```
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'
        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("*")</pre>
          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..O.
           -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
EI..RM.
            -0.0001474 0.0164597 -0.009 0.993
            -0.0173123 0.3458867 -0.050
Total
                                           0.960
PAO
             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.
             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 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.
                       0.324314 -0.103
            -0.033461
                                          0.918
BFI..C.
                       0.543706 0.284
             0.154399
                                          0.776
BFI..N.
             0.062337 0.295745 0.211
                                          0.833
BFI..O.
            0.504
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. check
BFI..E.
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 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
                   -4.170e-02 2.832e-01 -0.147 0.883
       BFI..A.
       BFI..C.
                    1.188e-01 4.719e-01 0.252 0.801
       BFI..N.
                    9.358e-02 2.512e-01 0.373 0.709
                 -7.562e-02 3.670e-01 -0.206 0.837
       BFI..O.
       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
       Total
                   -9.119e-02 3.408e-01 -0.268 0.789
       PA0
                     6.153e-02 2.703e-01 0.228
                                                   0.820
        (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.
                         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.
                     EI..Self.M. check
       EI..Social.A. EI..Social.A. check
       EI..RM.
                          EI..RM. check
       Total
                           Total check
       PAQ
                              PAQ check
        [1] "-----"
In [2]: # 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)
    bootstrap_sample <- data[random_indices, ]

# Store the bootstrap sample in data2
    data2[i, ] <- bootstrap_sample
}

# Now data2 contains the bootstrapped data with the new sample size</pre>
```

```
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"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.. =</pre>
"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.. =</pre>
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"
```

```
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 vario
         # 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>
```

```
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
                    MAE
 0.4985334 0.3803909 0.4062544
______
```

In []: