MH3510
Regression Analysis

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Group Project Report

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Modelling Linear Regression Model with R

1. Load Required Libraries

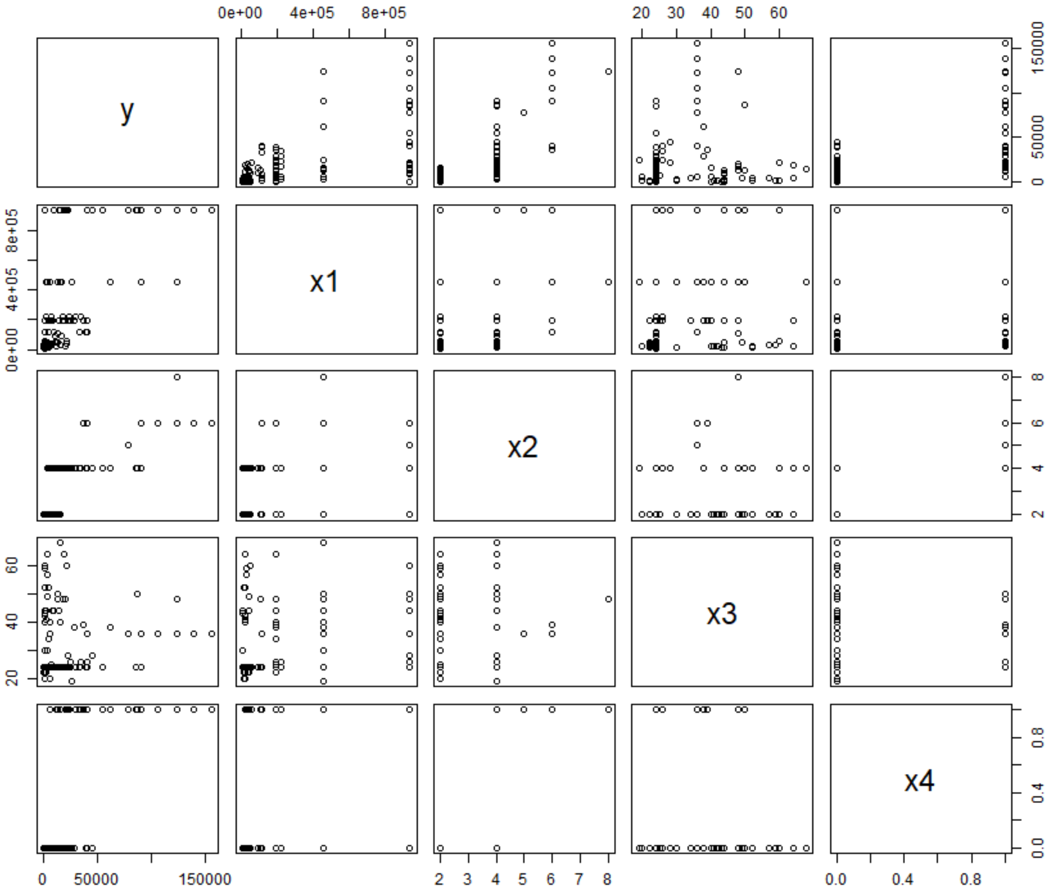
```
library(dplyr)
library(caret)
```

2. Data Preparation

```
# Load raw data
data_raw <- read.table('aadt.txt', header = FALSE)
df <- data.frame(y = data_raw$V1, x1 = data_raw$V2, x2 = data_raw$V3, x3 =
data_raw$V4, x4 = data_raw$V5)

# Convert x4 values of 2 to 0
df$x4[df$x4 == 2] <- 0

# Scale the data (optional)
df_scaled <- df
```

3. Exploratory Data Analysis

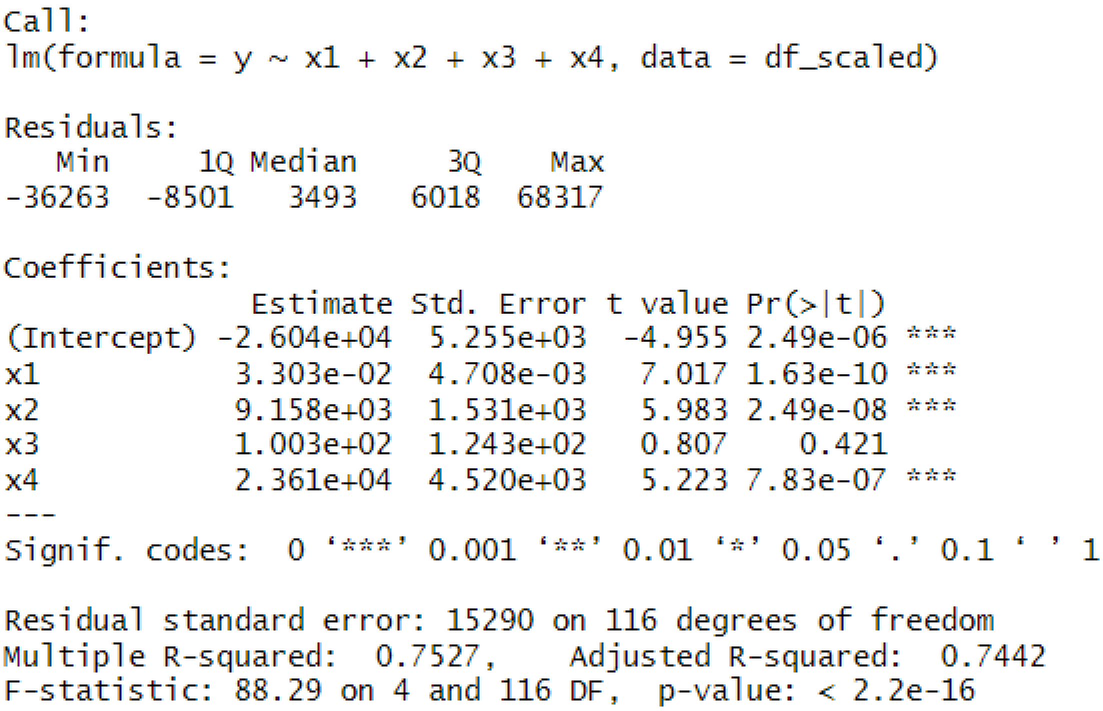
```
# Graphical display of the observed data
plot(df)
```



- **y vs. x1**: There seems to be some clustering or grouping in the data points. The relationship doesn't appear clearly linear.
- **y vs. x2**: The plot between y and x2 does not show a clear trend. The clustering observed here might imply the presence of some categorical elements or distinct groups within the dataset.
- **y vs. x3**: There appears to be minimal linear correlation between y and x3. The scatter is widespread, indicating that x3 might not be a significant predictor for y.
- **y vs. x4**: The points between y and x4 indicate a distinct grouping with many points overlapping at zero. This might indicate that x4 is binary or categorical.
- **x1 vs. x2**: There is no clear linear relationship between x1 and x2.
- **x2 vs. x3**: The scatter plot is widely spread, indicating that x2 and x3 are likely not correlated with each other.
- **x3 vs. x4**: There is significant correlation between x3 and x4.

4. Multiple Linear Regression Model

```
# Fit a multiple linear regression model
mlr <- lm(y ~ x1 + x2 + x3 + x4, data = df)
summary(mlr)
```

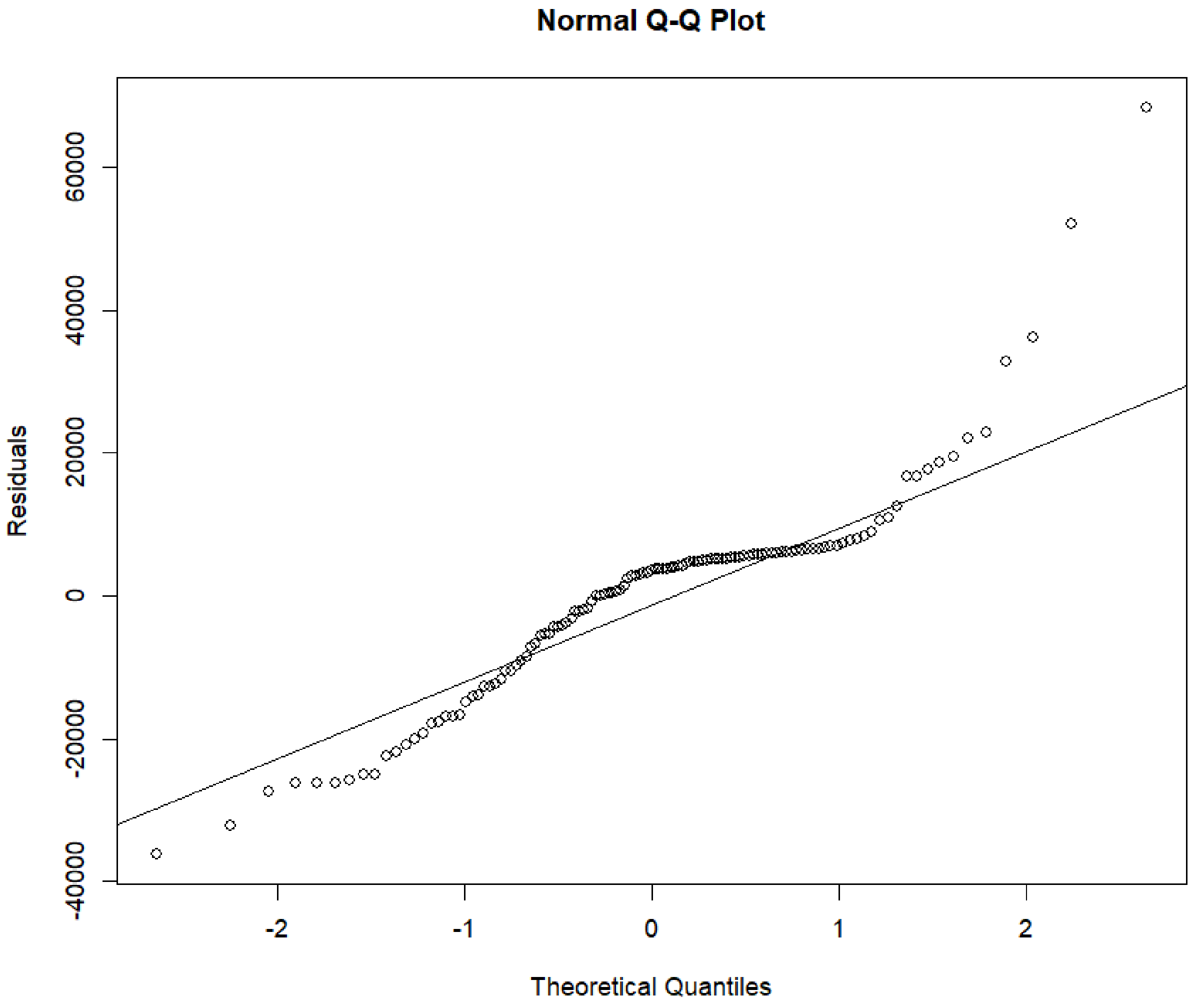


```
Call:
lm(formula = y ~ x1 + x2 + x3 + x4, data = df_scaled)

Residuals:
   Min     1Q Median     3Q    Max 
-36263  -8501   3493   6018  68317 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept) -2.604e+04  5.255e+03  -4.955 2.49e-06 ***
x1           3.303e-02  4.708e-03   7.017 1.63e-10 ***
x2           9.158e+03  1.531e+03   5.983 2.49e-08 ***
x3           1.003e+02  1.243e+02   0.807    0.421    
x4           2.361e+04  4.520e+03   5.223 7.83e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 15290 on 116 degrees of freedom
Multiple R-squared:  0.7527,	Adjusted R-squared:  0.7442 
F-statistic: 88.29 on 4 and 116 DF,  p-value: < 2.2e-16
```

- **Coefficients:**
    - Coefficient of **x3** has a p-value of 0.421 which is greater than the significance level of 0.05, thus H_0: $\beta_3 = 0$ is not rejected. Hence, **x3** is the least significant variable to the model in terms of t-test
    - Coefficients of **x1**, **x2** and **x4** have p-values which are smaller than 0.05, thus H_0: $\beta_i = 0$ for i = 1, 2, 4 are rejected. Hence, **x1**, **x2** and **x4** are highly significant variables.
- **R^2 Statistic:**
    - Multiple R-squared = 0.7527 indicates that approximately 75.27% of the variability in the response variable **y** is explained by the model.
    - Adjusted R-squared = 0.7442 is slightly lower than the R-squared value, indicating that the model fits the data well, considering the number of predictors.
- **F-statistic**:
    - 88.29 on 4 and 116 degrees of freedom, with a p-value < 2.2e-16. This suggests that the model is significant overall, and at least one of the predictors is related to **y**

5. Normality Check of Residuals

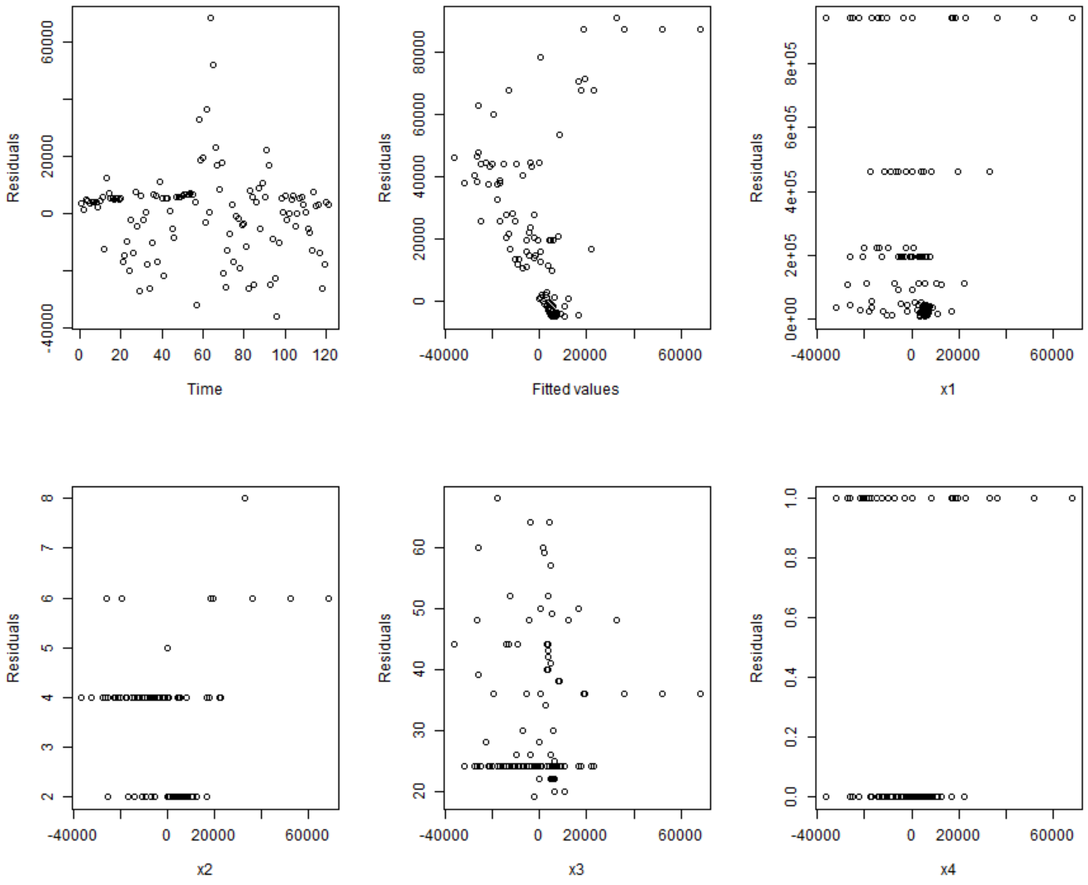
```
# Normality checking
qqnorm(residuals(mlr), ylab = 'Residuals')
qqline(residuals(mlr))
```



- Points generally follow the normal line on the QQ plot, except for some deviations in the upper tail.
- This suggests that the data mostly follows a normal distribution but has a few outliers in the upper tail.

6. Residual Analysis

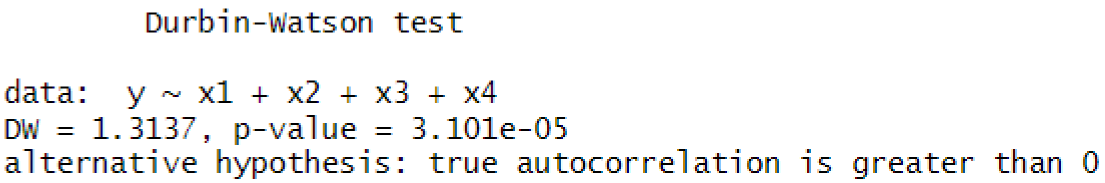
```
# Draw some plots of residuals
par(mfrow = c(2, 3))
plot(residuals(mlr), ylab = 'Residuals', xlab = 'Time')
plot(residuals(mlr), fitted(mlr), ylab = 'Residuals', xlab = 'Fitted values')
plot(residuals(mlr), df_scaled$x1, ylab = 'Residuals', xlab = 'x1')
plot(residuals(mlr), df_scaled$x2, ylab = 'Residuals', xlab = 'x2')
plot(residuals(mlr), df_scaled$x3, ylab = 'Residuals', xlab = 'x3')
plot(residuals(mlr), df_scaled$x4, ylab = 'Residuals', xlab = 'x4')
par(mfrow = c(1, 1))
```



- **Residuals vs. Time:** The points are somehow distributed around the zero line. There doesn't appear to be a strong trend over time, suggesting no clear temporal pattern.
- **Residuals vs. Fitted Values:** The plot shows a funnel-shaped pattern, which means that the variability of residuals is not constant across different levels of the fitted values.
- **Residuals vs. Predictors (x1, x2, x3, x4):** There are noticeable patterns and clusters, particularly for **x2** and **x3**, which may indicate non-linearity.The residuals for **x4** are clustered, suggesting **x4** might be categorical

7. Durbin-Watson Test

```
library(lmtest)
dwtest(y ~ x1 + x2 + x3 + x4, data = df)
```

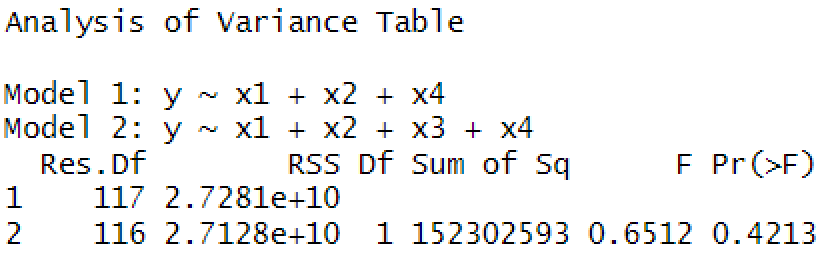


```
        Durbin-Watson test

data:  y ~ x1 + x2 + x3 + x4
DW = 1.3137, p-value = 3.101e-05
alternative hypothesis: true autocorrelation is greater than 0
```

- DW = 1.3137 suggests positive autocorrelation of residuals, meaning that consecutive residuals are correlated in a positive manner
- The p-value is **3.101e-05**, which is very small. The null hypothesis for the Durbin-Watson test is that there is no autocorrelation in the residuals. Since the p-value is much smaller than typical significance levels, we reject the null hypothesis. This indicates that autocorrelation is present in the residuals.

8. Model Comparison with F-tests

I.
```
# Model without x3
mlr1 <- lm(y ~ x1 + x2 + x4, data = df)
anova(mlr1, mlr)
```

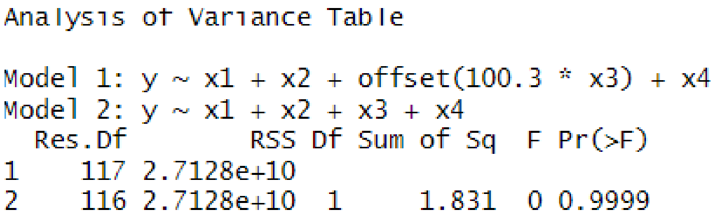


```
Analysis of Variance Table

Model 1: y ~ x1 + x2 + x4
Model 2: y ~ x1 + x2 + x3 + x4
  Res.Df        RSS Df Sum of Sq      F Pr(>F)
1    117 2.7281e+10
2    116 2.7128e+10  1 152302593 0.6512 0.4213
```

- The p-value is 0.4213. Since the p-value is greater than common significance levels, we fail to reject the null hypothesis, meaning that adding **x3** does not significantly improve the model.

II. # Model where $\hat{\beta}_3$ is constant using offset

```
mlr3 <- lm(y ~ x1 + x2 + offset(100.3 * x3) + x4, data = df)
summary(mlr3)
anova(mlr3, mlr)
```

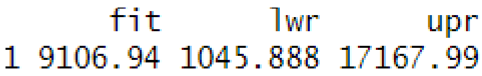


```
Analysis of Variance Table

Model 1: y ~ x1 + x2 + offset(100.3 * x3) + x4
Model 2: y ~ x1 + x2 + x3 + x4
  Res.Df        RSS Df Sum of Sq  F Pr(>F)
1    117 2.7128e+10
2    116 2.7128e+10  1     1.831  0 0.9999
```

- From the results of the MLR, we get $\hat{\beta}_3 = 100.3$
- To determine if setting a constant coefficient for **x3** improves model fitting, we specified 100.3 as an offset for β_3
- The p-value obtained is 0.9999. Since p-value is extremely high, we fail to reject the null hypothesis. It would be appropriate to treat **x3** as an offset or consider removing it altogether, as it does not add value in terms of improving model fit.

9. Prediction

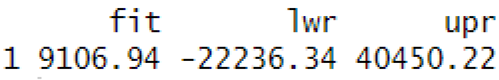
```
con <- data.frame(x1 = 50000, x2 = 3, x3 = 60, x4 = 0)

# Confidence interval prediction
predict(mlr, con, interval = 'confidence', level = 0.95)
```



```
      fit      lwr      upr
1 9106.94 1045.888 17167.99
```

- fit: The predicted value for the given input is 9106.94.
- lwr (Lower Bound): 1045.888 is the lower bound of the 95% confidence interval.
- upr (Upper Bound): 17167.99 is the upper bound of the 95% confidence interval.
- Interpretation: We are 95% confident that the mean response will fall between 1045.888 and 17167.99.

```
# Prediction interval prediction
predict(mlr, con, interval = 'prediction', level = 0.95)
```

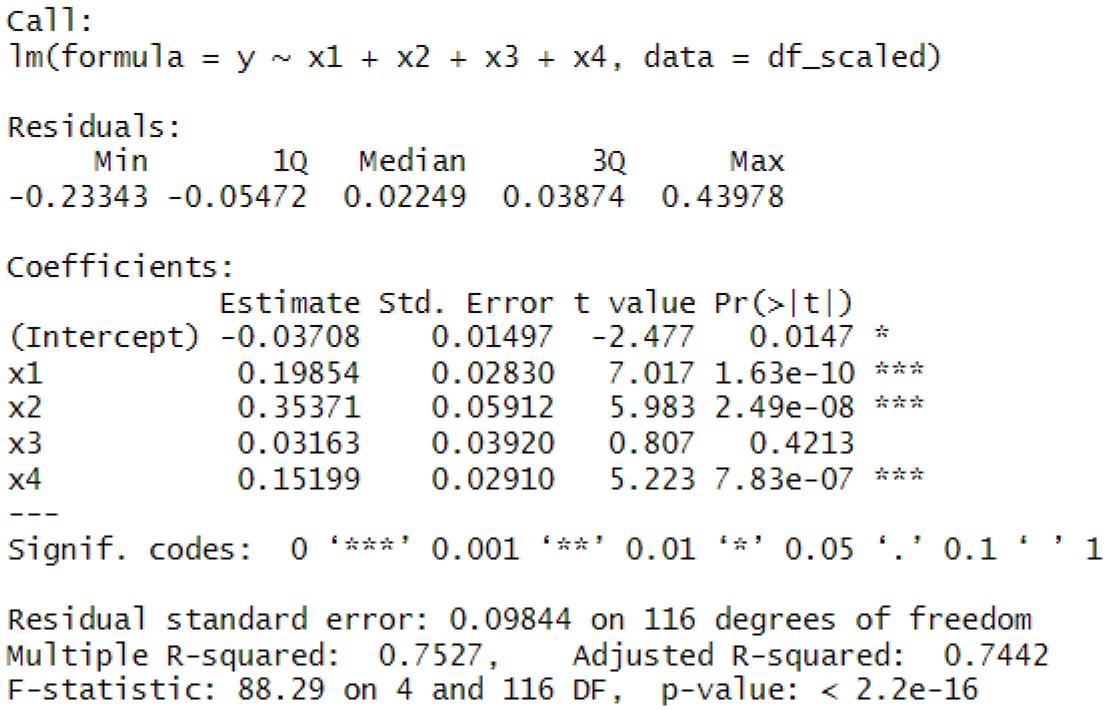


```
      fit       lwr      upr
1 9106.94 -22236.34 40450.22
```

- fit: The predicted value for the given input is 9106.94.
- lwr (Lower Bound): -22236.34 is the lower bound of the 95% prediction interval.
- upr (Upper Bound): 40450.22 is the upper bound of the 95% prediction interval.
- Interpretation: The prediction interval is very wide, ranging from -22236.34 to 40450.22, which suggests a lot of uncertainty in predicting individual responses.

10. Consideration of normalised data

```
# Normalised data
process <- preProcess(df, method=c("range"))
df_scaled <- predict(process, df)

mlr_scaled <- lm(y ~ x1+x2+x3+x4, data=df_scaled)
summary(mlr_scaled)
```



```
Call:
lm(formula = y ~ x1 + x2 + x3 + x4, data = df_scaled)

Residuals:
     Min       1Q   Median       3Q      Max 
-0.23343 -0.05472  0.02249  0.03874  0.43978 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) -0.03708    0.01497  -2.477   0.0147 *  
x1           0.19854    0.02830   7.017 1.63e-10 ***
x2           0.35371    0.05912   5.983 2.49e-08 ***
x3           0.03163    0.03920   0.807   0.4213    
x4           0.15199    0.02910   5.223 7.83e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.09844 on 116 degrees of freedom
Multiple R-squared:  0.7527,	Adjusted R-squared:  0.7442 
F-statistic: 88.29 on 4 and 116 DF,  p-value: < 2.2e-16
```

- The result shows that the normalised data does not improve the model fitting. Therefore, normalised data is not necessary.

11. Annex A (source code)

```
library(dplyr)
library(caret)

# Graphical display of the observed data.
data_raw <- read.table('aadt.txt',header=FALSE)
df <-
data.frame(y=data_raw$V1,x1=data_raw$V2,x2=data_raw$V3,x3=data_raw$V4,x4=data_raw$V5)
df$x4[df$x4 == 2]<-0
process <- preProcess(df, method=c("range"))
df_scaled <- predict(process, df)
plot(df)
plot(df_scaled)

# Fit a multiple linear regression model for both scaled and non-scaled data.
mlr <- lm(y ~ x1+x2+x3+x4, data=df)
summary(mlr)
mlr_scaled <- lm(y ~ x1+x2+x3+x4, data=df_scaled)
summary(mlr_scaled)

# Normality checking.
qqnorm(residuals(mlr),ylab='Residuals')
qqline(residuals(mlr))
qqnorm(residuals(mlr_scaled),ylab='Residuals')
qqline(residuals(mlr_scaled))

# Draw some plots of residuals.
par(mfrow=c(2,3))
plot(residuals(mlr),ylab='Residuals',xlab='Time')
plot(residuals(mlr),fitted(mlr),ylab='Residuals',xlab='Fitted values')
plot(residuals(mlr),df$x1,ylab='Residuals',xlab='x1')
plot(residuals(mlr),df$x2,ylab='Residuals',xlab='x2')
plot(residuals(mlr),df$x3,ylab='Residuals',xlab='x3')
plot(residuals(mlr),df$x4,ylab='Residuals',xlab='x4')
par(mfrow=c(1,1))
# scaled data
par(mfrow=c(2,3))
plot(residuals(mlr_scaled),ylab='Residuals',xlab='Time')
plot(residuals(mlr_scaled),fitted(mlr),ylab='Residuals',xlab='Fitted values')
plot(residuals(mlr_scaled),df_scaled$x1,ylab='Residuals',xlab='x1')
plot(residuals(mlr_scaled),df_scaled$x2,ylab='Residuals',xlab='x2')
plot(residuals(mlr_scaled),df_scaled$x3,ylab='Residuals',xlab='x3')
plot(residuals(mlr_scaled),df_scaled$x4,ylab='Residuals',xlab='x4')
par(mfrow=c(1,1))

# Durbin-Watson tests.
# install.packages( "lmtest" )
library(lmtest)
dwtest(y ~ x1+x2+x3+x4, data=df)
dwtest(y ~ x1+x2+x3+x4, data=df_scaled)
```

```
# Some F-tests.
mlr1 <- lm(y ~ x1+x2+x4,data=df)  #remove x3 as insignificant from above
anova(mlr1,mlr)

mlr1_scaled <- lm(y ~ x1+x2+x4,data=df_scaled)  #remove x3 as insignificant from above
anova(mlr1_scaled,mlr_scaled)

mlr2 <- lm(y ~ x1+x2+offset(100.3*x3)+x4,data=df)  # from MLR results, B3^=100.3
summary(mlr2)
anova(mlr2,mlr)

mlr2_scaled <- lm(y ~ x1+x2+offset(0.03*x3)+x4,data=df_scaled)  # from MLR(scaled)
results, B3^=0.03163
summary(mlr2_scaled)
anova(mlr2_scaled,mlr_scaled)

# Predicting non-scaled inputs
con <- data.frame(x1=50000,x2=3,x3=60,x4=0)
predict(mlr,con,interval='confidence',level=0.95)
predict(mlr,con,interval='prediction',level=0.95)

# Predicting scaled inputs
# scaling new input
new_input <- data.frame(y=-1,x1=50000,x2=3,x3=60,x4=0)
df_input <- rbind(new_input,df)
process <- preProcess(df_input[c('x1','x2','x3','x4')], method=c("range"))
df_input_scaled <- predict(process, df_input)
## scaled input: x1=0.045286737 ,x2=0.1666667 ,x3=0.83673469  ,x4=0
to_predict <- data.frame(x1=0.045286737 ,x2=0.1666667 ,x3=0.83673469  ,x4=0)
predict(mlr_scaled,to_predict,interval='confidence',level=0.95)
predict(mlr_scaled,to_predict,interval='prediction',level=0.95)

predicted_val <- (0.05732971*(max(df['y'])-min(df['y'])))+min(df['y'])
predicted_lwr_conf <- (0.00543876*(max(df['y'])-min(df['y'])))+min(df['y'])
predicted_upr_conf <- (0.1092207*(max(df['y'])-min(df['y'])))+min(df['y'])
predicted_lwr_pred <- (-0.1444346 *(max(df['y'])-min(df['y'])))+min(df['y'])
predicted_upr_pred <- (0.259094*(max(df['y'])-min(df['y'])))+min(df['y'])
conf<-data.frame(fit=predicted_val,lwr=predicted_lwr_conf,upr=predicted_upr_conf)
pred<-data.frame(fit=predicted_val,lwr=predicted_lwr_pred,upr=predicted_upr_pred)
conf
pred
```