

```

In [1]: install.packages("mediation")
library(mediation)

# Assume your dataset is named "Data" with columns: study_time, motivation, and
data <- read.csv("Complete_Data_Modified.csv")

# Step 1: Check for normality in the data
# Shapiro-Wilk test for normality
shapiro_test_BFI_E <- shapiro.test(data$BFI..E.)
shapiro_test_PAQ <- shapiro.test(data$PAQ)
shapiro_test_Panas <- shapiro.test(data$Panas..)

# Check the results
print("Shapiro-Wilk Test for Normality:")
print(paste("BFI..E. p-value:", shapiro_test_BFI_E$p.value))
print(paste("PAQ p-value:", shapiro_test_PAQ$p.value))
print(paste("Panas.. p-value:", shapiro_test_Panas$p.value))

#Part2

# Function to perform Shapiro-Wilk test for normality and display p-values
perform_shapiro_test <- function(column_name) {
  shapiro_test <- shapiro.test(data[[column_name]])
  cat("Shapiro-Wilk Test for Normality of", column_name, ":\n")
  print(paste("p-value:", shapiro_test$p.value))
}

# List of columns to test for normality
columns_to_test <- c('Panas..', 'Panas...1', 'BFI..E.', 'BFI..A.', 'BFI..C.', 'B

# Perform Shapiro-Wilk test for normality for each column
for (column in columns_to_test) {
  perform_shapiro_test(column)
}

#Part3

#the code to check the p-values from the Shapiro-Wilk test and display "Check" i

# Create a vector with column names to test
columns_to_test <- c('Panas..', 'Panas...1', 'BFI..E.', 'BFI..A.', 'BFI..C.', 'B

# Function to perform Shapiro-Wilk test and display the result
check_normality <- function(column) {
  shapiro_test_result <- shapiro.test(data[[column]])
  if (shapiro_test_result$p.value < 0.05) {
    return("Check")
  } else {
    return("Okay")
  }
}

# Check for normality in each column
normality_results <- sapply(columns_to_test, check_normality)

```

```
# Display the results
print("Shapiro-Wilk Test Results:")
for (i in seq_along(columns_to_test)) {
  print(paste(columns_to_test[i], ":", normality_results[i]))
}
```

also installing the dependencies 'pkgbuild', 'diffobj', 'brio', 'desc', 'pkgload', 'praise', 'waldo', 'checkmate', 'testthat', 'gridExtra', 'htmlTable', 'viridis', 'Formula', 'minqa', 'nloptr', 'mvtnorm', 'sandwich', 'lpSolve', 'Hmisc', 'lme4'

Updating HTML index of packages in '.Library'

Making 'packages.html' ...  
done

Loading required package: MASS

Loading required package: Matrix

Loading required package: mvtnorm

Loading required package: sandwich

mediation: Causal Mediation Analysis  
Version: 4.5.0

```

[1] "Shapiro-Wilk Test for Normality:"
[1] "BFI..E. p-value: 3.29237521349037e-21"
[1] "PAQ p-value: 1.95572976553528e-19"
[1] "Panas.. p-value: 7.56102739778441e-18"
Shapiro-Wilk Test for Normality of Panas.. :
[1] "p-value: 7.56102739778441e-18"
Shapiro-Wilk Test for Normality of Panas...1 :
[1] "p-value: 1.91915341924237e-23"
Shapiro-Wilk Test for Normality of BFI..E. :
[1] "p-value: 3.29237521349037e-21"
Shapiro-Wilk Test for Normality of BFI..A. :
[1] "p-value: 8.09747790119096e-19"
Shapiro-Wilk Test for Normality of BFI..C. :
[1] "p-value: 1.88065272166195e-20"
Shapiro-Wilk Test for Normality of BFI..N. :
[1] "p-value: 5.36904642737447e-19"
Shapiro-Wilk Test for Normality of BFI..O. :
[1] "p-value: 2.5812672934441e-23"
Shapiro-Wilk Test for Normality of EI..Self.A. :
[1] "p-value: 0.000230365680987184"
Shapiro-Wilk Test for Normality of EI..Self.M. :
[1] "p-value: 0.0005207026265117"
Shapiro-Wilk Test for Normality of EI..Social.A. :
[1] "p-value: 1.52105617368305e-07"
Shapiro-Wilk Test for Normality of EI..RM. :
[1] "p-value: 0.0116185274778922"
Shapiro-Wilk Test for Normality of Total :
[1] "p-value: 8.24612819044015e-12"
Shapiro-Wilk Test for Normality of PAQ :
[1] "p-value: 1.95572976553528e-19"
Shapiro-Wilk Test for Normality of CBCL :
[1] "p-value: 9.33865775872313e-19"
[1] "Shapiro-Wilk Test Results:"
[1] "Panas.. : Check"
[1] "Panas...1 : Check"
[1] "BFI..E. : Check"
[1] "BFI..A. : Check"
[1] "BFI..C. : Check"
[1] "BFI..N. : Check"
[1] "BFI..O. : Check"
[1] "EI..Self.A. : Check"
[1] "EI..Self.M. : Check"
[1] "EI..Social.A. : Check"
[1] "EI..RM. : Check"
[1] "Total : Check"
[1] "PAQ : Check"
[1] "CBCL : Check"

```

```

In [3]: # Load required library for Kolmogorov-Smirnov test
if (!requireNamespace("lawstat", quietly = TRUE)) {
  install.packages("lawstat")
}
library(lawstat)

data <- read.csv("Complete_Data_Modified.csv")

# Perform Kolmogorov-Smirnov test for normality for each column
for (col_name in colnames(data)) {

```

```

ks_test_result <- ks.test(data[[col_name]], "pnorm")
print(paste("Column:", col_name))
print(paste("Test statistic:", ks_test_result$statistic))
print(paste("P-value:", ks_test_result$p.value))
if (ks_test_result$p.value < 0.05) {
  print("The distribution is significantly different from normal.")
} else {
  print("The distribution is not significantly different from normal.")
}
cat("\n")
}

```

Warning message in ks.test.default(data[[col\_name]], "pnorm"):  
 "ties should not be present for the Kolmogorov-Smirnov test"

```

[1] "Column: Panas.."
[1] "Test statistic: 0.841344746068543"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."

```

Warning message in ks.test.default(data[[col\_name]], "pnorm"):  
 "ties should not be present for the Kolmogorov-Smirnov test"

```

[1] "Column: Panas...1"
[1] "Test statistic: 0.841344746068543"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."

```

Warning message in ks.test.default(data[[col\_name]], "pnorm"):  
 "ties should not be present for the Kolmogorov-Smirnov test"

```

[1] "Column: BFI..E."
[1] "Test statistic: 0.841344746068543"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."

```

Warning message in ks.test.default(data[[col\_name]], "pnorm"):  
 "ties should not be present for the Kolmogorov-Smirnov test"

```

[1] "Column: BFI..A."
[1] "Test statistic: 0.841344746068543"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."

```

Warning message in ks.test.default(data[[col\_name]], "pnorm"):  
 "ties should not be present for the Kolmogorov-Smirnov test"

```

[1] "Column: BFI..C."
[1] "Test statistic: 0.841344746068543"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."

```

Warning message in ks.test.default(data[[col\_name]], "pnorm"):  
 "ties should not be present for the Kolmogorov-Smirnov test"

```

[1] "Column: BFI..N."
[1] "Test statistic: 0.923851809799394"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."

```

Warning message in ks.test.default(data[[col\_name]], "pnorm"):  
 "ties should not be present for the Kolmogorov-Smirnov test"

```
[1] "Column: BFI..O."
[1] "Test statistic: 0.894725596207161"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."
```

```
Warning message in ks.test.default(data[[col_name]], "pnorm"):
"ties should not be present for the Kolmogorov-Smirnov test"
```

```
[1] "Column: EI..Self.A."
[1] "Test statistic: 1"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."
```

```
Warning message in ks.test.default(data[[col_name]], "pnorm"):
"ties should not be present for the Kolmogorov-Smirnov test"
```

```
[1] "Column: EI..Self.M."
[1] "Test statistic: 1"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."
```

```
Warning message in ks.test.default(data[[col_name]], "pnorm"):
"ties should not be present for the Kolmogorov-Smirnov test"
```

```
[1] "Column: EI..Social.A."
[1] "Test statistic: 1"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."
```

```
Warning message in ks.test.default(data[[col_name]], "pnorm"):
"ties should not be present for the Kolmogorov-Smirnov test"
```

```
[1] "Column: EI..RM."
[1] "Test statistic: 1"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."
```

```
Warning message in ks.test.default(data[[col_name]], "pnorm"):
"ties should not be present for the Kolmogorov-Smirnov test"
```

```
[1] "Column: Total"
[1] "Test statistic: 0.928706178731432"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."
```

```
Warning message in ks.test.default(data[[col_name]], "pnorm"):
"ties should not be present for the Kolmogorov-Smirnov test"
```

```
[1] "Column: PAQ"
[1] "Test statistic: 0.841344746068543"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."
```

```
Warning message in ks.test.default(data[[col_name]], "pnorm"):
"ties should not be present for the Kolmogorov-Smirnov test"
```

```
[1] "Column: CBCL"
[1] "Test statistic: 0.841344746068543"
[1] "P-value: 0"
[1] "The distribution is significantly different from normal."
```

```
In [4]: # Load required library for Shapiro-Wilk test
if (!requireNamespace("stats", quietly = TRUE)) {
  install.packages("stats")
}
```

```
}  
library(stats)  
  
data <- read.csv("Complete_Data_Modified.csv")  
  
# Perform Shapiro-Wilk test for normality for each column  
for (col_name in colnames(data)) {  
  shapiro_test_result <- shapiro.test(data[[col_name]])  
  print(paste("Column:", col_name))  
  print(paste("Test statistic:", shapiro_test_result$statistic))  
  print(paste("P-value:", shapiro_test_result$p.value))  
  if (shapiro_test_result$p.value < 0.05) {  
    print("The distribution is significantly different from normal.")  
  } else {  
    print("The distribution is not significantly different from normal.")  
  }  
  cat("\n")  
}
```

```
[1] "Column: Panas.."
[1] "Test statistic: 0.735732456276337"
[1] "P-value: 7.56102739778441e-18"
[1] "The distribution is significantly different from normal."

[1] "Column: Panas...1"
[1] "Test statistic: 0.518613225763599"
[1] "P-value: 1.91915341924237e-23"
[1] "The distribution is significantly different from normal."

[1] "Column: BFI..E."
[1] "Test statistic: 0.617177554096594"
[1] "P-value: 3.29237521349037e-21"
[1] "The distribution is significantly different from normal."

[1] "Column: BFI..A."
[1] "Test statistic: 0.704828178305341"
[1] "P-value: 8.09747790119096e-19"
[1] "The distribution is significantly different from normal."

[1] "Column: BFI..C."
[1] "Test statistic: 0.646791650473648"
[1] "P-value: 1.88065272166195e-20"
[1] "The distribution is significantly different from normal."

[1] "Column: BFI..N."
[1] "Test statistic: 0.698864559678619"
[1] "P-value: 5.36904642737447e-19"
[1] "The distribution is significantly different from normal."

[1] "Column: BFI..O."
[1] "Test statistic: 0.524770217806934"
[1] "P-value: 2.5812672934441e-23"
[1] "The distribution is significantly different from normal."

[1] "Column: EI..Self.A."
[1] "Test statistic: 0.970130140690256"
[1] "P-value: 0.000230365680987184"
[1] "The distribution is significantly different from normal."

[1] "Column: EI..Self.M."
[1] "Test statistic: 0.972891364629576"
[1] "P-value: 0.0005207026265117"
[1] "The distribution is significantly different from normal."

[1] "Column: EI..Social.A."
[1] "Test statistic: 0.93971326712911"
[1] "P-value: 1.52105617368305e-07"
[1] "The distribution is significantly different from normal."

[1] "Column: EI..RM."
[1] "Test statistic: 0.982508397052503"
[1] "P-value: 0.0116185274778922"
[1] "The distribution is significantly different from normal."

[1] "Column: Total"
[1] "Test statistic: 0.878581522917102"
[1] "P-value: 8.24612819044015e-12"
[1] "The distribution is significantly different from normal."
```

```
[1] "Column: PAQ"  
[1] "Test statistic: 0.683825869387246"  
[1] "P-value: 1.95572976553528e-19"  
[1] "The distribution is significantly different from normal."  
  
[1] "Column: CBCL"  
[1] "Test statistic: 0.706877246551081"  
[1] "P-value: 9.33865775872313e-19"  
[1] "The distribution is significantly different from normal."
```

In [ ]: