QMST 5334 Final Report

Analysis of hospital readmissions for patients with diabetes

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1.0 Introduction

The prediction of hospital readmission is a significant healthcare research area from data analytics and information systems perspective. It aims to develop and analyze models using historical medical data to predict probability of a patient returning to hospital in a certain period, e.g., 30 or 90 days, after the discharge (Wang & Zhu, 2022). Prediction of hospital readmission is a complex research problem due to the intricate nature of various diseases and healthcare eco-systems (Hospital Readmissions, 2018). As data scientists, we can provide solutions to the healthcare sector for optimizing resources and reducing the readmissions and associated costs using technology and various analytical tools in hand. Apart from the tangible outcomes associated with these solutions, the development and implementation of analytical models for hospital readmissions is significant from humanitarian point of view: in a way that helps patients with better treatment, care, and support (Healthstream, 2021). The motivation of choosing this study is to apply data analytics, specifically statistical analytical tools to identify underlying causes for readmissions, to achieve meaningful and transparent predictions for effective decision making. The report is divided into various sections describing purpose and description of dataset, basic statistics, descriptive plots, linear regression, analysis of residuals and analysis of variance.

The dataset used for this project focuses on hospital readmissions data in United States. The data was collected in the form of comprehensive clinical records across hospitals throughout United States by Health Facts database – Cerner Corporation, Kansas City. The data was submitted to UCI Machine Learning Repository (UCI Machine Learning Repository, 2014) in 2014 on behalf of the Center for Clinical and Translational Research, Virginia Commonwealth University, a recipient of NIH CTSA grants UL1 TR00058 and a recipient of the CERNER data (Strack, et al., 2014). The dataset represents 10 years (1999-2008) of clinical care at 130 US hospitals and integrated delivery networks. It includes 55 features representing patient and hospital outcomes. Appendix A of the report presents the data dictionary for the variables in the dataset. Information was extracted from the database for encounters that satisfied the following criteria:

i. It is an inpatient encounter (a hospital admission).
ii. It is a diabetic encounter, that is, one during which any kind of diabetes was entered to the system as a diagnosis.
iii. The length of the stay was at least 1 day and at most 14 days.
iv. Laboratory tests were performed during the encounter.
v. Medications were administered during the encounter.

2.0 Descriptive Analytics

Exploratory analysis is the first and critical step in the data analysis process. It involves performing initial data investigations to discover patterns, spot anomalies, test hypothesis and check assumptions. It is done by describing distributions through summary statistics and graphical representations. For this study, we have chosen variable of significance from the dataset as Time in Hospital. It is also called Length of Stay (LOS). It is a clinical metric that measures the length of time elapsed between a patient's hospital admittance and discharge. Figure 1 shows an illustration of the dataset indicating the data variable 'time_in_hospital'.

	A	B	C	D	E	F	G	H	I	J
1	encounter	patient_nl	race	gender	age	weight	admission	discharge_	admission	time_in_hospital
2	2278392	8222157	Caucasian	Female	[0-10)	?	6	25	1	1
3	149190	55629189	Caucasian	Female	[10-20)	?	1	1	7	3
4	64410	86047875	AfricanAm	Female	[20-30)	?	1	1	7	2
5	500364	82442376	Caucasian	Male	[30-40)	?	1	1	7	2
6	16680	42519267	Caucasian	Male	[40-50)	?	1	1	7	1
7	35754	82637451	Caucasian	Male	[50-60)	?	2	1	2	3
8	55842	84259809	Caucasian	Male	[60-70)	?	3	1	2	4
9	63768	1.15E+08	Caucasian	Male	[70-80)	?	1	1	7	5
10	12522	48330783	Caucasian	Female	[80-90)	?	2	1	4	13
11	15738	63555939	Caucasian	Female	[90-100)	?	3	3	4	12
12	28236	89869032	AfricanAm	Female	[40-50)	?	1	1	7	9
13	36900	77391171	AfricanAm	Male	[60-70)	?	2	1	4	7
14	40926	85504905	Caucasian	Female	[40-50)	?	1	3	7	7
15	42570	77586282	Caucasian	Male	[80-90)	?	1	6	7	10

Figure 1: Illustration of 'time_in_hospital' variable from dataset(UCI Machine Learning Repository, 2014)

To visualize the basic statistics, we noted that the data type of the variable as numeric, (specifically integer) with the units as 'days. It was observed that no null values exist for the variable and the exploratory analysis can be carried out on 101766 observations. Table 1 shows the measures of centre and spread obtained for length of stay. It is observed that the average length of stay is 4.39 days. The national average for a hospital stay is 4.5 days, according to the Agency for Healthcare Research and Quality, at an average cost of $10,400 per day. The statistical analysis of this variable is significant as it is an Important indicator of efficiency of hospital management, patient quality of care, functional evaluation. It is reported that shorter hospital stays reduce the burden of medical fees, increase the bed turnover rate. This in turn increases the profit margin of hospitals, while lowering the social costs. Additionally, it is important for further analysis: determination of impact of length of stay on readmission risk.

Table 1: Summary of basic statistics of time in hospital

Measures of Location (in Days)	
Mean	4.395987
Median	4
Mode	3
Measures of spread (in Days)	
Range	13
IQR	4
Variance	8.910868
Standard Deviation	2.985108

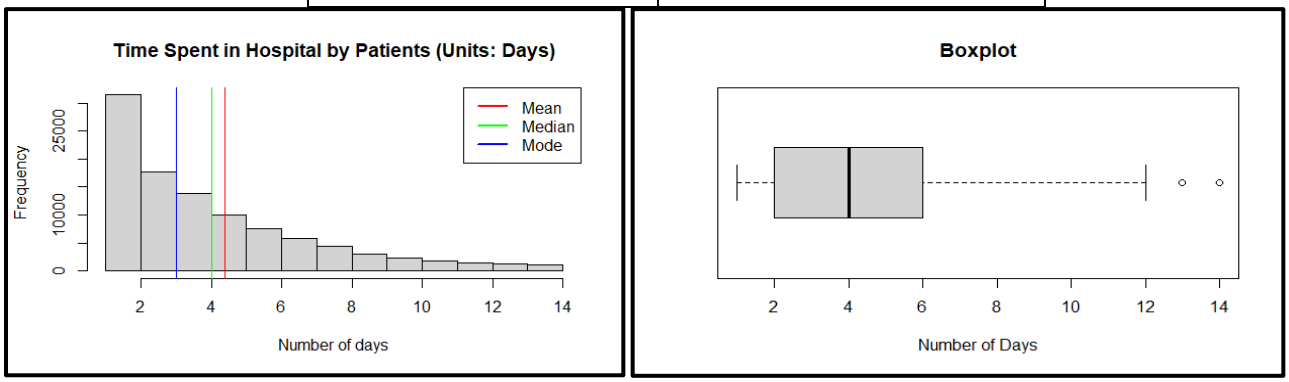


Figure 2: Graphical description of time in hospital using histogram (left) and boxplot (right)

Figure 2 shows the graphical description of the variable in the form of histogram (including mean, median and mode) and boxplots. The plots depict that the variable is a skewed distribution. The box plots show that the minimum and maximum values are 1 and 14 respectively while the three quartiles are 2, 4 and 6, respectively. The findings of the basic statistical analysis are: (i) Mean of time in hospital (4.395 days) obtained for this dataset is close to the national average of 4.5 days. (ii) Descriptive statistics indicate that time in hospital is a positively skewed distribution. (iii) 50% of the patients spent 2-6 days in the hospital (iv) 2252 patients who stayed in hospital for 13 days and 14 days are identified as outliers. Consequently, it was intriguing to understand that time in hospital could be analysed in association with other variables in the dataset from different perspectives. For further analysis we take a closer look at the number of medications administered and number of lab procedures carried out for the patients during their hospital stay. Figure 3 shows the distribution of number of medications administered to the patients in histogram and box plot representations. The histogram and box plot visual representations for number of lab procedures is shown in Figure 4. These figures indicate that the distributions are right skewed. Also, there are many outliers present in these distributions. From Table 2, it is noted that on an average 16 medicines were administer to the patients and 43 lab tests/ procedures were carried out. It would be interesting to determine correlation of length of stay with readmissions and severity and type of diagnosis variables in the dataset: whether patients with a lower length of stays were readmitted more frequently to the hospital, how many medications were administered, were any lab procedures carried out?

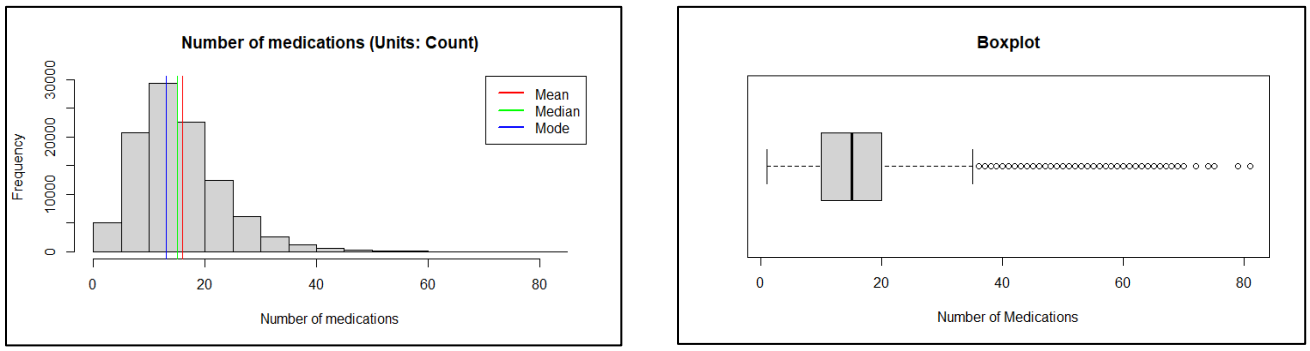
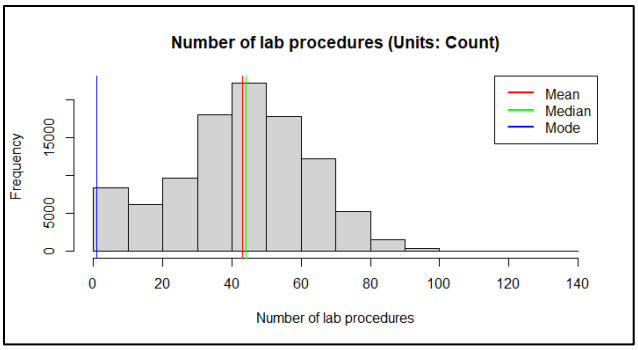


Figure 3: Graphical description of num of medications using histogram (left) and boxplot (right)



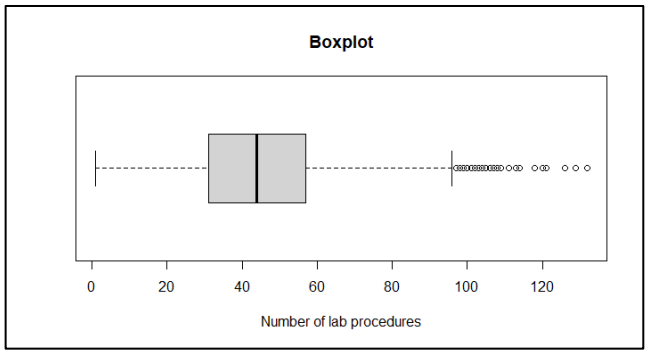


Figure 4: Graphical description of num of lab procedures using histogram (left) and boxplot (right)

Table 2: Summary of basic statistics

Num_medications	Num_lab_procedures
Five Number Stat: 1 10 15 20 81	Five Number Stat: 1 31 44 57 132
Mean - 16.02184 Median - 15 Mode - 13 Range - 80 IQR - 10 Variance - 66.05733 Standard Deviation - 8.1275	Mean - 43.095 Median - 44 Mode - 1 Range - 131 IQR - 26 Variance - 387.0805 Standard Deviation - 19.6743

3.0 Analysis of Variance (ANOVA)

Regression Analysis is a way of predicting the value of one variable from another. It is a hypothetical model of the relationship between two variables. The models we have used are linear ones. Therefore, we describe the relationship using the equation of a straight line. A model is used to predict an outcome (Y) based on set of predictors (X). For both the Simple and Multiple Regression Models we are considering the entire sample of the dataset of almost 100,000 samples.

In the simple regression model developed for this project, we wanted to see how the value of time_in_hospital (in days) varies for patients who have been re-admitted in hospital within 30 days based on the number of medications administered. Using outcome variable: time_in_hospital ($\hat{Y}$) And predictor variable: Num_medications (X_1), the equation of the model is: time_in_hospital = b_1(num_medications)+b_0. Pearson's and spearman correlation tests helped us to determine the relationship as shown in Figure 5. The correlation tests display estimate value with -1 to +1 so an estimate that is close to -1 is strong negative and the closer it gets to zero the weaker it gets and vice versa for the positive estimate. In our case we got both the test estimates to be around 0.48, which indicates a moderate positive correlation. By performing preliminary assessments using scatter plots we determine the correlation between the outcome and predictor variables. In the scatter plot, as depicted in Figure 6a, we cannot fully understand the relationship between the two variables time_in_hospital and num_medications as the variables are measured on a discrete scale, this presents us with a challenge. However, there could still be a linear relationship difficult to deduce. So, by using the heat map R scatter plot along with some base R functions such as smooth scatter and contour functions based on defining colors to regions according to the density of data instances present, we obtain heatmap R scatter plot shown in Figure 6b. From the heat map it is a positive correlation as confirmed by the tests. We obtain the equation with intercept and slope coefficients as: *time_in_hospital = 0.17929 (num_medications) + 1.73771*

```
        Pearson's product-moment correlation

data:  diabetic_data.less$time_in_hospital and diabetic_data.less$num_medications
t = 58.207, df = 11355, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.4650899 0.4934226
sample estimates:
      cor
0.4793812
```

```
        Spearman's rank correlation rho

data:  diabetic_data.less$time_in_hospital and diabetic_data.less$num_medications
S = 1.286e+11, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
     rho
0.4732401
```

Figure 5: Pearson's and Spearman's correlation test values

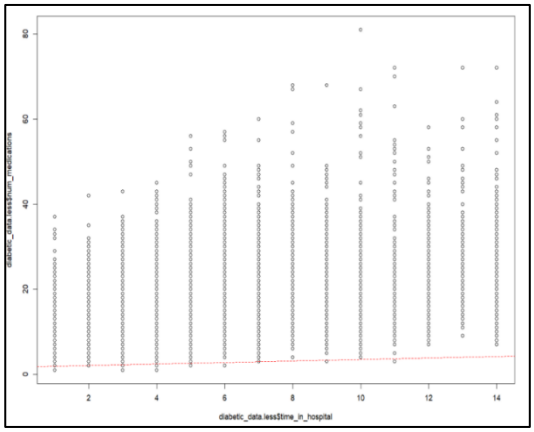


Figure 6a: Scatter Plot to depict the correlation between outcome and predictor variables.

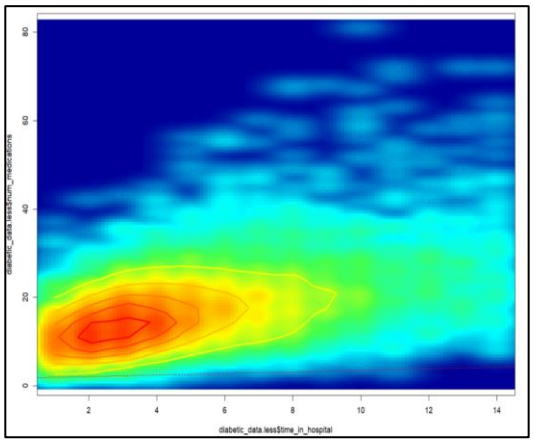


Figure 6b: Heat map for depicting the correlation between the outcome and predictor variables.

```
Call:
lm(formula = time_in_hospital ~ num_medications, data = diabetic_data.less)

Residuals:
    Min      1Q  Median      3Q     Max
-7.3714 -1.8892 -0.5306  1.4215 11.0073

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     1.73771    0.05773   30.10   <2e-16 ***
num_medications 0.17929    0.00308   58.21   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.658 on 11355 degrees of freedom
Multiple R-squared:  0.2298,    Adjusted R-squared:  0.2297
F-statistic:  3388 on 1 and 11355 DF,  p-value: < 2.2e-16
```

Figure 7: Summarized Output of the Simple Linear Model

```
                   2.5 %     97.5 %
(Intercept)     1.6245487 1.8508677
num_medications 0.1732509 0.1853263
```

Figure 8: Confidence Interval for Slope

From Figure 7, we understand that the num_medications coefficient suggests for every 10-count increase in the count of medications of the patient, we can expect increase in length of stay by 0.17929 * 10 = 1.7929 days, on average. Is the Slope statistically significant? Yes. It is, because the value of slope (b_1) in the Interval doesn't contain zero. Also, if the coefficient is large compared to the standard error, then statistically our coefficient will not be zero. From the 95% confidence interval test, shown in Figure 8, we can say with 95% confidence that slope lies between 0.1732 and 0.1853. Figure 5 also shows that num_medications coefficient is 58.21 standard errors away from zero and it is far from zero. The larger our t-statistic, the more certain we can be that the coefficient is not zero. The p-value is calculated using t-statistic from the t distribution and helps us understand our coefficient's significance to the model. In practical terms any p-value below 0.05 is significant. In our model, we can see that the intercept and num_medications have p-value of 2e-16 which is extremely small, and it is even below 0.001. We can conclude that the coefficients in this model are not zero. The residual standard error is a measure of how well the model fits the data. From our model summary, we can see that on average, the actual values are 2.658 days away from regression line on average. The F-statistic and overall p-value help us determine the result of our Hypothesis test. It is common for the F-statistic to be close to 1 if we have lot of predictors. However, for smaller models, a larger F-statistic and a small p-value indicates that null hypothesis should be rejected, and it clearly indicates that the coefficient in the model is not zero.

For Multiple Linear Regression model, we wanted to see how the value of time_in_hospital (in Days) varies for patients who have been re-admitted in hospital within 30 days based on the number of medications they have also used number of lab procedures they have undergone. In this case, The equation of the model: time_in_hospital = b_1(num_medications)+b_2(num_lb_procedures)+ b_0. We obtain the multicollinearity scatter plot shown in Figure 9. To quantify the correlation among the variables we use a function in R and obtain the correlation matrix as depicted in Figure 10. The equation with intercept and slope coefficients is obtained as 0.1578 (Num_medications) + 0.0299 (Num_lab_procedures) +

0.7758. From the summarized view of multiple regression model shown in Figure 11, the p-value of F-statistic is <2.2e-16, which is highly significant, this means at least one of the predictor variables is significantly related to the outcome variable. Also, change in number of num_medications and num_lab_procedures, the time_in_hospital of a patient is associated. For instance, for 10 count increase in the number of medications taken by the patient, we can expect an increase of 0.1578 * 10 = 1.578 days of patient staying in hospital (when the num_lab_procedures are constant). The confidence interval for model coefficients is shown in Figure 12. What about the goodness of fit for the Model? The adjusted R-squared value for multiple regression model is 0.2627, meaning that 26.27% of the variance in measure of days can be predicted by num_medications and num_lab_procedures number count. This model is better than the simple linear model with only num_medications which had an adjusted R-squared of 0.2297. The RSE gives us a measure of error of prediction. The multiple linear regression model gives an RSE rate of 54%, which is better than the simple linear regression model where the RSE was 0.558 (i.e., 55.8% error rate).

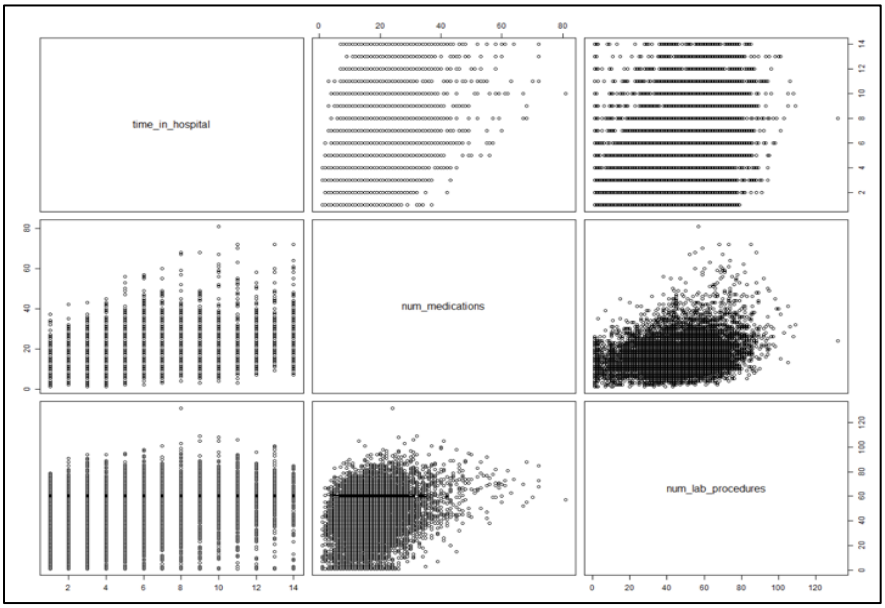


Figure 9: Multi Collinearity Scatter plot

	time_in_hospital	num_medications	num_lab_procedures
time_in_hospital	1.0000000	0.4793812	0.3176553
num_medications	0.4793812	1.0000000	0.3009453
num_lab_procedures	0.3176553	0.3009453	1.0000000

Figure 10: Correlation Matrix

```
Call:
lm(formula = time_in_hospital ~ num_medications + num_lab_procedures,
    data = diabetic_multi)

Residuals:
    Min      1Q  Median      3Q     Max
-6.9334 -1.8217 -0.5187  1.3418 11.9016

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.775825   0.070760   10.96   <2e-16 ***
num_medications   0.157830   0.003160   49.95   <2e-16 ***
num_lab_procedures 0.029951   0.001327   22.57   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.6 on 11354 degrees of freedom
Multiple R-squared:  0.2629,    Adjusted R-squared:  0.2627
F-statistic:  2024 on 2 and 11354 DF,  p-value: < 2.2e-16
```

Figure 11: Summary of the Multiple Linear Regression Model

	2.5 %	97.5 %
(Intercept)	0.57467654	0.66329459
num_medications	0.14865545	0.15269200
num_lab_procedures	0.03079195	0.03245947

Figure 12: Confidence Interval for the model coefficients

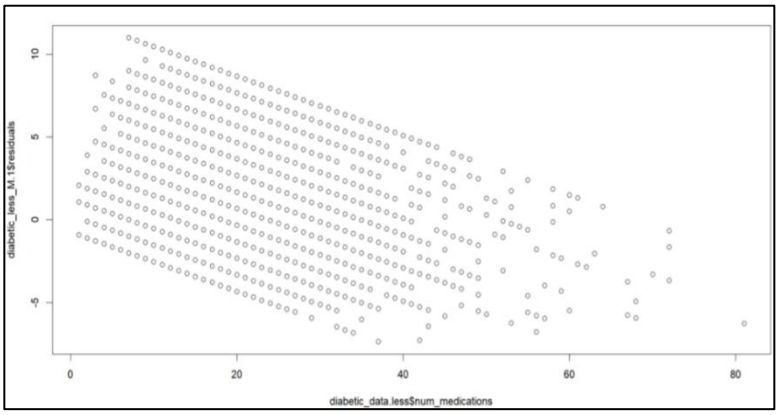


Figure 13: Residual Plot for the Simple Regression Model

For both models, we analyzed the residuals, to verify the Gauss Markov Theorem conditions. Additionally, we also try to explain and diagnose what multicollinearity is and explain how violations to the theorem affect the model. The residuals plot for the simple regression model is shown in Figure 13. From Simple linear regression Model, we used in regression analysis, we compute the mean value of residuals, i.e., -3.671336e^{-16}. Therefore, the first condition of Gauss Markov Theorem that errors have expectation zero is satisfied. Next, we test the residuals are not correlated among themselves, for this we do the Durbin Watson test. From Figure 14, the results of Durbin Watson test show that with a low p-value we reject the null hypothesis. We conclude that the residuals are correlated with each other. We then perform Breusch-Pagan test (Figure 15) to see if the Homoscedastic condition is satisfied or not satisfied. Based on the small p-value we reject the hypothesis that residuals are homoscedastic. We conclude that the errors do not have equal variances. We test for normality of the residuals by using Histogram (Figure 16) and QQ-plot (Figure 17). We observe that the distribution of errors is rightly skewed. Therefore, normality condition is not satisfied.

```
        Durbin-Watson test

data:  diabetic_less_M.1
DW = 1.9549, p-value = 0.0081
alternative hypothesis: true autocorrelation is greater than 0
```

Figure 14: Results for Durbin Watson Test

```
        studentized Breusch-Pagan test

data:  diabetic_less_M.1
BP = 256.68, df = 1, p-value < 2.2e-16
```

Figure 15: Results for Breusch Pagan Test

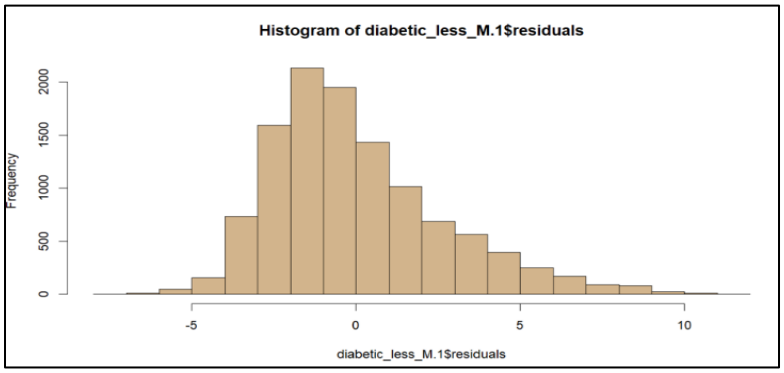


Figure 16: Histogram to test normality

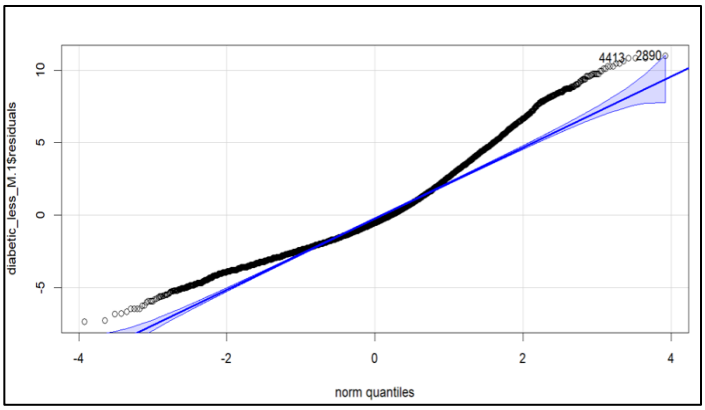


Figure 17: QQ-plot for the residuals

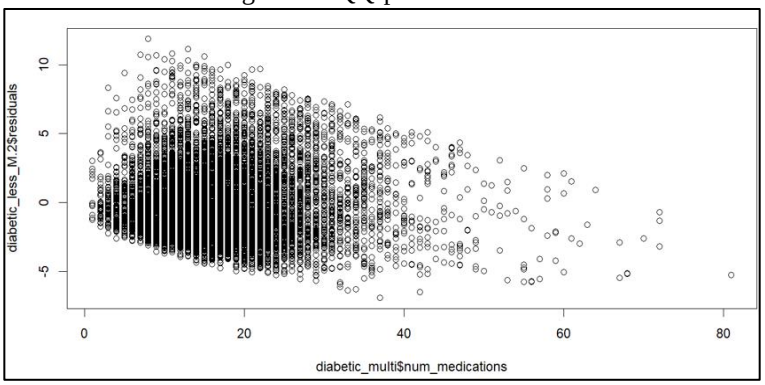


Figure 18: Residual plot for predictor variable Num_medications

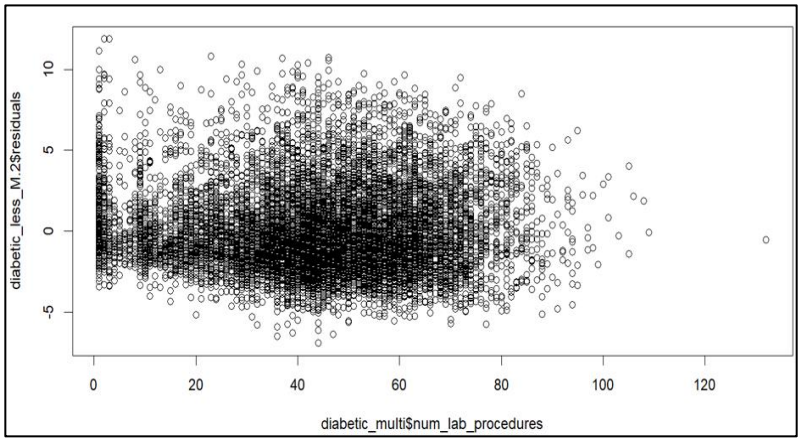


Figure 19: Residual Plot for predictor num_lab_procedures

From Figure 17, the qq-plot shows that few samples lie within the confidence band and by this we can state that the normality conditions are not satisfied. We try to test for normality Shapiro-Wilk test, if the residuals are Gaussian Distributed or not and since the number of samples is too large, we could not conduct this formal test. Therefore, from the above test we can say there is correlation between the variables we considered for the simple linear regression model. Similar analysis of residuals is carried out for multiple linear regression models. Figures 18 and 19 show the model's residuals with respect to the number of medications and lab procedures. For the multiple regression model, we computed the mean of residuals, i.e., 5.223827e-16, therefore the first condition of Gauss Markov theorem that errors have expectation of zero is satisfied. Next, we test to see if the residuals are correlated with each other or not, using Durbin Watson test, a low p-value is obtained, we reject null hypothesis. We conclude that the residuals are correlated with each other. Next, we perform Breusch-Pagan test to see if the homoscedasticity condition is satisfied or not. We reject the hypothesis that the residuals show homoscedasticity. Due to the p value being exceedingly small, we conclude that the errors do not have equal variances.

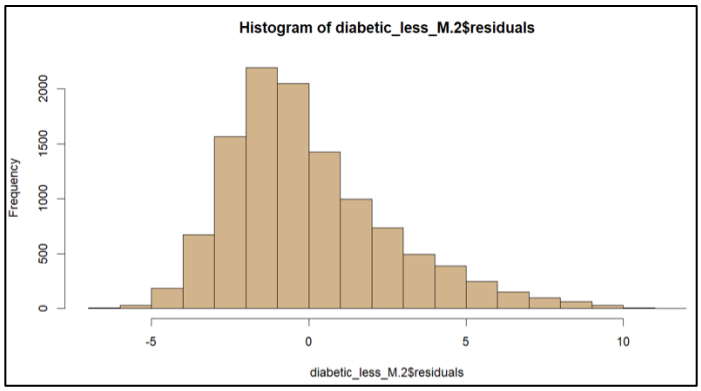


Figure 20: Histogram to check normality

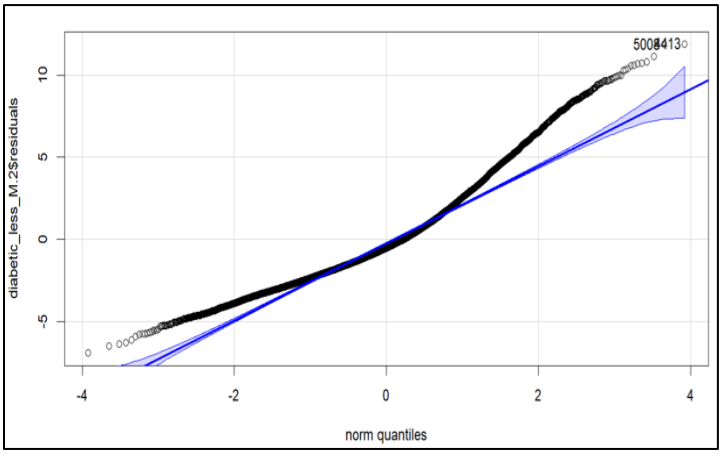


Figure 21: QQ-plot of multiple linear regression model's residuals to check normality

Using histogram shown in Figure 20, we conclude that there is no normality of the residuals as it is right skewed, and from the QQ-plot depicted in Figure 21, we conclude that the samples do not lie in the confidence band which results in not being normal. As seen from the simple linear regression model, the Shapiro-Wilk test does not work for the multiple linear regression model as well since the number of samples we have been working on for the model is large. Consequently, we checked for the multicollinearity between the variables, which indicates whether the predictors are correlated. If the predictors are correlated, the estimation of regression coefficients gets affected which indicates multicollinearity!

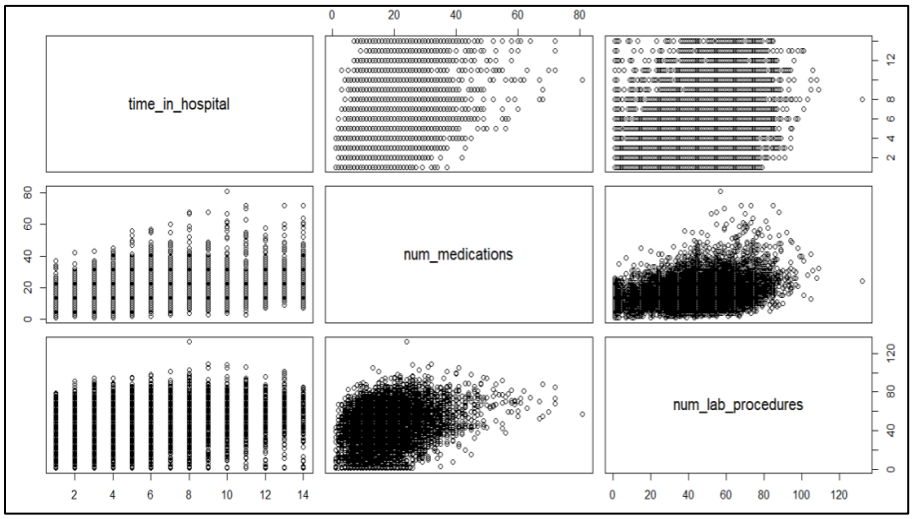


Figure 22: Scatter plots for three variables to test multicollinearity

	time_in_hospital	num_medications	num_lab_procedures
time_in_hospital	1.0000	0.4794	0.3177
num_medications	0.4794	1.0000	0.3009
num_lab_procedures	0.3177	0.3009	1.0000

Figure 23: Correlation Matrix for the Multiple linear regression model

From Figure 22, we can see the trend of the collinearity among the three variables, however using the correlation function, we try to quantify the correlation which is said to be positive if the estimate is greater than 0. As displayed in Figure 23, we observe that the predictors number of medications and number of lab procedures are correlated. The square root of the VIF (Variance Inflation Factor) says how much larger the standard error is, as compared to the case of predictors that are uncorrelated. So, we calculated the VIF for the model which is obtained as 1.099588. Our model has VIF > 1 which indicates there is no reason for concern, and it is possible to say that there is correlation between the two predictors. Looking at the results of both models, it is safe to say that regression models 1 and 2 satisfy only one of the four conditions of the Gauss-Markov theorem conditions, i.e., expectation of errors is zero. From the tests conducted it is visible that residuals are correlated and display heteroscedasticity and are not normally distributed. Since the number of samples is greater than 5000, the formal Shapiro-Wilk test cannot be performed on our data. There is evidence of multicollinearity among the predictors used in regression model 2.

With the results obtained from regression testing and analysis of residuals it is evident that analyzing models with continuous variables or numerical data is not always an appropriate modelling approach. With the help of the methodologies used in analysis of variance, we can use categorical variables. We create models by factoring the categorical variables and adding them to the linear models.

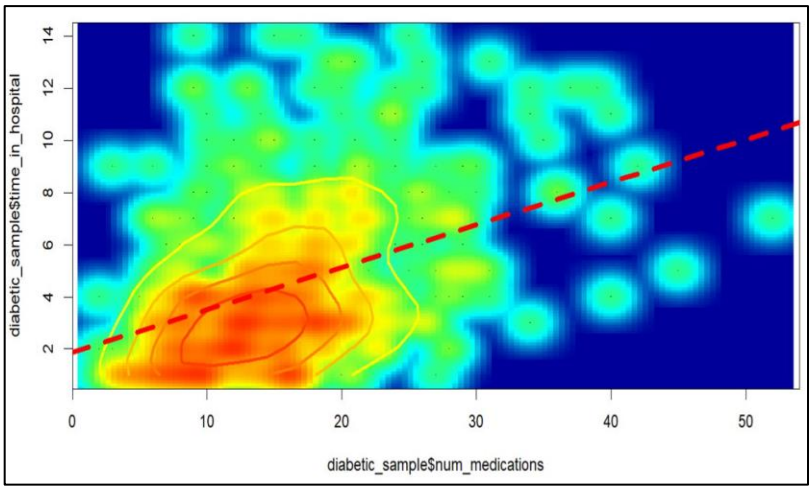


Figure 24: Heat scatter plot for displaying correlation between the variables

```
Call:
lm(formula = time_in_hospital ~ num_medications, data = diabetic_sample)

Residuals:
    Min      1Q  Median      3Q     Max
-5.2753 -1.8590 -0.5552  1.1888 10.6530

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.88288    0.28703   6.560 1.35e-10 ***
num_medications  0.16268    0.01661   9.794  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.745 on 498 degrees of freedom
Multiple R-squared:  0.1615,    Adjusted R-squared:  0.1598
F-statistic: 95.92 on 1 and 498 DF,  p-value: < 2.2e-16
```

Figure 25: Summarized Output of the Simple Linear Model

By performing analysis of variance (ANOVA) we can determine up to what percent of the samples have been explored, and how much are yet to be extracted and explained, and instead of creating multiple t-tests we use ANOVA groups differences by comparing means of each group. Like a t-test, we use ANOVA test with a null hypothesis that the means are the same. Since we can know the method that will let us use categorical variable in our linear models, we are designing new models with random 500 samples from the total 100,000 samples. We are considering the same simple linear regression model as in the before section, i.e., outcome variable is time_in_hospital ($\hat{Y}$) And predictor variable is num_medications (X_1). The equation of the model: $\hat{Y} = b_1X_1 + b_0$.From Figure 24, we show a density heat scatter plot to understand correlation using R programming base functions such as Smooth scatter and contour. We computed Pearson's coefficient which resulted in sample estimate of 0.40187 and 95% confidence intervals as 0.32 and 0.47. These results show that there is a positive correlation.

```
                    2.5 %    97.5 %
(Intercept)     1.3189358 2.446823
num_medications 0.1300476 0.195320
```

Figure 26: 95% confidence intervals

```
Call:
lm(formula = time_in_hospital ~ num_medications + readmitted,
    data = diabetic_sample)

Residuals:
    Min      1Q  Median      3Q     Max
-5.6834 -1.9336 -0.4633  1.3895 10.2281

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      1.53738    0.43497   3.534 0.000447 ***
num_medications  0.16175    0.01657   9.763  < 2e-16 ***
readmitted>30    0.77882    0.39601   1.967 0.049780 *
readmittedNO     0.16120    0.37987   0.424 0.671484
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.732 on 496 degrees of freedom
Multiple R-squared:  0.1726,    Adjusted R-squared:  0.1676
F-statistic:  34.5 on 3 and 496 DF,  p-value: < 2.2e-16
```

Figure 27: Summarized Output of the Multiple Regression Linear Model

From the summary shown in Figure 25, we can understand that the slope is significant since it is not equal to zero, and t value is not small. Additionally, the p-value is highly significant when we consider the alpha to be 95% which is 0.05. We check the 95% confidence interval for the values of intercept and slope, as shown in Figure 26. The goodness of fit of the model is 0.6204048, and with all the values and interpretation we can assume the model to be a good one. For the multiple linear regression model the outcome variable is same as the previous model i.e., time_in_hospital, but this time in the predictor variables instead of just having numerical variable we have taken an addition of a categorical variable. The outcome variable time_in_hospital ($\hat{Y}$). The predictors variables are num_medications (X_1) & readmitted (X2). The equation of the model: $\hat{Y} = b_1X_1 + b_2X_2 + b_0$. From the summary shown in Figure 27, for the new multiple regression model, we can see that both the predictor variables are significant, since the estimate coefficients are not equal to zero, but when analyzing the t-value the readmittedNO is closer to zero since it is 0.424, and the rest three are 2 and above. The p values are significant, but it varies based on the alpha we assume for the study. Since the alpha we take is 0.05, only readmitted<30 and readmitted>30 is significant and not readmittedNO.

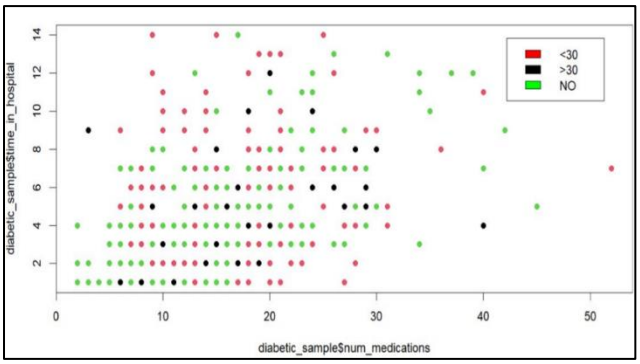


Figure 28: Scatter plot based on groups of the categorical variable

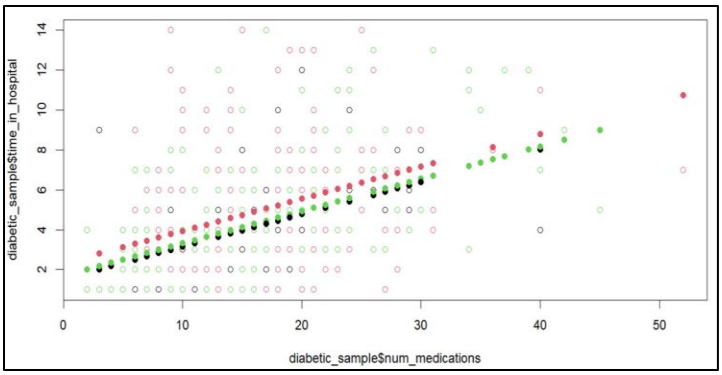


Figure 29: Linear regression analysis predicted lines

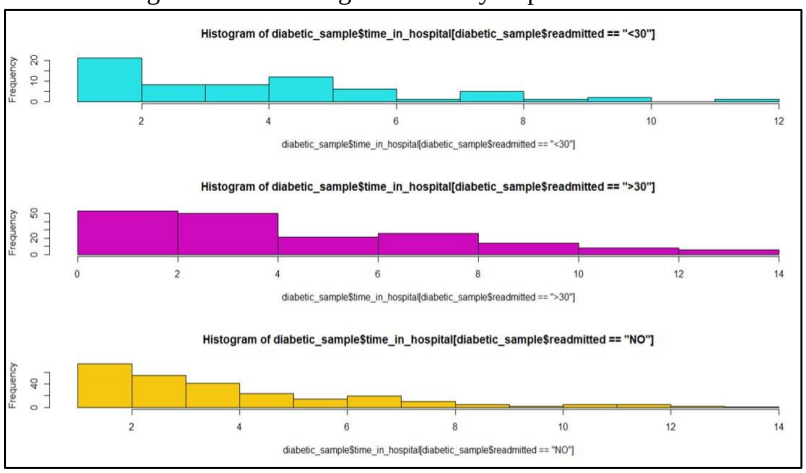


Figure 30: Histogram to visualize time in hospital based on categorical variables

When comparing the multiple models with linear model, the adjusted R-squared is better as 0.1676 > 0.1598. Also, the residual standard error is less for the multiple regression model when compared to the simple model. So, we can say that the new multiple linear regression model is better than the simple model. Figure 28 shows the scatter plot of the three groups of the categorical variable with respect to number of medications and number of days in the hospital. It is interesting to note that most of the samples lie between number of days around 1-10 days and number of medications administered as 1-30. Using linear regression analysis, the predicted lines are obtained and shown in Figure 29. To check the variability in each group, we plot the histograms of the categories separately. The histograms are shown in Figure 30. The box plots are shown in Figure 31 to explain the variability of observations in each group.

We designate readmitted<30 as the base group and outcome variable as time_in_hospital. The equation of the regression model considering the categorical variables is: $\widehat{y_i} = b_0 + b_1(readmitted > 30)_i + b_2\,(readmitted\ NO)_i$. The results obtained for ANOVA are depicted in Figure 32. It is observed that intercept (base category) is significant as compared to readmittedNO and readmitted>30. In addition, this model shows that a low R squared value id obtained for this categorical variable as a predictor for time in hospital. The amount of variability is explained by F-ratio. In this case, the F-ratio is 3.43. It is an indicator of amount of variability explained by the model and compared to the error in the model. Since the F-ratio is high, it means that there is a difference in means. Similar conclusions can be drawn from the summary of the ANOVA analysis from Figure 33. Since the ANOVA reflects whether the experiment was successful or not, additional tests are required to find out where the differences lie. We use Tukey post-hoc test to compare all pairs of means as shown in Figure 34. In the Tukey Post-hoc tests, a single-step multiple comparison procedure is followed to find means that are significantly different from each other. It compares all pairs of means. It is based on a studentized range distribution (q). From the Tukey post-hoc tests and confidence intervals, there is a difference in the means of the different groups. Figure 35 shows the confidence intervals for multiple comparisons of means using Tukey contrasts. In conclusion, we can perform analysis of variance on the outcome variable time in hospital. It would be interesting to test our model for logistic regression as a part of further investigation.

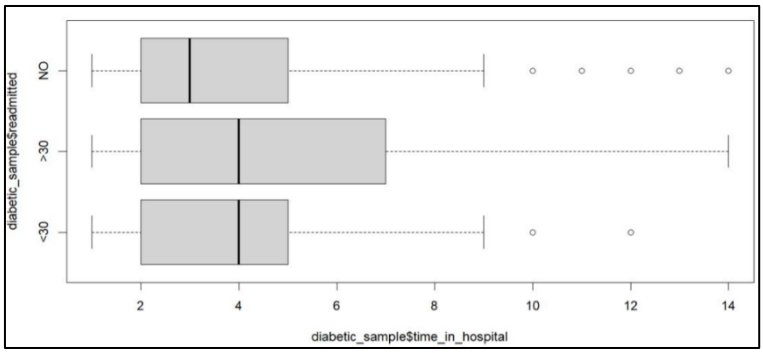


Figure 31: Visual comparison using boxplots to account for variability of observations within each group

```
> anova_m1 <- lm(time_in_hospital~readmitted, data=diabetic_sample)
> summary(anova_m1)

Call:
lm(formula = time_in_hospital ~ readmitted, data = diabetic_sample)

Residuals:
    Min      1Q  Median      3Q     Max
-3.8933 -2.1556 -0.8933  1.8444  9.8444

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   4.20000    0.36961  11.363   <2e-16 ***
readmitted>30  0.69326    0.43185   1.605    0.109
readmittedNO  -0.04436    0.41371  -0.107    0.915
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 2.98 on 497 degrees of freedom
Multiple R-squared:  0.01363,   Adjusted R-squared:  0.009657
F-statistic: 3.433 on 2 and 497 DF,  p-value: 0.03306
```

Figure 32: Summary of regression model (ANOVA)

```
> summary(anova.1)
             Df Sum Sq Mean Sq F value Pr(>F)
readmitted    2     61   30.48   3.433 0.0331 *
Residuals   497   4413    8.88
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Figure 33: Summary of regression model (ANOVA)

```
        Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts


Fit: aov(formula = anova_m1)

Linear Hypotheses:
               Estimate Std. Error t value Pr(>|t|)
>30 - <30 == 0  0.69326    0.43185   1.605   0.2392
NO - <30 == 0  -0.04436    0.41371  -0.107   0.9936
NO - >30 == 0  -0.73762    0.29058  -2.538   0.0296 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Adjusted p values reported -- single-step method)
```

Figure 34: Tukey Post Hoc tests for the model

```
> confint(postHocs)

         Simultaneous Confidence Intervals

Multiple Comparisons of Means: Tukey Contrasts


Fit: aov(formula = anova_m1)

Quantile = 2.3377
95% family-wise confidence level


Linear Hypotheses:
                    Estimate lwr       upr
>30 - <30 == 0  0.69326 -0.31625  1.70277
NO - <30 == 0  -0.04436 -1.01148  0.92276
NO - >30 == 0  -0.73762 -1.41689 -0.05834
```

Figure 35: Tukey Post Hoc confidence intervals

This report summarises the basic descriptive statistics, analysis of the length of stay of patients with respect to factors such as gender and readmission. In the post mid-term part of the project, we studied the correlations and performed regression analysis for different variables. We conducted the analysis of residuals and analysis of variance for the dataset. In conclusion, this project was a great learning opportunity for statistical methodology for real-life application.

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Appendix A: Data Dictionary

S.No.	Field Name	Field Type	Description and Values
1	Encounter ID	Numeric	Unique identifier of an encounter
2	Patient number	Numeric	Unique Identifier of a patient
3	Race	Character	Values: Caucasian, Asian, African American, Hispanic, and other
4	Gender	Character	Values: male, female, and unknown/invalid
5	Age	Character	Grouped in 10-year intervals: [0, 10), [10, 20) ..., [90, 100)
6	Weight	Numeric	Weight in pounds
7	Admission Type	Character	Integer identifier corresponding to 8 distinct values, for example, emergency, urgent, elective, newborn, and not available
8	Discharge Disposition	Character	Integer identifier corresponding to 29 distinct values, for example, discharged to home, expired, discharged/transferred to another type of inpatient care institution and not available
9	Admission source	Character	Integer identifier corresponding to 26 distinct values, for example, physician referral, clinic referral, court/law enforcement, emergency room, and transfer from a hospital
10	Time in Hospital	Numeric	Integer number of days between admission and discharge
11	Payer code	Character	Integer identifier corresponding to 23 distinct values, for example, Blue Cross\BlueShield, Medicare, and self-pay
12	Medical Specialty	Character	Integer identifier of a specialty of the admitting physician, corresponding to 84 distinct values, for example, cardiology, internal medicine, family\general practice, and surgeon
13	Number of lab procedures	Numeric	Number of lab tests performed during the encounter
14	Number of procedures	Numeric	Number of procedures (other than lab tests) performed during the encounter
15	Number of medications	Numeric	Number of distinct generic names administered during the encounter
16	Number of outpatient visits	Numeric	Number of outpatient visits of the patient in the year preceding the encounter
17	Number of emergency visits	Numeric	Number of emergency visits of the patient in the year preceding the encounter
18	Number of inpatient visits	Numeric	Number of inpatient visits of the patient in the year preceding the encounter
19	Diagnosis 1	Character	The primary diagnosis (coded as first three digits of ICD9); 848 distinct values
20	Diagnosis 2	Character	Secondary diagnosis (coded as first three digits of ICD9); 923 distinct values
21	Diagnosis 3	Character	Additional secondary diagnosis (coded as first three digits of ICD9); 954 distinct values
22	Number of Diagnoses	Numeric	Number of diagnoses entered to the system
23	Glucose serum test result	Character	Indicates the range of the result or if the test was not taken. Values: “>200,” “>300,” “normal,” and “none” if not measured
24	Alc test result	Character	Indicates the range of the result or if the test was not taken. Values: “>8” if the result was greater than 8%, “>7” if the result was greater than 7% but less than 8%, “normal “if the result was less than 7%, and “none” if not measured.
25	Change of medications	Character	Indicates if there was a change in diabetic medications (either dosage or generic name). Values: “change” and “no change”
26	Diabetes medications	Character	Indicates if there was any diabetic medication prescribed. Values: “yes” and “no”

27	24 features for medications	Character	For the generic names: metformin, repaglinide, Nate glinide, chlorpropamide, glimepiride, acetohexamide, glipizide, glyburide, tolbutamide, pioglitazone, rosiglitazone, acarbose, miglitol, troglitazone, tolazamide, examide, sitagliptin, insulin, glyburide-metformin, glipizide-metformin, glimepiride-pioglitazone, metformin-rosiglitazone, and metformin-pioglitazone, the feature indicates whether the drug was prescribed or there was a change in the dosage. Values: "up" if the dosage was increased during the encounter, "down" if the dosage was decreased, "steady" if the dosage did not change, and "no" if the drug was not prescribed
28	Readmitted	Character	Days to inpatient readmission. Values: "<30" if the patient was readmitted in less than30 days, ">30" if the patient was readmitted in more than 30 days, and "No" for no record of readmission.