<u>Assignment: 1</u> <u>Statistical Model and Regression analysis</u>

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Q:1 Given that, we have a data set with five predictors, X1 = GPA, X2 = IQ, X3 = Level (1 for College and 0 for High School), X4 = Interaction between GPA and IQ, and X5 = Interaction between GPA and Level. The response is starting salary after graduation (in thousands of dollars). Suppose we use least squares to fit the model, and get β 0 = 50, β 1 = 20, β 2 = 0.07, β 3 = 35, β 4 = 0.01, β 5 = -10.

Fitted regression model eq will be-

Salary =
$$\beta$$
0 + β 1*GPA + β 2*IQ + β 3*Level + β 4*(GPA×IQ) + β 5*(GPA×Level)

- (a) The correct answer is (ii) For a fixed value of IQ and GPA, college graduates earn more, on average, than high school graduates. Because the coefficient , $\beta 3 = 35$ represents the difference in starting salary between college graduates (Level = 1) and high school graduates (Level = 0) when all other predictors are held fixed. Since $\beta 3 = 35$ is positive, it implies that, on average, college graduates earn more than high school graduates, for a fixed value of IQ and GPA.
- **(b)** We have to predict the salary of a college graduate if IQ is 110 and a GPA is 4.0.

Salary=
$$50+20\times4.0+0.07\times110+35+0.01\times(4.0\times110)-10\times(4.0\times1)$$

Salary=136.1

So, the predicted salary of a college graduate with IQ of 110 and a GPA of 4.0 will be approximately \$136,100.

(c) False. Even though the coefficient for the GPA/IQ interaction term (β =0.01) is small, it doesn't necessarily mean there is very little evidence of an interaction effect. The significance of an interaction effect depends on various factors, including the scale and context of the data. Therefore, the small coefficient alone does not provide conclusive

evidence for or against an interaction effect. Additional statistical tests or analysis would be needed to determine the significance of the interaction effect.

Q:2 (a) create a vector, x

x <- rnorm(100, mean = 0, sd = 1)

(b) create a vector, eps

eps <- rnorm(100, mean = 0, sd = sqrt(0.25))

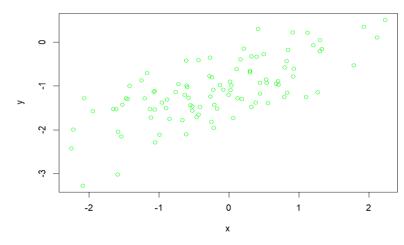
(c) Using x and eps, generate a vector y according to the model

$$y < -1 + 0.5*x + eps$$

The length of the vector y will be 100. In this linear model, $\beta 0 = -1$ and $\beta 1 = 0.5$.

(d) Scatterplot displaying the relationship between x and y.

Scatter plot btw x and y



Here we can see that positive correlation between x and y, it means that as the value of one variable x increases, the value of the other variable y also tends to increase.

(e) Fit a least squares linear model to predict y using x:

Fitted least squares regression line eq will be

 $y = \beta_0 = \beta_1 = -0.99770$ and $\beta_1 = 0.48777$

estimating coefficients β_0 cap = -0.99770 and β_1 cap = 0.48777 both are close to β_0 and β_1 respectivey. It indicates that the linear regression model has effectively captured the underlying relationship between the predictor variable X and the target variable Y.

R2 = 0.50 (say), then it indicates the model explained 50% of the variation that is there in the response. Thus, the fitted regression model is given by y = -0.99770 + 0.48777*x

RSE =
$$0.4873$$
, R2_adj = 0.4967 and R2 = 0.5018

Note that p-value< 2.2×10^{-16} is very small and hence, we should reject the overall hypothesis H0 : $\beta 0_{cap} = \beta 1_{cap} = 0$.

Check model is statistically significate or not: Use significance level $\alpha = 0.05$

Testing Hypothisis: For β0_cap (intercept)

```
H01 : \beta0_cap = 0 vs. H11 : \beta0_cap != 0 p - value < 2 × 10^-16
```

i.e., $p = value < \alpha$ and hence H01 is rejected.

Testing Hypothisis: For $\beta1$ _cap (slop)

 $H01 : β1_cap = 0 vs. H11 : β1_cap != 0$

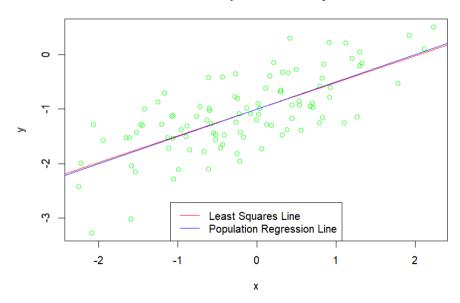
p-value < 2×10^{-16}

i.e., p-value $< \alpha$ and hence H01 is rejected.

Hence model a statistically significant.

(f) Display the least squares line and the population regression line on the scatterplot

Scatter plot btw x and y



Q:3 In task given that, we have to use Bostan data set. And we have to use per capita crime rate is the response and the predictors are as follows: zn, indus, nox, rm, dis, tax, medy from the Boston data set.

(a) Fit simple linear regression models for each predictor.

(i) Fit simple linear regression model for response variable crime rate and predictor zn-

The fitted regression model1 eq will be- crime rate = b1 + m1 * zn, here b1 = 4.45369 and m1 = -0.07393

(ii) Fit simple linear regression model for response variable crime rate and predictor indus-

The fitted regression model2 eq will be- crime rate = b2 + m2 * indus, here b2 = -2.06374 and m2 = 0.50978

(iii) Fit simple linear regression model for response variable crime rate and predictor nox-

The fitted regression model3 eq will be- crime rate = b3 + m3 * nox, here b3 = 4.45369 and m3 = -0.07393

(iv) Fit simple linear regression model for response variable crime rate and predictor rm-

The fitted regression model4 eq will be- crime rate = b4 + m4 * rm, here b4 = 20.482 and m4 = -2.684

(v) Fit simple linear regression model for response variable crime rate and predictor dis-

The fitted regression model 5 eq will be-crime rate = b5 + m5 * dis, here b5 = 9.4993 and m5 = -1.5509

(vi) Fit simple linear regression model for response variable crime rate and predictor tax-

The fitted regression model6 eq will be- crime rate = b6 + m6 * tax, here b6 = -8.528369 and m6 = 0.029742

(vii) Fit simple linear regression model for response variable crime rate and predictor medv-

The fitted regression model7 eq will be- crime rate = b7 + m7 * medv, here b7 = 11.79654 and m7 = -0.36316

To determine whether there is a statistically significant association between a predictor variable and a response variable in models we will perform hypothesis testing. For testing the association between a predictor and a response, the null hypothesis usually states that there is no association (the coefficient for the predictor is zero), while the alternative hypothesis states that there is a nonzero association.

Null Hypothesis (H0): There is no association between the predictor and the response. Alternative Hypothesis (H1): There is an association between the predictor and the response.

Use significance level $\alpha = 0.05$

For model1:

Testing Hypothisis: For b1 (intercept)

H01: b1 = 0 vs. H11: b1!= 0

p - value < 2×10^{-16}

i.e., p = value < α and hence H01 is rejected.

Testing Hypothisis: For m1 (slop)

H01: m1 = 0 vs. H11: m1!= 0

$$p$$
-value < 5.51 × 10^-6

i.e., p-value $< \alpha$ and hence H01 is rejected.

For model2:

Testing Hypothisis: For b2 (intercept)

H02: b2 = 0 vs. H12: b2!= 0

p-value = 0.00209

i.e., p-value $< \alpha$ and hence H02 is rejected.

Testing Hypothisis: For m2 (slop)

H02: m2 = 0 vs. H12: m2!= 0

p-value < 2×10^{-16}

i.e., p-value $< \alpha$ and hence H02 is rejected.

For model3:

Testing Hypothisis: For b3 (intercept)

H03: b3 = 0 vs. H12: b3!= 0

p-value < 2 × 10^-16

i.e., p-value $< \alpha$ and hence H03 is rejected.

Testing Hypothisis: For m3 (slop)

H03: m3 = 0 vs. H13: m3!= 0

p-value = 5.51 x 10^-6

i.e., p-value < α and hence H03 is rejected.

For model4:

Testing Hypothisis: For b4 (intercept)

H04: b4 = 0 vs. H14: b3!= 0

p-value < 2.27 × 10^-9

i.e., p-value $< \alpha$ and hence H04 is rejected.

Testing Hypothisis: For m4 (slop)

H04: m4 = 0 vs. H14: m4!= 0

p-value = 6.35 x 10^-7

i.e., p-value $< \alpha$ and hence H04 is rejected.

For model5:

Testing Hypothisis: For b5 (intercept)

H05: b5 = 0 vs. H15: b5!= 0

p-value < 2×10^{-16}

i.e., p-value $< \alpha$ and hence H05 is rejected.

Testing Hypothisis: For m5 (slop)

H05: m5 = 0 vs. H15: m5!= 0

p-value = 2 x 10^-16

i.e., p-value $< \alpha$ and hence H05 is rejected.

For model6:

Testing Hypothisis: For b6 (intercept)

H06: b6 = 0 vs. H16: b6!= 0

p-value < 2 × 10^-16

i.e., p-value < α and hence H06 is rejected.

Testing Hypothisis: For m6 (slop)

H06 : m6 = 0 vs. H16 : m6 != 0

p-value = 2 x 10^-16

i.e., p-value $< \alpha$ and hence H06 is rejected.

For model7:

Testing Hypothisis: For b7 (intercept)

H07: b7 = 0 vs. H17: b7! = 0

p-value < 2×10^{-16}

i.e., p-value $< \alpha$ and hence H07 is rejected.

Testing Hypothisis: For m7 (slop)

H07 : m7 = 0 vs. H14 : m7 != 0

p-value = 2 x 10^-16

i.e., p-value < α and hence H07 is rejected.

Hence, We can see that each model there is a statistically significant association between the predictor and the response.

Check godness of Fit of models-

Model-1: RSE = 8.435, R2_adj = 0.03828 and R2 = 0.04019

Model-2: RSE = 7.866, R2_adj = 0.1637 and R2 = 0.1653,

Model-3: RSE = 8.435, R2_adj = 0.03828 and R2 = 0.04019,

Model-4: RSE = 8.401, R2_adj = 0.04618 and R2 = 0.04807

Model-5: RSE = 7.965, R2_adj = 0.1425 and R2 = 0.1441

Model-6: RSE = 6.997, R2_adj = 0.3383 and R2 = 0.3396

Model-7: RSE = 7.934, R2_adj = 0.1491 and R2 = 0.1508

(b) Fit a multiple regression model to predict the response using all of the predictors.

The fitted regression model eq will be

```
crim = \beta0 + \beta1*zn + \beta2*indus + \beta3*nox + \beta4*rm + \beta5*dis + \beta6*tax + \beta7*medv
```

Summary of multiple regression model:

```
> multi_model <- lm(crim ~ zn+indus+nox+rm+dis+tax+medv, Data_set)</pre>
> summary(multi_model)
lm(formula = crim \sim zn + indus + nox + rm + dis + tax + medv,
   data = Data_set)
Residuals:
Min 1Q Median
-12.573 -2.856 -0.577
           1Q Median 3Q Max
856 -0.577 1.302 74.911
Coefficients:
Estimate Std. Error t value Pr(>|t|) (Intercept) 2.417290 4.735683 0.510 0.60997
                                        0.03517 *
                     0.018539
           0.039158
                                2.112
           indus
nox
           rm
           -1.138369
                      0.278208 -4.092 4.99e-05 ***
dis
tax
            0.026635
                       0.002809
                                9.481 < 2e-16 ***
                       0.051763 -4.548 6.82e-06 ***
medv
           -0.235403
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
Residual standard error: 6.795 on 498 degrees of freedom
Multiple R-squared: 0.3845,
                              Adjusted R-squared: 0.3759
F-statistic: 44.45 on 7 and 498 DF, p-value: < 2.2e-16
```

R2 = 0.3845 (say), then it indicates the model explained 38% of the variation that is

there in the response. Thus, the fitted regression model is given by

```
crim = 2.417 + 0.039*zn - 0.226798*indus - 3.107230*nox + 0.596972*rm - 1.138369*dis + 0.026635*tax - 0.235403*medv
```

Note that p-value < 2.2×10^{-16} is very small and hence, we should reject the overall hypothesis H0 : $\beta 0 = \beta 1 = \beta 2 = \beta 3 = \beta 4 = \beta 5 = \beta 6 = 0$

We have F0 = 44.45 i.e. model is not too good.

Test hypothesis on Individual Regression Coefficients:

Level- α -test with $\alpha = 0.05$

Testing Problem 1 (For intercept): $H01 : \beta 0 = 0 \text{ vs. } H11 : \beta 0 != 0$

p - value = 0.60997

i.e., p-value > α and hence H01 is accepted.

Testing Problem 2 (For coefficient of zn): $H02 : \beta 1 = 0$ vs. $H12 : \beta 1 != 0$

p - value = 0.03517

i.e., p-value $< \alpha$ and hence H02 is rejected.

Testing Problem 3 (For coefficient of indus): H03 : β 2 = 0 vs. H13 : β 2 != 0

p - value = 0.00678

i.e., p-value < α and hence H03 is rejected.

Testing Problem 4 (For coefficient of nox): $H04 : \beta 3 = 0 \text{ vs. } H14 : \beta 3 != 0$

p - value = 0.52922

i.e., p-value > α and hence H04 is accepted.

Testing Problem 5 (For coefficient of rm): $H05 : \beta 4 = 0 \text{ vs. } H15 : \beta 4 != 0$

p - value = 0.32725

i.e., p-value > α and hence H05 is accepted.

Testing Problem 6 (For coefficient of dis): H06 : β 5 = 0 vs. H16 : β 5 != 0

 $p - value = 4.99 X 10^{-5}$

i.e., p-value $< \alpha$ and hence H06 is rejected.

Testing Problem 7 (For coefficient of tax): H07 : β 6 = 0 vs. H17 : β 6 != 0

p - value < 2e X 10^-16

i.e., p-value $< \alpha$ and hence H07 is rejected.

Testing Problem 8 (For coefficient of medv): $H08 : \beta 7 = 0 \text{ vs. } H18 : \beta 7 != 0$

 $p - value = 6.82 \times 10^{-6}$

i.e., p-value $< \alpha$ and hence H08 is rejected.

Hence, for zn, indus, dis, tax ans medv predictors we can reject the null hypothesis.

(C) First of all we will check is there any outlier in our data or not by using Cook's Distance, DFDITS, DFBETA, COVRATIO.

Leverage points in our data set -

```
> Leverage_point_values
        58
                   65
                                        121
                                                   122
                                                              123
                                                                         124
                                                                                     125
0.03257538 0.03187811 0.02943673 0.04842189 0.04890818 0.04881315 0.04997225 0.04923036
      126
                 127
                             143
                                        144
                                                   145
                                                              146
                                                                         147
0.04878971 0.05075272 0.03496255 0.03512634 0.03927612 0.03516511 0.03465780 0.04046433
      149
                 150
                             151
                                        152
                                                   153
                                                              154
                                                                         155
                                                                                     156
0.03933303 0.03478728 0.03556228 0.03841873 0.04020408 0.03592916 0.03544033 0.03576184
      157
                 160
                             162
                                        163
                                                   164
                                                              167
                                                                         196
0.03709908 0.03763297 0.04043182 0.04112410 0.04649398 0.04178245 0.03202719 0.03113536
       201
                  202
                             204
                                        205
                                                   226
                                                              253
                                                                          254
0.03062041 0.02835231 0.04511526 0.04646273 0.03446388 0.02788501 0.05136878 0.03302948
       258
                  263
                             266
                                        268
                                                   284
                                                               291
                                                                          292
0.04268769 0.03719959 0.03008273 0.02964522 0.03789945 0.03173803 0.02933236 0.03179830
       352
                  353
                             354
                                        355
                                                   356
                                                              365
                                                                          366
0.03547234 0.03599164 0.05630926 0.03714091 0.03520699 0.05829266 0.08621304 0.05868991
                  370
                             371
                                        372
                                                   373
                                                              375
0.10628219 0.05397890 0.04904638 0.06332713 0.07293835 0.03313435 0.03134333
```

Influential Points in our data set: Detect using Cook's Distance, DFBETAS, DFFITS, COVRATIO -

```
> Influential_Points <- which(cook > cutoff)
```

```
381 399 405 406 411 415 419 428
0.35360784 0.02011448 0.02103295 0.10510491 0.05058565 0.05590810 0.09961697 0.01638663
```

Detect using DFBETAS-

> Influential_Points_values <- cook[Influential_Points]</pre>

> Influential_Points_values

```
> DFBETAS_Points <- which(abs(def) > cutoff_)
> DFBETAS_Points_values <- abs(def)[DFBETAS_Points]</pre>
> DFBETAS_Points_values
  [1] 0.10087191 0.15899205 0.12707966 0.23223600 0.09828860 0.12279276 0.61940816 0.09549808
  [9] 0.12555279 0.09369549 0.12211434 0.15884931 0.32136545 0.13686767 0.21558832 0.37728215
 [17] 0.10692348 0.09730661 0.10779941 0.10630662 0.21078997 0.10456931 0.24761851 0.10463419
 [25] 0.13275412 0.14628877 0.13065373 0.11502323 0.11318643 0.09922125 0.11786592 0.10311781
 [33] 0.10464834 0.22307935 0.18687395 0.14395281 0.17008762 0.19186447 0.17841147 0.19157216
 [41] 0.16885314 0.12416095 0.29903560 0.39735214 0.15244756 0.13281924 0.17865030 0.16379212
 [49] 0.14643285 0.10480949 0.28645887 0.13475292 0.10759500 0.14853057 0.09659675 0.10199022
 [57] 0.15617507 0.11713195 1.47859116 0.12402442 0.16961091 0.19519190 0.18673571 0.15218081
 [65] 0.18879957 0.45392954 0.29709997 0.15899005 0.15963915 0.17074348 0.20320405 0.50404282
  [73] \quad 0.14554614 \quad 0.12105279 \quad 0.36160941 \quad 0.34082992 \quad 0.12348900 \quad 0.15224940 \quad 0.23695866 \quad 0.11326723 
 [81] 0.10238045 0.10119925 0.09125607 0.10472920 0.33074522 0.10152224 0.14325402 0.21690381
 [89] 0.34430212 0.17092424 0.20804789 0.31608836 0.12571701 0.09159583 0.13484183 0.10861910
 [97] 0.09092688 0.10578498 0.16472548 0.15468498 1.35088332 0.21534689 0.13238849 0.15182814
[105] 0.61720785 0.54718333 0.19658882
```

Detect using DFFITS-

A measure of model performance: COVRATIO

```
> outliers <- which(cv < 1 | cv > u)
> outlier_values <- cv[outliers]</pre>
> outlier_values
     57
             58
                     67 121
                                    122
                                            123
                                                   124
                                                           125
1.0434526 1.0498043 1.0415028 1.0599996 1.0623366 1.0623284 1.0658118 1.0640576 1.0617841
    127 143 144 145 146 147 148 149
1.0671781 1.0524343 1.0532012 1.0564569 1.0510258 1.0514523 1.0582282 1.0575489 1.0522436
            152
                    153
                            154 155
                                            156
                                                   157 160
1.0532227 1.0561578 1.0565047 1.0538090 1.0516166 1.0538114 1.0543331 1.0555897 1.0523521
    163 164 167 196 200
                                            201
                                                   203
                                                           204
1.0522410 1.0598009 1.0525926 1.0473120 1.0465842 1.0448306 1.0440956 1.0620150 1.0630658
                            256 257 258 262 263
            254 255
    226
1.0495948 1.0559746 1.0425732 1.0440888 1.0480233 1.0601112 1.0442885 1.0534956 1.0458275
    268 284 285
                            287 291
                                            292 293
                                                           346
1.0447073 1.0499626 1.0437167 1.0419718 1.0489746 1.0467129 1.0490379 1.0417893 1.0419215
    348 352 353
                            354 355
                                            356 365
1.0420992 1.0535830 1.0538272 1.0535305 1.0553819 1.0530895 1.0521909 1.1080768 1.0722724
            370 371
                            372
                                    373
                                            381
                                                   399
1.1364966 1.0738710 1.0678576 1.0766657 1.0901096 0.1045145 0.8368439 0.7727634 0.3512559
    411 414 415
                            419
                                    428
0.5971289 0.9318098 0.7024977 0.2569325 0.8257339
```

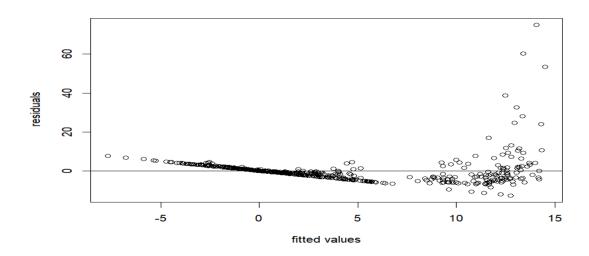
Hence, in our data outlier present.

Model Assumptions:

(i) The error term has zero mean:

```
> error <- multi_model$residuals
> mean(error)
[1] 3.833105e-16
```

(ii) Check the error term has constant variance or not: Plot graph between residuals and fitted values.



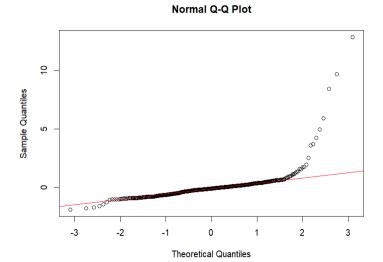
By above graph we can see that error term has not constant variance.

(iii) Check Uncorreleated error assumption: Use DurbinWatsonTest for this.

The Durbin-Watson test statistic (DW) is approximately 1.3535, and the p-value is very small (close to zero) for all three alternative hypotheses:Alternative = "less": The p-value is 1. This indicates that there is no evidence to suggest that the autocorrelation is less than 0 (i.e., negative autocorrelation). Alternative = "greater": The p-value is approximately 2.531×10^{4} . This indicates strong evidence to suggest that the autocorrelation is greater than 0 (i.e., positive autocorrelation). Alternative = "two.sided": The p-value is also very small, approximately 5.061×10^{4} . This indicates strong evidence to suggest that the autocorrelation is not equal to 0.

Based on these results, we can conclude that there is strong evidence of positive autocorrelation in the errors of the regression model. This means that consecutive residuals are correlated with each other, violating the assumption of independence of errors.

(iv) Normality assumption: Normality check by using Q-Q plot for studentized residuals-



By graph we can see that distribution of the studentized residual positive skew. It indicates that the residuals are not normally distributed.

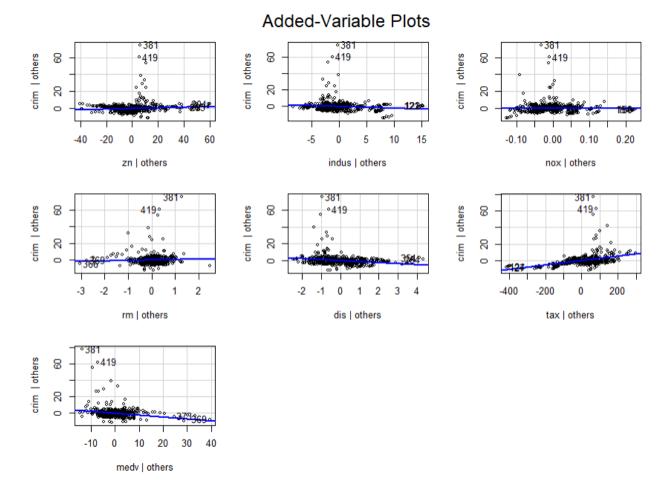
(v) Check the Multicollinearity-

The minimum eigenvalue of variance-covariance matrix is approximately 0, it is indicating that one or more variables are linear combinations of other variables, suggesting multicollinearity.

We can also check by VIF:

```
> library(mctest)
> imcdiag(multi_model, method = "VIF")
 library(mctest)
imcdiag(mod = multi_model, method = "VIF")
VIF Multicollinearity Diagnostics
         VIF detection
      2.0446
zn
indus 3.5818
      3.5763
2.0008
nox
                       0
rm
dis
      3.7533
tax
      2.4786
medv
       VIF Method Failed to detect multicollinearity
0 --> COLLINEARITY is not detected by the test
```

(vi) Check for linearity assumption:



By above plot we can see that the relationship btw response variable and predictor variable are linear so linearity assumption hold.

Fix non-normality and non-constant variance problem be transformation of response variable: Use Box-Cox method

```
> library(car)
> p <- powerTransform(crim ~ zn+indus+nox+rm+dis+tax+medv, family = "bcPower",Data_set)
> summary(p)
bcPower Transformation to Normality
  Est Power Rounded Pwr Wald Lwr Bnd Wald Upr Bnd
     -0.0405
                   -0.04
                              -0.0746
                                           -0.0064
Υ1
Likelihood ratio test that transformation parameter is equal to 0
(log transformation)
                           LRT df
                                      pval
LR test, lambda = (0) 5.528272 1 0.018712
Likelihood ratio test that no transformation is needed
                           LRT df
                                        pval
LR test, lambda = (1) 2786.602 1 < 2.22e-16
```

The estimated transformation parameter is $\lambda = -0.0405$

After applying the Box-Cox transformation, the updated data has approximately normal distribution with constant variance.

```
> new_MLR_model <- lm(bcPower(crim, p$roundlam, jacobian.adjusted = TRUE)~ zn+indus+nox+rm+dis+tax+
medv, Data_set)
> summary(new_MLR_model)
lm(formula = bcPower(crim, p$roundlam, jacobian.adjusted = TRUE) ~
   zn + indus + nox + rm + dis + tax + medv, data = Data_set
Residuals:
   Min
            1Q Median
                            3Q
-1.79179 -0.27606 0.02866 0.31543 1.04643
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
-0.0074602 0.0011810 -6.317 5.92e-10 ***
indus
         -0.0063652 0.0053139 -1.198
                                      0.232
                             8.542 < 2e-16 ***
          2.6853020 0.3143615
nox
          -0.0017209 0.0387784 -0.044
                                      0.965
         -0.0290243 0.0177221 -1.638
dis
                                      0.102
         tax
medv
         0.0002168 0.0032973 0.066
                                    0.948
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
Residual standard error: 0.4329 on 498 degrees of freedom
Multiple R-squared: 0.8062, Adjusted R-squared: 0.8034
F-statistic: 295.9 on 7 and 498 DF, p-value: < 2.2e-16
```

R2 = 0.8062 (say), then it indicates the model explained 81% of the variation that is

there in the response. Thus, the fitted regression model is given by

```
crim = -2.9110237 + -0.0074602*zn - 0.0063652*indus + 2.6853020*nox - 0.0017209*rm - 0.0290243*dis + 0.0031805*tax + 0.0002168*medv
```

Note that p-value < 2.2×10^{-16} is very small and hence, we should reject the overall hypothesis H0 : $\beta 0 = \beta 1 = \beta 2 = \beta 3 = \beta 4 = \beta 5 = \beta 6 = 0$

------END------