbl> <chr>  <chr>     <dbl>  <dbl>     <dbl>     <dbl>  <dbl>   <dbl> <chr>
## 1   385 Male   No           21      8         23         15     19       2 No
## # ... with 2 more variables: is.outlier <lgl>, is.extreme <lgl>, and
## #   abbreviated variable name 1: Regulation
```

Hence, there is no extreme outliers in *"Leader" variable*.

Checking the **"Persevere" variable**.

```
identify_outliers(AMOD5210_Part1, Persevere)
```

```
## # A tibble: 5 x 12
##      ID Gender Student Honesty Leader Persevere Regulat~1 Health Depress Dstatus
##   <dbl> <chr>  <chr>     <dbl>  <dbl>     <dbl>     <dbl>  <dbl>   <dbl> <chr>
## 1   249 Female No           13     22         10          9     21      20 Yes
## 2   180 Female Yes          20     14         10         17     26       6 No
## 3   498 Female Yes          24     16         10          6     21      18 Yes
## 4    47 Female Yes          15     13         10         14     25      14 No
## 5   714 Female No           22     18          8         14     18       9 No
## # ... with 2 more variables: is.outlier <lgl>, is.extreme <lgl>, and
## #   abbreviated variable name 1: Regulation
```

Hence, there is no extreme outliers in *"Persevere" variable*.

Checking the **"Regulation" variable**.

```
identify_outliers(AMOD5210_Part1, Regulation)
```

```
## # A tibble: 1 x 12
##      ID Gender Student Honesty Leader Persevere Regulat~1 Health Depress Dstatus
##   <dbl> <chr>  <chr>     <dbl>  <dbl>     <dbl>     <dbl>  <dbl>   <dbl> <chr>
## 1   498 Female Yes          24     16         10          6     21      18 Yes
## # ... with 2 more variables: is.outlier <lgl>, is.extreme <lgl>, and
## #   abbreviated variable name 1: Regulation
```

Hence, there is no extreme outliers in *"Regulation" variable*.

Now, we will check if the data is **normaly distributed** or not. For that, we will use the *Shapiro-Wilks Test* for this. If $p > 0.05$, the data is normal.

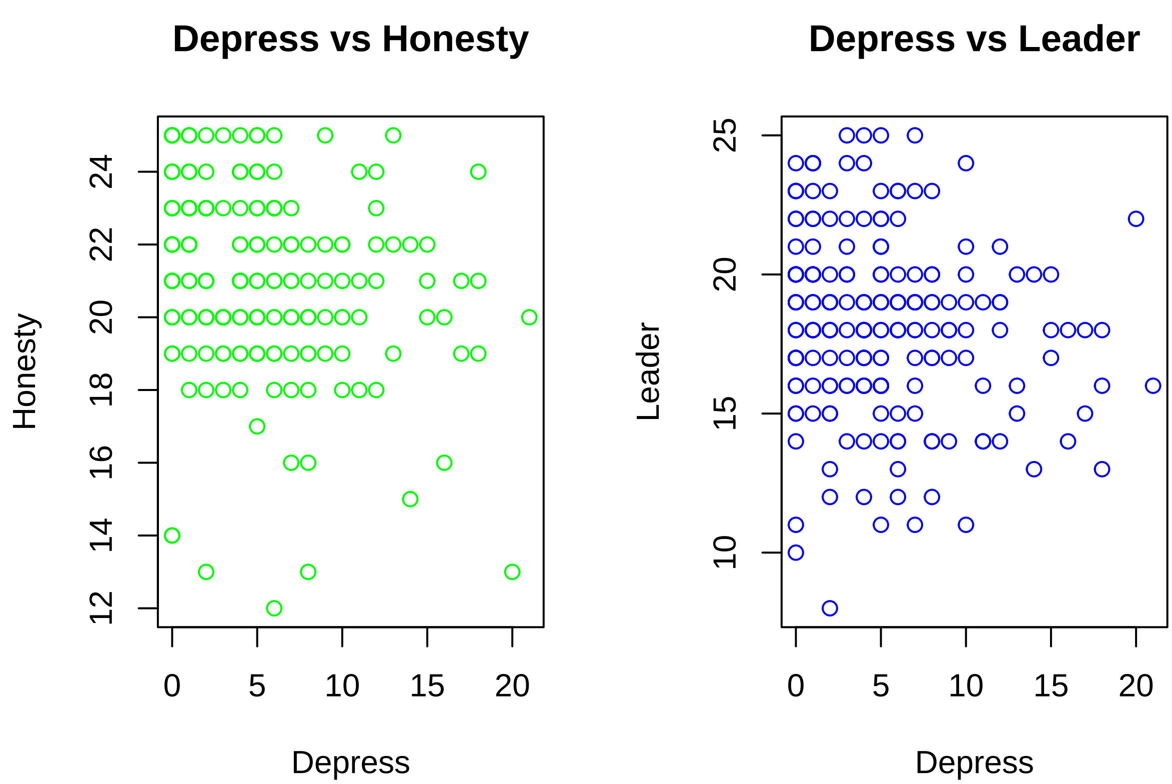
```
shapiro_test(AMOD5210_Part1, vars = c("Honesty", "Leader", "Persevere", "Regulation"))
```

```
## # A tibble: 4 x 3
##   variable   statistic            p
##   <chr>          <dbl>        <dbl>
## 1 Honesty        0.933 0.0000000641
## 2 Leader         0.982 0.0105
## 3 Persevere      0.959 0.0000151
## 4 Regulation     0.978 0.00305
```

Here, we can see that the $p < 0.05$ for all the four variables, that is, "Honesty", "Leader", "Persevere", "Regulation". And we can say that, the data is not Normal Distribution.

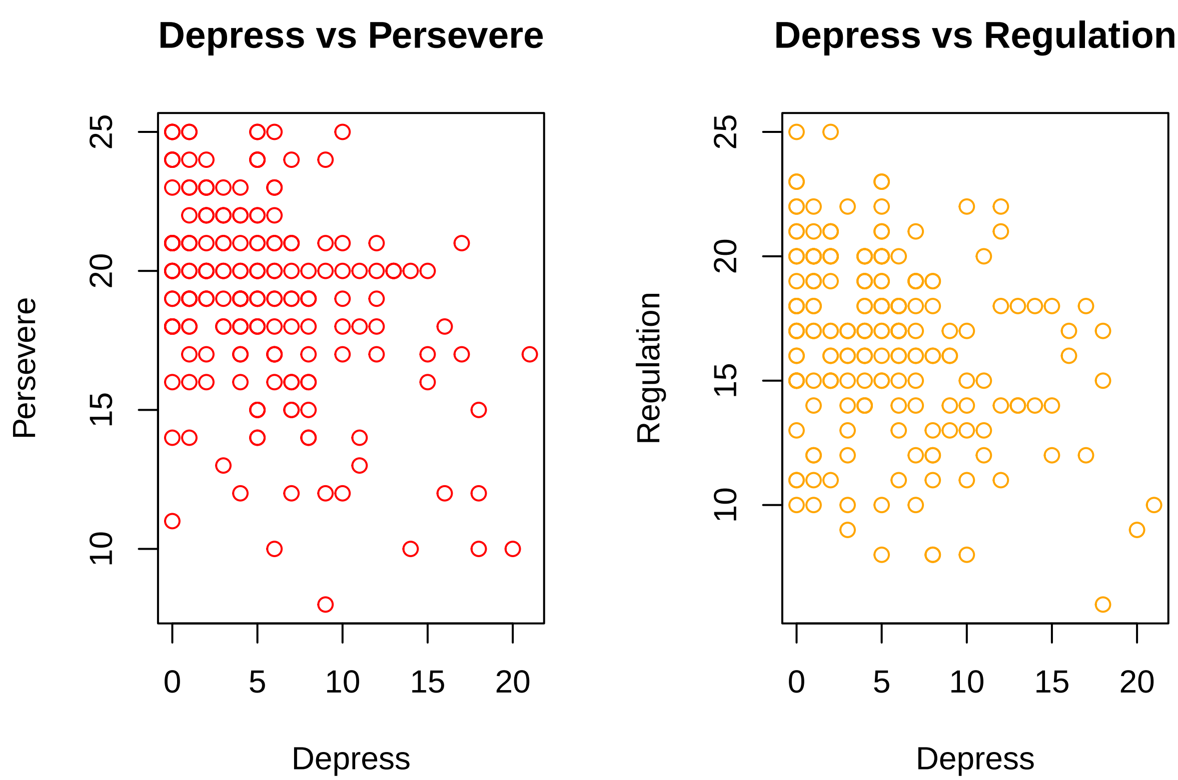
Finally, we need to check the *Linearity* for all the four variables, that is, "Honesty", "Leader", "Persevere", "Regulation".

```
# Checking Linearity for all of the four with respect to depress variable
par(mfrow=c(1,2))
plot(AMOD5210_Part1$Depress, AMOD5210_Part1$Honesty
     , col = "green", xlab = "Depress", ylab = "Honesty"
     , main = "Depress vs Honesty")
plot(AMOD5210_Part1$Depress, AMOD5210_Part1$Leader
     , col = "blue", xlab = "Depress", ylab = "Leader"
     , main = "Depress vs Leader")
```



```
par(mfrow=c(1,2))
plot(AMOD5210_Part1$Depress, AMOD5210_Part1$Persevere
     , col = "red", xlab = "Depress", ylab = "Persevere"
       , main = "Depress vs Persevere")

plot(AMOD5210_Part1$Depress, AMOD5210_Part1$Regulation
     , col = "orange", xlab = "Depress", ylab = "Regulation"
     , main = "Depress vs Regulation")
```



None of the four variables shows the Linearity. Hence, we can say that the Linearity condition is not satisfied.

Pearson's r Correlation test

Now, we will run **Pearson's r Correlation test** for all the four variables, that is, "Honesty", "Leader", "Persevere", "Regulation".

The proportion of variability in Depress variable explained by the other Honesty is given below:

```
corr_honesty <- corr.test(AMOD5210_Part1$Depress, AMOD5210_Part1$Honesty, method = "pearson")
corr_honesty
```

```
## Call:corr.test(x = AMOD5210_Part1$Depress, y = AMOD5210_Part1$Honesty,
##     method = "pearson")
## Correlation matrix
## [1] -0.24
## Sample Size
## [1] 200
```

```
## These are the unadjusted probability values.
##   The probability values  adjusted for multiple tests are in the p.adj object.
## [1] 0
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

The values are given below:

```
# p-Value is
corr_honesty$p
```

```
## [1] 0.0006999901
```

```
# R Value is
corr_honesty$r
```

```
## [1] -0.2377245
```

```
# R Square Value, coefficient of determination is
corr_honesty$r^2
```

```
## [1] 0.05651294
```

The *p-value* is **0.00069**.Here, $p - value < 0.05$, this Correlation for Depress vs Honesty is not significant.

The **Pearson's**, r is **-0.23** and **coefficient of determination**, r^2 is **0.056**. Hence, both shows **small** effect sizes.

The proportion of variability in Depress variable explained by the other Leader is given below:

```
corr_leader <- corr.test(AMOD5210_Part1$Depress, AMOD5210_Part1$Leader, method = "pearson")
corr_leader
```

```
## Call:corr.test(x = AMOD5210_Part1$Depress, y = AMOD5210_Part1$Leader,
##     method = "pearson")
## Correlation matrix
## [1] -0.16
## Sample Size
## [1] 200
## These are the unadjusted probability values.
##   The probability values  adjusted for multiple tests are in the p.adj object.
## [1] 0.03
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

The values are given below:

```
# p-Value is
corr_leader$p
```

```
## [1] 0.02792895
```

```r
# R Value is
corr_leader$r
```

```
## [1] -0.1554702
```

```r
# R Square Value, coefficient of determination is
corr_leader$r^2
```

```
## [1] 0.02417097
```

The *p-value* is **0.027**.Here, $p - value < 0.05$, this Correlation for Depress vs Honesty is not significant.

The **Pearson's**, r is **-0.15** and **coefficient of determination**, r^2 is **0.024**. Hence, both shows **small** effect sizes.

The proportion of variability in Depress variable explained by the other Persevere is given below:

```r
corr_persevere <- corr.test(AMOD5210_Part1$Depress, AMOD5210_Part1$Persevere, method = "pearson")
corr_persevere
```

```
## Call:corr.test(x = AMOD5210_Part1$Depress, y = AMOD5210_Part1$Persevere,
##     method = "pearson")
## Correlation matrix
## [1] -0.37
## Sample Size
## [1] 200
## These are the unadjusted probability values.
##   The probability values  adjusted for multiple tests are in the p.adj object.
## [1] 0
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

The values are given below:

```r
# p-Value is
corr_persevere$p
```

```
## [1] 5.462712e-08
```

```r
# R Value is
corr_persevere$r
```

```
## [1] -0.3727463
```

```r
# R Square Value, coefficient of determination is
corr_persevere$r^2
```

```
## [1] 0.1389398
```

The *p-value* is **5.462712e-08**.Here, $p-value < 0.05$, this Correlation for Depress vs Honesty is not significant.

The **Pearson's**, r is **-0.37** and **coefficient of determination**, r^2 is **0.14**. Hence, both shows **moderate** effect sizes.

The proportion of variability in Depress variable explained by the other Regulation is given below:

```
corr_regulation <- corr.test(AMOD5210_Part1$Depress, AMOD5210_Part1$Regulation, method = "pearson")
corr_regulation
```

```
## Call:corr.test(x = AMOD5210_Part1$Depress, y = AMOD5210_Part1$Regulation,
##     method = "pearson")
## Correlation matrix
## [1] -0.3
## Sample Size
## [1] 200
## These are the unadjusted probability values.
##   The probability values  adjusted for multiple tests are in the p.adj object.
## [1] 0
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

The values are given below:

```
# p-Value is
corr_regulation$p
```

```
## [1] 1.544422e-05
```

```
# R Value is
corr_regulation$r
```

```
## [1] -0.3004228
```

```
# R Square Value, coefficient of determination is
corr_regulation$r^2
```

```
## [1] 0.09025385
```

The *p-value* is **1.544422e-05**.Here, $p-value < 0.05$, this Correlation for Depress vs Honesty is not significant.

The **Pearson's**, r is $-$**0.3004** and **coefficient of determination**, r^2 is **0.0902**. Hence, both shows **moderate** effect sizes.

b) Using multiple linear regression, determine whether the four character strengths variables are significant predictors of depression symptoms. Report the slopes and p-values for each character strength and identify which character strengths were significant predictors. Also report and interpret the multiple R^2 for the overall model.

We can create our model using the lm() function and store the model as an object, to test **multiple regression test**. Then, we will check the summary.

```r
regress.model <- lm(Depress ~ Honesty + Leader + Persevere + Regulation
         , data = AMOD5210_Part1)
summary(regress.model)
```

```
##
## Call:
## lm(formula = Depress ~ Honesty + Leader + Persevere + Regulation,
##     data = AMOD5210_Part1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.1388 -2.8512 -0.8262  2.0204 13.3709
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 18.383330   2.787325   6.595 3.89e-10 ***
## Honesty     -0.099070   0.139200  -0.712 0.477496
## Leader      -0.005705   0.103353  -0.055 0.956038
## Persevere   -0.377685   0.109926  -3.436 0.000722 ***
## Regulation  -0.226089   0.091998  -2.458 0.014862 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.268 on 195 degrees of freedom
## Multiple R-squared:  0.1695, Adjusted R-squared:  0.1525
## F-statistic: 9.953 on 4 and 195 DF,  p-value: 2.382e-07
```

The slopes and $p - value$ for each charter strength variables are as followers:

1. Slopes are:

   Honesty -0.099070,
   Leader -0.005705,
   Persevere -0.377685,
   Regulation -0.226089

2. $p - value$ are:

   Honesty 0.477496,
   Leader 0.956038,
   Persevere 0.000722, Regulation 0.014862

We can observed from the values above that "Honesty" and "Leader" have $p-value$ greater than 0.05 making them a significant predictor.

The values of Multiple r^2 is **0.1695**.

According to Cohen's d (Cohen, 1988) conventions, the overall model explained a **moderate** proportion of variability in "Depress" variable.

Part 1: Question 4

Using an appropriate inferential statistic and effect size(s), determine whether participants had significantly different scores across the four character strengths ("honesty", "Leader", "Persevere", "Regulation").

We will use **One Way Repeated Measures ANOVA Test** Inferential Statistic, to check whether participants had significantly different scores across the four character strengths ("honesty", "Leader", "Persevere", "Regulation"). And to measure the effect size, we will use η_p^2, **partial eta squared**.

Step 1 : Hypothesis & Assumptions

The H_0 is Null hypothesis and H_A is Alternative hypothesis.

$$H_0 : \text{The participants does not had significantly different scores across the four character strengths}$$
$$\text{vs.}$$
$$H_A : \text{The participants had significantly different scores across the four character strengths}$$

```r
library(ez)
# Gathering data of different character strengths into one column
strength <- gather(data = AMOD5210_Part1
                    , key = "Character_Strength"
                    , value = "Score", Honesty, Leader, Persevere, Regulation)

# Storing the required data in a new dataframe
data_frame <- strength[ ,c("ID","Character_Strength","Score")]
tail(data_frame,5)
```

```
## # A tibble: 5 x 3
##      ID Character_Strength Score
##   <dbl> <chr>              <dbl>
## 1   186 Regulation            15
## 2   584 Regulation            16
## 3   520 Regulation            25
## 4   636 Regulation            15
## 5   831 Regulation            17
```

Now let's group the data and print the descriptive statistics:

```r
char_group <- group_by(data_frame, Character_Strength)
get_summary_stats(char_group, Score, type = "mean_sd")
```

```
## # A tibble: 4 x 5
##   Character_Strength variable     n  mean    sd
##   <chr>              <fct>    <dbl> <dbl> <dbl>
## 1 Honesty            Score      200  21.1  2.52
## 2 Leader             Score      200  18.2  3.22
## 3 Persevere          Score      200  19.1  3.40
## 4 Regulation         Score      200  16.6  3.60
```

Now, we need to test some **assumptions** about our data.

```
identify_outliers(char_group, Score)
```

```
## # A tibble: 14 x 5
##    Character_Strength    ID Score is.outlier is.extreme
##    <chr>              <dbl> <dbl> <lgl>      <lgl>
##  1 Honesty              249    13 TRUE       FALSE
##  2 Honesty              935    13 TRUE       FALSE
##  3 Honesty               23    13 TRUE       FALSE
##  4 Honesty               47    15 TRUE       FALSE
##  5 Honesty              666    12 TRUE       FALSE
##  6 Honesty              792    14 TRUE       FALSE
##  7 Honesty              344    14 TRUE       FALSE
##  8 Leader               385     8 TRUE       FALSE
##  9 Persevere            249    10 TRUE       FALSE
## 10 Persevere            180    10 TRUE       FALSE
## 11 Persevere            498    10 TRUE       FALSE
## 12 Persevere             47    10 TRUE       FALSE
## 13 Persevere            714     8 TRUE       FALSE
## 14 Regulation           498     6 TRUE       FALSE
```

Here, We get no outliers. We will now test for **normality** from the Score-data. For that, we will use the **Shapiro-Wilks Test**. If $p > 0.05$, the data is normal.

```
shapiro_test(char_group, Score)
```

```
## # A tibble: 4 x 4
##   Character_Strength variable statistic            p
##   <chr>              <chr>        <dbl>        <dbl>
## 1 Honesty            Score        0.933 0.0000000641
## 2 Leader             Score        0.982 0.0105
## 3 Persevere          Score        0.959 0.0000151
## 4 Regulation         Score        0.978 0.00305
```

Here, $p - value < 0.05$ and it can be seen that our data is not normally distributed for all groups. We are still going to proceed with the test.

Step 2 : Testing

Now we will performing **One Way Repeated Measures ANOVA Test**.

```
rep_ANOVA <- ezANOVA(data_frame, dv = Score, wid = ID
                      , within = Character_Strength, type=3
                      , return_aov = TRUE)
```

```
## Warning: Converting "ID" to factor for ANOVA.
```

```
## Warning: Converting "Character_Strength" to factor for ANOVA.
```

```r
# Printing rep_ANOVA
rep_ANOVA
```

```
## $ANOVA
##               Effect DFn DFd        F            p p<.05       ges
## 2 Character_Strength   3 597 99.29093 3.807505e-52     * 0.2016286
##
## $`Mauchly's Test for Sphericity`
##               Effect         W            p p<.05
## 2 Character_Strength 0.8616564 1.900668e-05     *
##
## $`Sphericity Corrections`
##               Effect      GGe        p[GG] p[GG]<.05      HFe        p[HF]
## 2 Character_Strength 0.907239 1.420815e-47         * 0.921045 2.964712e-48
##   p[HF]<.05
## 2         *
##
## $aov
##
## Call:
## aov(formula = formula(aov_formula), data = data)
##
## Grand Mean: 18.72
##
## Stratum 1: ID
##
## Terms:
##                 Residuals
## Sum of Squares    4058.28
## Deg. of Freedom       199
##
## Residual standard error: 4.515902
##
## Stratum 2: ID:Character_Strength
##
## Terms:
##                 Character_Strength Residuals
## Sum of Squares             2075.42   4159.58
## Deg. of Freedom                  3       597
##
## Residual standard error: 2.639597
## Estimated effects may be unbalanced
```

In the ANOVA section, since p-value is less than 0.05, we will **reject** the null hypothesis, H_O. Thus, we can conclude that participants had significantly different scores across the four character strengths.

Calculating **Partial Eta Squared Effect Size Calculation**

Now, need to calculate the **effect size**.

```r
eta_squared(rep_ANOVA$aov, partial = TRUE)
```

```
## # Effect Size for ANOVA (Type I)
```

```
##
## Group                  |          Parameter | Eta2 (partial) |       95% CI
## ---------------------------------------------------------------------------
## ID:Character_Strength | Character_Strength |           0.33 | [0.28, 1.00]
##
## - One-sided CIs: upper bound fixed at [1.00].
```

Hence, η_p^2 is 0.33 and based on Cohen's (1998) conventions, we have a Large Effect.

Now let's run our **post-hoc test**

```
t_test(data_frame, Score ~ Character_Strength, paired = TRUE, p.adjust.method = "bonferroni")
```

```
## # A tibble: 6 x 10
##   .y.   group1    group2        n1    n2 stati~1    df        p    p.adj p.adj~2
## * <chr> <chr>     <chr>      <int> <int>   <dbl> <dbl>    <dbl>    <dbl> <chr>
## 1 Score Honesty   Leader       200   200   12.0    199 2.91e-25 1.75e-24 ****
## 2 Score Honesty   Persevere    200   200    9.02   199 1.58e-16 9.48e-16 ****
## 3 Score Honesty   Regulation   200   200   16.8    199 3.85e-40 2.31e-39 ****
## 4 Score Leader    Persevere    200   200   -3.39   199 8.49e- 4 5   e- 3 **
## 5 Score Leader    Regulation   200   200    5.03   199 1.08e- 6 6.48e- 6 ****
## 6 Score Persevere Regulation   200   200    8.98   199 2.01e-16 1.21e-15 ****
## # ... with abbreviated variable names 1: statistic, 2: p.adj.signif
```

Since adjusted $p < 0.05$ for all of the comparisons, we can say that Scores were Significantly Different across each Character Strength.

calculating effect size for each Pairwise Comparison:

Next, we need to calculate our effect size for each pairwise comparison, cohen's d. Again, we need to use the cohens_d() function from the "rstatix" package, so we first have to detach the "effectsize" package.

```
detach("package:effectsize", unload = TRUE)
```

We also need to specify "paired = TRUE" to indicate the data is paired.

```
cohens_d(data_frame, Score ~ Character_Strength, paired = TRUE)
```

```
## # A tibble: 6 x 7
##   .y.   group1    group2     effsize    n1    n2 magnitude
## * <chr> <chr>     <chr>        <dbl> <int> <int> <ord>
## 1 Score Honesty   Leader       0.847   200   200 large
## 2 Score Honesty   Persevere    0.638   200   200 moderate
## 3 Score Honesty   Regulation   1.19    200   200 large
## 4 Score Leader    Persevere   -0.240   200   200 small
## 5 Score Leader    Regulation   0.356   200   200 small
## 6 Score Persevere Regulation   0.635   200   200 moderate
```

Step 3 : Conclusion

PART 2: DIAGNOSTIC EFFICIENCY STATISTICS

The following questions requires the use of **"diagnostic-data.xlsx"**.

Firstly, loading the required packages and then reading the excel file.

```
library(readxl)
diagnostic_dataset <- read_excel("diagnostic-data.xlsx")
```

Now, let's performing data extraction.

```
set.seed(0758054)
index <- sample(1:nrow(diagnostic_dataset),200)
AMOD5210_Part2 <- diagnostic_dataset[index, ]
```

Part 2: Question 1

Create a 2 x 2 contingency table for the variables Diagnosis and Test. The contingency table you create should include frequencies within each cell, and each row and column of the table should be meaningfully labelled.

To create a 2 x 2 contingency table for the variables Diagnosis and Test, we will first specify our variables are factors and add some labels.

```
AMOD5210_Part2$Test <- factor(AMOD5210_Part2$Test, labels = c("Yes", "No"))
AMOD5210_Part2$Diagnosis <- factor(AMOD5210_Part2$Diagnosis, labels = c("Yes", "No"))
```

Next we will now create a contingency table.

```
table(AMOD5210_Part2$Test, AMOD5210_Part2$Diagnosis, dnn = c("Test", "Diagnosis"))
```

```
##      Diagnosis
## Test  Yes  No
##   Yes 102  28
##   No   24  46
```

Part 2: Question 2

Report the following diagnostic efficiency statistics: a) sensitivity, b) specificity, c) positive prediction value, d) negative prediction value, e) overall correct classification, and f) Kappa

Now, we will use the confusionMatrix function to calculate our the given diagnostic efficiency statistics:

```
confusionMatrix(data = AMOD5210_Part2$Test
                , reference = AMOD5210_Part2$Diagnosis
                , positive = "Yes"
                , dnn = c("Test","Diagnosis"))
```

```
## Confusion Matrix and Statistics
##
##      Diagnosis
## Test  Yes  No
##   Yes 102  28
##   No   24  46
##
##                Accuracy : 0.74
##                  95% CI : (0.6734, 0.7993)
##     No Information Rate : 0.63
##     P-Value [Acc > NIR] : 0.0006357
##
##                   Kappa : 0.436
##
##  Mcnemar's Test P-Value : 0.6773916
##
##             Sensitivity : 0.8095
##             Specificity : 0.6216
##          Pos Pred Value : 0.7846
##          Neg Pred Value : 0.6571
##              Prevalence : 0.6300
##          Detection Rate : 0.5100
##    Detection Prevalence : 0.6500
##       Balanced Accuracy : 0.7156
##
##        'Positive' Class : Yes
##
```

Conclusion:

Following are diagnostic efficiency statistics:

a) Sensitivity = 0.8095,

b) Specificity = 0.6216,

c) Positive Prediction Value = 0.7846,

d) Negative Prediction Value = 0.6571,

e) Overall Correct Classification (Accuracy) = 0.74,

f) Kappa = 0.436

Part 2: Question 3

Based on the diagnostic efficiency statistics reported in Question 2, does the new test accurately diagnose individuals with breast cancer? Explain your answer.

We can observe, through the sensitivity value, that is, **0.8095**, that the test was better at identifying the true positive cases. Also, it was worse in identifying true negative cases. The new test was not accurate in diagnosing breast cancer in individuals due to its low kappa value, that is, **0.436** (As per the conventions for interpreting Kappa).