```
In [1]: #Glm Test for P-value
        # Load your data
        data <- read.csv("Pilot_modified_data_1.csv")</pre>
        # Define your variables
        independent_variables <- c('BFI..E.', 'BFI..A.', 'BFI..C.', 'BFI..N.', 'BFI..O.',</pre>
        mediator_variable <- 'PAQ'</pre>
        dependent variables <- c('Panas...', 'Panas...1', 'CBCL')</pre>
        # Function to calculate star ratings
        get star rating <- function(p value) {</pre>
          if (p_value < 0.001) return("***")</pre>
          else if (p_value < 0.01) return("**")</pre>
          else if (p_value < 0.05) return("*")
          else return("check")
        # Fit separate Poisson GLM models for each dependent variable
        for (dependent_variable in dependent_variables) {
          formula <- paste(dependent_variable, "~ . +", mediator_variable)</pre>
          poisson_model <- glm(formula, data = data, family = poisson(link = "log"))</pre>
          # Summarize the model
          cat("Summary for", dependent_variable, ":\n")
          model_summary <- summary(poisson_model)</pre>
          print(model_summary)
          # Get and print star ratings for p-values
          p_values <- model_summary$coefficients[, "Pr(>|z|)"]
          star_ratings <- sapply(p_values, get_star_rating)</pre>
          star_ratings_df <- data.frame(Coefficient = rownames(model_summary$coefficients),</pre>
          print(star ratings df)
          print("==========="")
```

```
Summary for Panas..:
Call:
glm(formula = formula, family = poisson(link = "log"), data = data)
Deviance Residuals:
               10
                      Median
                                   3Q
                                            Max
-0.127254 -0.030803 -0.004841 0.030804
                                        0.236661
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)
            0.8376069 2.7176884 0.308
                                          0.758
Panas...1 -0.0035951 0.2941212 -0.012
                                          0.990
BFI..E.
          -0.0490939 0.4710388 -0.104
                                         0.917
BFI..A.
           0.0071564 0.2813401 0.025
                                         0.980
BFI..C.
           0.0366116 0.4633167 0.079 0.937
BFI..N.
           0.0525955 0.2210784 0.238 0.812
BFI..0. -0.0122170 0.3629494 -0.034 0.973
EI..Self.A. 0.0008079 0.0183715 0.044 0.965
EI..Self.M. -0.0021908 0.0143532 -0.153 0.879
EI..Social.A. 0.0023679 0.0235086 0.101 0.920
           -0.0001474 0.0164597 -0.009 0.993
EI..RM.
Total
           -0.0173123 0.3458867 -0.050 0.960
PAQ
           0.0146337 0.2688049 0.054 0.957
CBCL
            -0.1406602 0.4055748 -0.347
                                         0.729
(Dispersion parameter for poisson family taken to be 1)
   Null deviance: 0.41816 on 33 degrees of freedom
Residual deviance: 0.15941 on 20 degrees of freedom
AIC: 117.4
Number of Fisher Scoring iterations: 3
              Coefficient Stars
(Intercept)
              (Intercept) check
Panas...1
              Panas...1 check
BFI..E.
                BFI..E. check
BFI..A.
                 BFI..A. check
BFI..C.
                BFI..C. check
BFI..N.
                BFI..N. check
BFI..O.
                 BFI..O. check
EI..Self.A. EI..Self.A. check
             EI..Self.M. check
EI..Self.M.
EI..Social.A. EI..Social.A. check
EI..RM.
                 EI..RM. check
Total
                   Total check
PAO
                     PAQ check
CBCL
                    CBCL check
[1] "-----"
Summary for Panas...1:
Call:
glm(formula = formula, family = poisson(link = "log"), data = data)
Deviance Residuals:
```

```
Min
            10
                 Median
                             3Q
                                     Max
-0.6553 -0.3270 -0.0017
                         0.2423
                                  0.5873
Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)
             0.889891 4.349013 0.205
                                          0.838
Panas..
            -0.149219
                      1.404358 -0.106
                                          0.915
BFI..E.
            -0.146126
                      0.531573 -0.275
                                          0.783
BFI..A.
            -0.033461 0.324314 -0.103
                                          0.918
BFI..C.
                      0.543706 0.284
            0.154399
                                          0.776
BFI..N.
             0.062337 0.295745 0.211
                                          0.833
BFI..O.
           -0.280332 0.419729 -0.668
                                          0.504
EI..Self.A.
             0.003700 0.020197 0.183
                                          0.855
EI..Self.M. -0.000276 0.017381 -0.016
                                          0.987
EI..Social.A. 0.002127 0.027020
                                0.079
                                          0.937
EI..RM.
            -0.007422 0.017756 -0.418
                                          0.676
Total
             0.060747 0.382359 0.159
                                          0.874
PAQ
             0.082828 0.304525 0.272
                                          0.786
CBCL
             0.089480 0.656400 0.136
                                          0.892
(Dispersion parameter for poisson family taken to be 1)
   Null deviance: 5.7187 on 33 degrees of freedom
Residual deviance: 3.8829 on 20 degrees of freedom
AIC: 110.93
Number of Fisher Scoring iterations: 4
              Coefficient Stars
(Intercept)
              (Intercept) check
Panas..
                  Panas.. check
BFI..E.
                  BFI..E. check
                 BFI..A. check
BFI..A.
                  BFI..C. check
BFI..C.
BFI..N.
                  BFI..N. check
BFI..O.
                  BFI..O. check
EI..Self.A.
             EI..Self.A. check
EI..Self.M.
             EI..Self.M. check
EI..Social.A. EI..Social.A. check
EI..RM.
                  EI..RM. check
Total
                    Total check
PAO
                      PAQ check
CBCL
                     CBCL check
[1] "-----"
Summary for CBCL :
glm(formula = formula, family = poisson(link = "log"), data = data)
Deviance Residuals:
    Min
              1Q
                    Median
                                 3Q
                                         Max
-0.60355 -0.06141
                   0.02928
                            0.07397
                                     0.28235
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)
             2.104e+00 3.339e+00
                                   0.630
                                           0.529
```

```
Panas..
                   -8.260e-01 1.114e+00 -0.741
                                                    0.459
        Panas...1
                    2.974e-02 3.034e-01 0.098
                                                    0.922
        BFI..E. -1.124e-01 4.808e-01 -0.234 0.815
BFI..A. -4.170e-02 2.832e-01 -0.147 0.883
        BFI..C.
                    1.188e-01 4.719e-01 0.252 0.801
        BFI..N.
                    9.358e-02 2.512e-01 0.373 0.709
        BFI..O. -7.562e-02 3.670e-01 -0.206 0.837
        EI..Self.A. 1.366e-04 1.894e-02 0.007 0.994
        EI..Self.M. -3.774e-03 1.527e-02 -0.247 0.805
        EI..Social.A. 7.694e-03 2.340e-02 0.329 0.742
        EI..RM. -1.222e-05 1.706e-02 -0.001 0.999
                   -9.119e-02 3.408e-01 -0.268 0.789
        Total
                    6.153e-02 2.703e-01 0.228 0.820
        PA0
        (Dispersion parameter for poisson family taken to be 1)
           Null deviance: 2.2148 on 33 degrees of freedom
        Residual deviance: 1.1489 on 20 degrees of freedom
        AIC: 115.56
        Number of Fisher Scoring iterations: 4
                       Coefficient Stars
        (Intercept)
                      (Intercept) check
        Panas..
                         Panas.. check
        Panas...1
                       Panas...1 check
        BFI..E.
                         BFI..E. check
                         BFI..A. check
        BFI..A.
        BFI..C.
                         BFI..C. check
        BFI..N.
                         BFI..N. check
        BFI..O.
                         BFI..O. check
       EI..Self.A. EI..Self.A. check
EI..Self.M. EI..Self.M. check
        EI..Social.A. EI..Social.A. check
                         EI..RM. check
        EI..RM.
        Total
                            Total check
        PAQ
                              PAQ check
        [1] "-----"
In [5]: # Bootstrapping code to run for 150 iterations . Can be expanded later
        # Load your data (assuming 'data' is already loaded)
        # data <- read.csv("your_data.csv")</pre>
        data <- read.csv("Pilot_modified_data_1.csv")</pre>
        # Define your variables
        independent_vars <- c('BFI..E.', 'BFI..A.', 'BFI..C.', 'BFI..N.', 'BFI..O.', 'EI..S
        dependent_vars <- c('Panas...', 'Panas...1', 'CBCL')</pre>
        mediator_var <- 'PAQ'</pre>
        # Set the new sample size , here taken 150
        new_sample_size <- 150</pre>
        # Create an empty data frame to store the bootstrapped data
        data2 <- data.frame(matrix(NA, ncol = length(independent_vars) + length(dependent_v</pre>
        colnames(data2) <- c(independent_vars, dependent_vars, mediator_var)</pre>
```

```
# Perform bootstrapping
for (i in 1:new_sample_size) {
 # Generate a random sample with replacement from the original data
  random_indices <- sample(nrow(data), replace = TRUE)</pre>
  bootstrap_sample <- data[random_indices, ]</pre>
 # Store the bootstrap sample in data2
  data2[i, ] <- bootstrap_sample</pre>
# Now data2 contains the bootstrapped data with the new sample size
head(data2)
```

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Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
"replacement element 13 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
"replacement element 14 has 34 rows to replace 1 rows"
```

```
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
"replacement element 1 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
c(2L, :
"replacement element 2 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
c(2L, :
"replacement element 3 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
c(2L, :
"replacement element 4 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
"replacement element 5 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
"replacement element 6 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
c(2L, :
"replacement element 7 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
c(2L, :
"replacement element 8 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
c(2L, :
"replacement element 9 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
c(2L, :
"replacement element 10 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
"replacement element 11 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
"replacement element 12 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
c(2L, :
"replacement element 13 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
c(2L, :
"replacement element 14 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
c(2L, :
"replacement element 1 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
"replacement element 2 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
"replacement element 3 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
c(2L, :
"replacement element 4 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
c(2L, :
```

```
"replacement element 5 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
c(2L, :
"replacement element 6 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
c(2L, :
"replacement element 7 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
"replacement element 8 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
"replacement element 9 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
c(2L, :
"replacement element 10 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =</pre>
c(2L, :
"replacement element 11 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
c(2L, :
"replacement element 12 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
c(2L, :
"replacement element 13 has 34 rows to replace 1 rows"
Warning message in `[<-.data.frame`(`*tmp*`, i, , value = structure(list(Panas.. =
"replacement element 14 has 34 rows to replace 1 rows"
```

A data.frame: 6×14

	BFIE.	BFIA.	BFIC.	BFIN.	BFIO.	ElSelf.A.	ElSelf.M.	ElSocial.A.	EIRM.	Total	Panas
	<int></int>	<int< th=""></int<>									
1	2	1	2	2	2	2	3	73	65	62	7
2	2	1	2	3	2	3	2	89	62	88	7
3	2	1	2	3	2	2	3	67	68	74	6
4	2	1	2	2	2	1	2	67	49	74	6
5	2	2	1	2	2	2	2	70	76	79	7
6	2	2	2	2	1	3	2	79	62	62	5

```
In [7]: #Confidence levels for the dependent variables Only
         # Load your data (assuming 'data' is already loaded)
         # data <- read.csv("your_data.csv")</pre>
         data <- read.csv("Pilot_modified_data_1.csv")</pre>
         # Define your variables
         independent vars <- c('BFI..E.', 'BFI..A.', 'BFI..C.', 'BFI..N.', 'BFI..O.', 'EI..S
         dependent_vars <- c('Panas...', 'Panas...1', 'CBCL')</pre>
         mediator_var <- 'PAQ'</pre>
         # Set the new sample size, here taken 150
```

```
new_sample_size <- 150</pre>
        # Number of bootstrapping iterations
        num_iterations <- 1000 # You can adjust this number as needed
        # Create empty data frames to store bootstrapped statistics and confidence interval
        bootstrap_stats <- data.frame(matrix(NA, ncol = length(dependent_vars), nrow = num_
        colnames(bootstrap_stats) <- dependent_vars</pre>
        confidence intervals <- data.frame(matrix(NA, ncol = length(dependent vars), nrow =
        rownames(confidence_intervals) <- c("Lower", "Upper")</pre>
        colnames(confidence_intervals) <- dependent_vars</pre>
        # Perform bootstrapping
        for (i in 1:num_iterations) {
         for (dependent var in dependent vars) {
           # Generate a random sample with replacement from the original data
           random_indices <- sample(nrow(data), replace = TRUE)</pre>
           bootstrap_sample <- data[random_indices, ]</pre>
           # Calculate the statistic of interest for the bootstrap sample
           # Here, you can calculate any statistic you're interested in (e.g., mean, media
           bootstrap_statistic <- mean(bootstrap_sample[[dependent_var]]) # Example: mean</pre>
           # Store the bootstrap statistic in the bootstrap_stats data frame
           bootstrap_stats[i, dependent_var] <- bootstrap_statistic</pre>
          }
        # Calculate and display confidence intervals
        for (dependent_var in dependent_vars) {
          lower <- quantile(bootstrap_stats[, dependent_var], 0.025)</pre>
          upper <- quantile(bootstrap_stats[, dependent_var], 0.975)</pre>
          confidence_intervals["Lower", dependent_var] <- lower</pre>
          confidence_intervals["Upper", dependent_var] <- upper</pre>
          cat("Confidence Interval for", dependent_var, ":\n")
         cat("Lower Bound:", lower, "\n")
         cat("Upper Bound:", upper, "\n")
          cat("========\n")
        Confidence Interval for Panas..:
        Lower Bound: 2
        Upper Bound: 2.088235
        Confidence Interval for Panas...1:
        Lower Bound: 1.352941
        Upper Bound: 1.705882
        ______
        Confidence Interval for CBCL:
        Lower Bound: 1.764706
        Upper Bound: 1.970588
        ______
In [8]: #Confidence levels for the all variables/columns Only After Bootstrapping
        # Load your data (assuming 'data' is already loaded)
```

```
data <- read.csv("Pilot_modified_data_1.csv")</pre>
# Define your variables
columns_to_bootstrap <- names(data) # Include all columns in the bootstrapping
# Set the new sample size, here taken 150
new_sample_size <- 150</pre>
# Number of bootstrapping iterations
num_iterations <- 1000 # You can adjust this number as needed
# Create empty data frames to store bootstrapped statistics and confidence interval
bootstrap_stats <- data.frame(matrix(NA, ncol = length(columns_to_bootstrap), nrow
colnames(bootstrap_stats) <- columns_to_bootstrap</pre>
confidence intervals <- data.frame(matrix(NA, ncol = length(columns to bootstrap),</pre>
rownames(confidence_intervals) <- c("Lower", "Upper")</pre>
colnames(confidence_intervals) <- columns_to_bootstrap</pre>
# Perform bootstrapping
for (i in 1:num iterations) {
 # Generate a random sample with replacement from the original data
 random indices <- sample(nrow(data), replace = TRUE)</pre>
 bootstrap_sample <- data[random_indices, ]</pre>
 # Calculate the statistic of interest for the bootstrap sample for all columns
 bootstrap_statistics <- sapply(data[, columns_to_bootstrap], function(col) mean(c
 # Store the bootstrap statistics in the bootstrap stats data frame
 bootstrap_stats[i, columns_to_bootstrap] <- bootstrap_statistics</pre>
# Calculate and display confidence intervals for all columns
for (col in columns_to_bootstrap) {
 lower <- quantile(bootstrap_stats[, col], 0.025)</pre>
 upper <- quantile(bootstrap_stats[, col], 0.975)</pre>
 confidence_intervals["Lower", col] <- lower</pre>
 confidence_intervals["Upper", col] <- upper</pre>
 cat("Confidence Interval for", col, ":\n")
 cat("Lower Bound:", lower, "\n")
 cat("Upper Bound:", upper, "\n")
 cat("========\n")
```

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```
Confidence Interval for Panas..:
Lower Bound: 2.029412
Upper Bound: 2.029412
_____
Confidence Interval for Panas...1:
Lower Bound: 1.529412
Upper Bound: 1.529412
______
Confidence Interval for BFI..E.:
Lower Bound: 1.970588
Upper Bound: 1.970588
______
Confidence Interval for BFI..A.:
Lower Bound: 2.088235
Upper Bound: 2.088235
_____
Confidence Interval for BFI..C.:
Lower Bound: 2
Upper Bound: 2
______
Confidence Interval for BFI..N. :
Lower Bound: 2.058824
Upper Bound: 2.058824
______
Confidence Interval for BFI..O. :
Lower Bound: 2.294118
Upper Bound: 2.294118
______
Confidence Interval for EI..Self.A. :
Lower Bound: 77
Upper Bound: 77
_____
Confidence Interval for EI..Self.M. :
Lower Bound: 65.64706
Upper Bound: 65.64706
______
Confidence Interval for EI.. Social.A. :
Lower Bound: 77.76471
Upper Bound: 77.76471
_____
Confidence Interval for FI..RM. :
Lower Bound: 70.41176
Upper Bound: 70.41176
______
Confidence Interval for Total:
Lower Bound: 2.823529
Upper Bound: 2.823529
______
Confidence Interval for PAQ:
Lower Bound: 1.617647
Upper Bound: 1.617647
______
Confidence Interval for CBCL:
Lower Bound: 1.882353
Upper Bound: 1.882353
______
```

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> In [6]: #To display the entire new data set "data2" print(data2)

	BFIE.	BFIA.	BFIC.	BFIN.	BFIO.	EISelf.A.	EISelf.M.
1	2	1	2	2	2	2	3
2	2	1	2	3	2	3	2
3	2	1	2	3	2	2	3
4	2	1	2	2	2	1	2
5	2	2	1	2	2	2	2
6	2	2	2	2	1	3	2
7	2	2	1	1	2	2	2
8	2	2	2	2	2	2	2
9	2	2	2	2	2	2	2
10	2	1	2	3	2	3	2
11	2	2	1	1	2	2	2
12	2	2	2	2	2	2	2
13	2	2	2	2	2	3	2
14	2	2	2	3	2	2	2
15	2	1	2	2	3	2	3
16	2	1	2	2	3	2	3
17	3	1	2	3	2	3	3
		1			2		
18	2		2	2		2	2
19	2	1	2	2	2	2	3
20	2	2	2	3	2	2	2
21	2	1	2	1	1	3	2
22	2	1	2	2	2	1	2
23	2	2	2	2	2	2	2
24	2	2	2	3	2	2	2
25	2	2	2	3	2	2	2
26	2	1	2	2	2	2	3
27	2	2	2	2	1	3	2
28	2	2	1	1	2	2	2
29	2	2	2	2	2	2	2
30	2	2	2	2	2	2	3
31	2	2	1	1	2	2	2
32	2	2	2	2	2	2	3
33	2	1	2	2	2	2	2
34	2	2	2	2	2	2	2
35	2	2	2	2	2	2	2
36	2	2	2	2	2	2	2
37	2	1	2	1	2	2	2
38	2	2	1	1	2	2	2
39	2	2	2	3	2	2	2
40	2	1	2	1	2	2	2
41	2	1	2	2	2	2	3
42	2	1	2	2	2	2	3
43	2	2	2	2	2	3	2
44	2	2	2	2	2	1	2
45	2	1	2	2	2	1	2
46	2	2	2	2	2	2	2
47	2	1	2	2	3	2	3
48	2	1	2	3	2	2	3
46 49	2	1	2	2	2	1	2
50 51	2	2	2	2	2	2	2
51	2	2	2	2	2	1	2
52	2	1	2	3	2	2	3
53	2	1	2	3	2	2	3
54	2	2	2	1	2	3	2
55	2	1	2	2	2	1	2

56	2	1	2	1	1	3	2
						3	
57	2	2	2	2	2		2
58	2	2	2	2	2	2	2
59	2	1	2	2	2	2	2
60	2	2	2	2	2	2	3
61	2	2	3	2	3	2	2
62	2	2	1	1	2	2	2
63	2	2	2	1	2	3	2
64	3	1	2	3	2	3	3
65	2	1	2	2	2	2	3
66	2	2	2	2	2	2	2
67	2	1	2	2	2	3	2
68	2	2	3	2	3	2	
							2
69	2	2	2	2	2	1	2
70	2	1	2	2	2	3	2
71	2	2	1	2	2	2	2
72	2	2	2	2	2	2	2
73	2	1	2	2	2	1	2
74	2	2	2	3	2	2	2
75	2	2	2	2	2	2	2
76	3	1	2	3	2	3	3
77	2	1	2	2	3	2	3
78	2	1	2	2	2	2	3
79	2	1	2	2	2	1	2
80	2	1	2	2	2	3	2
81	2	2	2	2	2	2	2
82	2	2	2	3	2	2	2
83	2	2	2	2	2	1	2
84	2	2	2	2	2	1	2
85	2	2	2	2	2	2	2
86	2	2	2	2	2	2	3
87	2	2	2	3	2	2	2
88	2	2	2	2	2	2	2
89	2	2	2	2	2	3	2
90	3	1	2	3	2	3	3
91	2	1	2	2	2	2	3
92	2	1	2	2	2	1	3
93	2	1	2	2	2	2	3
94	2	1	2	2	2	3	2
95	3	1	2	3	2	3	3
96	2	2	2	1	2	3	2
97	2	2	2	2	1	3	2
98	2	1	2	3	2	3	2
99	2	1	2	2	2	2	3
100	2	2	2	2	2	2	2
101	2	1	2	2	2	2	3
102	2	1	2	2	2	1	2
103	2	2	2	1	2	3	2
104	2	2	2	2	2	2	2
105	2	2	2	2	2	2	3
106	2	2	2	2	2	3	2
107	2	2	2	2	2	2	2
108	2	1	2	2	2	3	2
109	2	1	2	3	2	2	3
110	2	2	2	2	2	3	2
	2	1			2	2	3
111	2	T	2	3	2	۷	3

112	3		1		2	3		2		3		
113	2		1		2	2		2		3		
114	2		2		2	2		2		2		
115	2		2		2	2		2		2		
116	2		1	2	2	2		2		2		
117	2		2	2	2	2		2		2		
118	2		1		2	2		2		1		
119	2		1		<u>-</u> 2	2		2		2		
120	2		1		2	2		2		1		
121	2		1		2	1		1		3		
122	2		2		2	3		2		2		
123	2		1	2	2	1		1		3		
124	2		2	2	2	2		2		3		
125	3		1		2	3		2		3		
126	2		1		2	2		2		1		
127	2		2		- L	2		2		2		
128	2		1		2	3		2		2		
129	2		1		2	2		2		2		
130	2		1		2	2		2		1		
131	2		1	2	2	3		2		3		
132	2		2	3	3	2		3		2		
133	2		2		2	1		2		3		
134	2		2		2	2		2		2		
135	2		1		<u>-</u> 2	2		2		1		
136	2		2		2	2		2		2		
137	2		2		2	3		2		2		
138	2		2		2	2		2		2		
139	2		1	2	2	3		2		3		
140	2		2	2	2	2		2		2		
141	2		2	2	2	2		2		2		
142	2		1		2	2		2		3		
143	2		2		2	2		2		2		
144	2		1		<u>-</u> 2	2		3		2		
145	2		2		2	3		2		2		
146	2		2	2		1		2		3		
147	2		1	2		1		1		3		
148	2		1	2	2	1		2		2		
149	2		1	2	2	2		3		2		
150	2		2	2	2	3		2		2		
	EISocial	Α.	EIRM	. 1	Total	Panas	5	Panas	.1 (CBCL P.	ΑO	
1		73	6		62		70		2	1	2	
2		89	6		88		77		3	1	2	
3		67	6		74		61		2	2	2	
4		67	4		74		65		2	2	2	
5		70	7	6	79		77		3	1	2	
6		79	6	2	62		56		2	2	2	
7		85	8		81		86		4	1	2	
8		77	7		72		83		3	1	1	
9		79	7		88		78		3	2	2	
										1		
10		89	6		88		77		3		2	
11		85	8		81		86		4	1	2	
12		79	7		88		78		3	2	2	
13		79	7		79		78		3	1	2	
14		46	4	9	88		53		4	3	2	
15		79	6	2	77		67		3	1	2	
16		79		2	77		67		3	1	2	

17	77	37	77	70	2	2	1
18	83	52	77	89	3	2	2
19	73	65	62	70	2	1	2
20	77	71	70	53	2	2	2
21	67	62	70	65	2	1	2
22	67	49	74	65	2	2	2
23	79	73	88	78	3	2	2
24	76	68	68	56	2	3	2
25	46	49	88	53	4	3	2
	74						
26		36	81	75 56	2	2	2
27	79	62	62	56	2	2	2
28	85	85	81	86	4	1	2
29	85	93	93	59	4	2	2
30	67	45	64	43	1	2	2
31	85	85	81	86	4	1	2
32	85	62	93	89	4	2	2
33	83	52	77	89	3	2	2
34	90	75	68	53	3	2	2
35	85	62	90	78	3	1	2
36	77	74	72	83	3	1	1
37	76	73	90	77	3	1	2
38	85	85	81	86	4	1	2
39	77	71	70	53	2	2	2
40	76	73	90	77	3	1	2
41	73	65	62	70	2	1	2
42	74	36	81	75	2	2	2
43	79	78	79	78	3	1	2
44	76	74	88	86	4	1	2
45	83	91	81	77	4	1	1
46	85	80	81	77	4	3	2
47	79	62	77	67	3	1	2
48	76	45	72	75	2	2	2
49					2	1	
	72	49	76	67			2
50	85	62	90	78	3	1	2
51	76	74	88	86	4	1	2
52	67	68	74	61	2	2	2
53	67	68	74	61	2	2	2
54	79	78	81	70	3	1	2
55	72	49	76	67	2	1	2
56	67	62	70	65	2	1	2
57	79	78	79	78	3	1	2
58	85	93	93	59	4	2	2
59	83	52	77	89	3	2	2
60	67	45	64	43	1	2	2
61	77	62	79	75	3	1	2
62	85	85	81	86	4	1	2
63	79	78	81	70	3	1	2
64	77	37	77	70	2	2	1
65	83	78	70	59	3	2	1
66	85	93	93	59	4	2	2
67	79	96	77	80	4	2	2
68	77	62	79	75	3	1	2
69	76	74	88	86	4	1	2
70	70 79	96	77	80	4	2	2
70	7 <i>9</i> 70	76	7 <i>7</i>	77	3	1	2
						1	
72	77	74	72	83	3	Т	1

73	72	49	76	67	2	1	2
74	77	71	70	53	2	2	2
75	85	80	81	77	4	3	2
76	77	37	77	70	2	2	1
77	79	62	77	67	3	1	2
78	73	65	62	70	2	1	2
79	67	49	74	65	2	2	2
80	79	96	77	80	4	2	2
81	85	62	90	78	3	1	2
82	77	71	70	53	2	2	2
83	76	74	88	86	4	1	2
84	76	74	88	86	4	1	2
85	90	75	68	53	3	2	2
86	85	62	93	89	4	2	2
87	77	71	70	53	2	2	2
88	85	93	93	59	4	2	2
89	79	78	79	78	3	1	2
90	77	37	77	70	2	2	1
91	73	65	62	70	2	1	2
92	76	40	74	70	2	1	2
93	74	36	81	75	2	2	2
94	79	96	77	80	4	2	2
95	77	37	77	70	2	2	1
96	79	78	81	70	3	1	2
97	79	62	62	56	2	2	2
98	89	62	88	77	3	1	2
99	73	65	62	70	2	1	2
100	85	80	81	77	4	3	2
101	74	36	81	75	2	2	2
102	83	91	81	77	4	1	1
103	79	78	81	70	3	1	2
104	77	74	72	83	3	1	1
105	67	45	64	43	1	2	2
106	79	78	79	78	3	1	2
107	85	93	93	59	4	2	2
108	79	96	77	80	4	2	2
109	76	45	72	75	2	2	2
110	79	78	79	78	3	1	2
111	67	68	74	61	2	2	2
112	77	37	77	70	2	2	1
113	79	96	77	80	4	2	2
114	77	74	72	83	3	1	1
115	79	73	88	78	3	2	2
116	83	52	77	89	3	2	2
117	85	80	81	77	4	3	2
118	76	40	74	70	2	1	2
119	73	65	62	70	2	1	2
120	67	49	74	65	2	2	2
121	67	62	70	65	2	1	2
122	77	71	70	53	2	2	2
123	67	62	70	65	2	1	2
124	79	78	79	78	3	1	2
125	77	37	77	70	2	2	1
126	76	40	74	70	2	1	2
127	70	76	79	77	3	1	2
128	67	68	74	61	2	2	2

```
129
           74
                  36
                      81
                             75
                                     2
                                         2
                                            2
130
           83
                  91
                      81
                             77
                                     4
                                         1
                                            1
                                     3
                                            2
           89
                  62
                      88
                             77
131
                                         1
132
           77
                  62
                      79
                             75
                                     3
                                       1
                                            2
133
           79
                  78
                      81
                             70
                                     3 1
                                            2
                                     3
134
           79
                  73
                      88
                             78
                                         2
                                            2
135
           83
                  91 81
                             77
                                     4 1 1
                                     3
136
           79
                  73
                      88
                             78
                                         2
                                            2
                                     2 3 2
                  68
137
           76
                      68
                             56
           90
                  75
                             53
                                     3 2
                                            2
138
                      68
139
           89
                  62
                      88
                             77
                                     3
                                            2
                                        1
140
           77
                 74 72
                             83
                                     3
                                        1
                                            1
141
           85
                  93
                             59
                                     4
                                         2
                                            2
                      93
                                     4 2 2
142
           79
                  96
                      77
                             80
           90
                  75
                             53
                                     3
                                         2
                                            2
143
                      68
           79
                                     3 1
144
                  62
                      77
                                            2
                             67
145
                 49 88
                             53
                                     4 3
                                            2
           46
                                     3
                                        1
                                            2
146
           79
                 78
                      81
                             70
           67
                  62 70
                                     2 1 2
147
                             65
148
           76
                  73
                      90
                             77
                                     3
                                       1
                                            2
                                     3 1 2
           79
                  62 77
149
                             67
                                     2
150
           76
                  68
                      68
                             56
                                         3
                                            2
```

```
In [4]: #Main Code
        #SOURCES ::
        # https://www.statology.org/k-fold-cross-validation-in-r/
        # https://www.geeksforgeeks.org/k-fold-cross-validation-in-r-programming/
        # http://www.sthda.com/english/articles/38-regression-model-validation/157-cross-va
         # https://cran.r-project.org/web/packages/caret/vignettes/caret.html
         # https://www.youtube.com/watch?v=CmOZy8WKpTM
         # Load necessary libraries
        library(caret)
         # Assuming you have already performed the GLM analysis and have the data in a varia
         # Set the number of folds for cross-validation (e.g., 5-fold)
         num_folds <- 5
         # Create a cross-validation control object
         cv <- trainControl(method = "cv", number = num_folds)</pre>
         # Define the independent variables and mediator variable
         independent_variables <- c('BFI..E.', 'BFI..A.', 'BFI..C.', 'BFI..N.', 'BFI..O.',</pre>
        mediator_variable <- 'PAQ'</pre>
         # Define a list of dependent variables
         dependent_variables <- c('Panas...', 'Panas...1', 'CBCL')</pre>
         # Loop through each dependent variable
         for (dependent_variable in dependent_variables) {
          # Define the formula for the model
          formula <- as.formula(paste(dependent_variable, "~ . +", mediator_variable))</pre>
```

```
# Fit the GLM model with 5-fold cross-validation
 glm_cv <- train(formula, data = data2, method = "glm", family = poisson(link = "1</pre>
 # View cross-validation results for each dependent variable
 cat("Cross-validation results for", dependent_variable, ":\n")
 print(glm_cv)
 cat("========\n")
Cross-validation results for Panas..:
Generalized Linear Model
150 samples
13 predictor
No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 119, 120, 121, 120, 120
Resampling results:
 RMSE
          Rsquared
 8.425976 0.5329223 6.37341
Cross-validation results for Panas...1:
Generalized Linear Model
150 samples
13 predictor
No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 120, 119, 122, 120, 119
Resampling results:
 RMSE
           Rsquared
                     MAE
 0.3540945 0.8263909 0.2384964
Cross-validation results for CBCL:
Generalized Linear Model
150 samples
13 predictor
No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 121, 119, 120, 120, 120
Resampling results:
 RMSE
           Rsquared
 0.4985334 0.3803909 0.4062544
______
```

```
In [1]: #Code to Check the confidence intervals of the K-fold Cross Validation
        # Load necessary libraries
        library(caret)
        data <- read.csv("Pilot_modified_data_1.csv")</pre>
        # Assuming you have already performed the GLM analysis and have the data in a varia
        # Set the number of folds for cross-validation (e.g., 5-fold)
        num_folds <- 5
        # Create a cross-validation control object
        cv <- trainControl(method = "cv", number = num_folds)</pre>
        # Define the independent variables and mediator variable
        independent_variables <- c('BFI..E.', 'BFI..A.', 'BFI..C.', 'BFI..N.', 'BFI..O.',</pre>
        mediator variable <- 'PAQ'
        # Define a list of dependent variables
        dependent_variables <- c('Panas...', 'Panas...1', 'CBCL')</pre>
        # Loop through each dependent variable
        for (dependent variable in dependent variables) {
          # Define the formula for the model
          formula <- as.formula(paste(dependent_variable, "~ . +", mediator_variable))</pre>
          # Fit the GLM model with 5-fold cross-validation
          glm_cv <- train(formula, data = data, method = "glm", family = poisson(link = "lo")</pre>
          # View cross-validation results for each dependent variable
          cat("Cross-validation results for", dependent_variable, ":\n")
          print(glm_cv)
          # Get and print confidence intervals
          confidence_level <- 0.95 # You can set the desired confidence Level</pre>
          conf_intervals <- confint(glm_cv$finalModel, level = confidence_level)</pre>
          cat("Confidence Intervals (", confidence_level * 100, "%):\n")
          print(conf_intervals)
          cat("=======\n")
        Loading required package: ggplot2
        Loading required package: lattice
        Warning message in train.default(x, y, weights = w, ...):
        "You are trying to do regression and your outcome only has two possible values Are
        you trying to do classification? If so, use a 2 level factor as your outcome colum
        n."
        Warning message in nominalTrainWorkflow(x = x, y = y, wts = weights, info = trainI
        nfo,:
        "There were missing values in resampled performance measures."
```

```
Cross-validation results for Panas..:
Generalized Linear Model
34 samples
13 predictors
No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 27, 28, 27, 27, 27
Resampling results:
  RMSE
            Rsquared
                       MAE
  0.2527456 0.2222222 0.1536952
Waiting for profiling to be done...
Confidence Intervals ( 95 %):
                   2.5 %
                             97.5 %
(Intercept) -4.52962974 6.19383713
Panas...1
            -0.58139715 0.57591853
BFI..E.
             -0.94538271 0.91902446
BFI..A.
            -0.55155455 0.55688115
BFI..C.
             -0.87269423 0.95169455
BFI..N.
            -0.38116926 0.48957416
BFI..O.
            -0.74325364 0.68585922
EI..Self.A. -0.03535082 0.03736765
EI..Self.M. -0.03086436 0.02567329
EI..Social.A. -0.04459332 0.04791043
EI..RM.
            -0.03208577 0.03272308
Total
             -0.70616649 0.66038196
PAQ
             -0.52554052 0.53362686
CBCL
             -0.90081535 0.70831595
Warning message in train.default(x, y, weights = w, ...):
"You are trying to do regression and your outcome only has two possible values Are
you trying to do classification? If so, use a 2 level factor as your outcome colum
n."
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type
"prediction from a rank-deficient fit may be misleading"
Cross-validation results for Panas...1:
Generalized Linear Model
34 samples
13 predictors
No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 27, 28, 27, 27
Resampling results:
  RMSE
            Rsquared
                       MAE
  0.8089249 0.3224103 0.6974561
```

```
Waiting for profiling to be done...
Confidence Intervals ( 95 %):
                   2.5 %
                            97.5 %
(Intercept)
             -7.67581222 9.78392888
Panas..
            -3.44866963 2.44509983
BFI..E.
            -1.16637525 0.94183865
            -0.68201205 0.59768039
BFI..A.
BFI..C.
            -0.90784178 1.23864245
BFI..N.
            -0.50794309 0.66014285
           -1.14248521 0.51574656
BFI..O.
EI..Self.A. -0.03630188 0.04361503
EI..Self.M. -0.03499845 0.03358241
EI..Social.A. -0.05176683 0.05481635
EI..RM.
            -0.04192160 0.02815058
Total
            -0.69532455 0.81425853
PAO
            -0.52931454 0.67185137
CBCL
            -1.13737476 1.48942119
_____
Warning message in train.default(x, y, weights = w, ...):
"You are trying to do regression and your outcome only has two possible values Are
you trying to do classification? If so, use a 2 level factor as your outcome colum
n."
Warning message in predict.lm(object, newdata, se.fit, scale = 1, type = if (type
"prediction from a rank-deficient fit may be misleading"
Warning message in nominalTrainWorkflow(x = x, y = y, wts = weights, info = trainI
"There were missing values in resampled performance measures."
Cross-validation results for CBCL:
Generalized Linear Model
34 samples
13 predictors
No pre-processing
Resampling: Cross-Validated (5 fold)
Summary of sample sizes: 27, 27, 28, 27, 27
Resampling results:
  RMSE
            Rsquared
                       MAE
  0.4844196 0.08302448 0.3497156
Waiting for profiling to be done...
```

9/24/23, 8:23 PM CrossValidation2

```
Confidence Intervals ( 95 %):
                 2.5 %
                         97.5 %
(Intercept) -4.20614399 9.44624851
Panas..
           -3.80116832 1.01994749
Panas...1
           -0.56454388 0.62989737
BFI..E.
           -1.03346545 0.87317891
BFI..A.
BFI..C.
          -0.60788946 0.50934793
          -0.81252554 1.04477742
BFI..N.
          -0.39524798 0.59674386
BFI..O.
          -0.81288041 0.63220966
EI..Self.A. -0.03735695 0.03758648
EI..Self.M. -0.03413890 0.02604045
EI..Social.A. -0.03917482 0.05293202
EI..RM.
          -0.03304823 0.03415683
Total
           -0.76991674 0.57731010
PAQ
           -0.48363315 0.58198734
_____
```