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D208 – Predictive Modeling, Task 2

October 11, 2023

Western Governors University

Part A1

Which variables influence the probability of a patient being readmitted within a month of release?

Part A2

The goal of the data analysis is to determine if the probability of the patient being readmitted within a month of release is influenced by other variables in the dataset.

Part B1

Logistic regression relies on four key assumptions: first, a linear relationship between predictor variables and the log-odds of the dependent variable; second, independence of observations, meaning that one observation's outcome does not influence another's; third, minimal or no multicollinearity among independent variables to prevent high correlation issues; and finally, a reasonably large sample size, typically with at least 10-20 observations per predictor variable to ensure the reliability of statistical inference. Adherence to these assumptions is crucial for accurate model estimation and interpretation.

Part B2

Two benefits of using R for logistic regression analysis are its open-source nature and extensive package ecosystem. Being open-source, R is freely available, making it accessible to a broad user base and eliminating licensing costs. Moreover, R has a large collection of packages tailored for statistical modeling, including logistic regression, allowing users to tap into a wealth of specialized functions and tools for data preprocessing, model building, and result interpretation. These advantages enhance the efficiency and versatility of logistic regression analysis in R.

Part B3

The target variable for this analysis is categorical. Logistic regression is appropriate for this analysis because it can help to understand the relationship between a categorical response variable and one or more explanatory variables that are continuous and/or categorical.

Part C1

The goals of the data cleaning process are to detect and treat duplicate values, missing values, and outlier values. The unique values for categorical variables also need to be detected to check for inconsistency in presentation of the data.

Duplicate values are detected using the `sum(duplicated())` functions. No duplicate values were detected.

Missing values are detected using the `colSums(is.na())` functions. No missing values were detected.

Outliers for quantitative variables are detected using a function that uses the mean(), sd(), and sum() functions to calculate the z-score and count how many z-scores have a value greater than three or less than negative three. Seven variables were found to have outliers.

For categorical variables, unique values are detected using the unique() function. None of the categorical variables had inconsistent presentation of the data.

Part C2

Summary statistics for dependent variable

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of ReAdmis	6331	3669	10000

Summary statistics for categorical independent variables

Column Labels <input type="button" value="v"/>				
	Female	Male	Nonbinary	Grand Total
Count of Gender	5018	4768	214	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of HighBlood	5910	4090	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of Stroke	8007	1993	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of Overweight	2906	7094	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of Arthritis	6426	3574	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of Diabetes	7262	2738	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of Hyperlipidemia	6628	3372	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of BackPain	5886	4114	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of Anxiety	6785	3215	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of Allergic_rhinitis	6059	3941	10000

Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of Reflux_esophagitis	5865	4135	10000

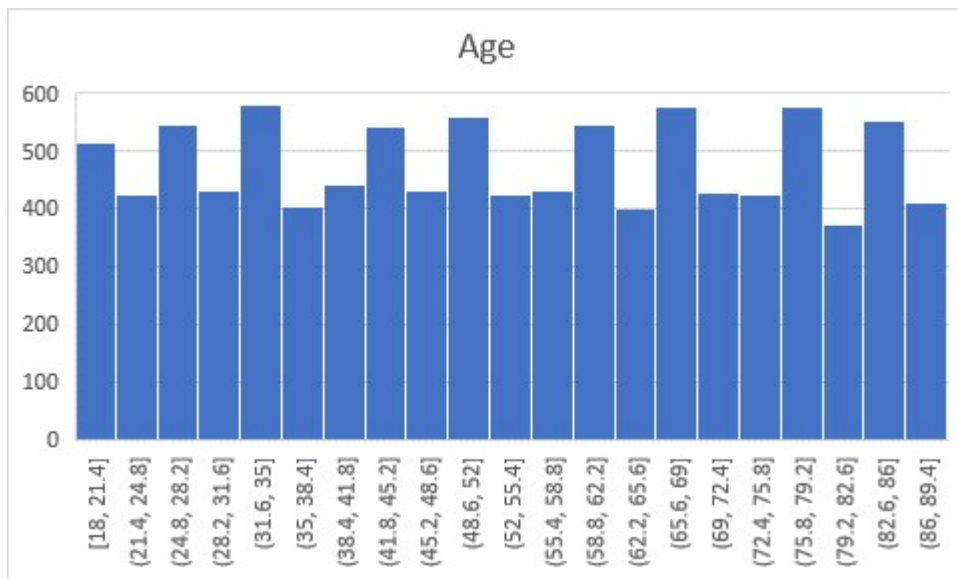
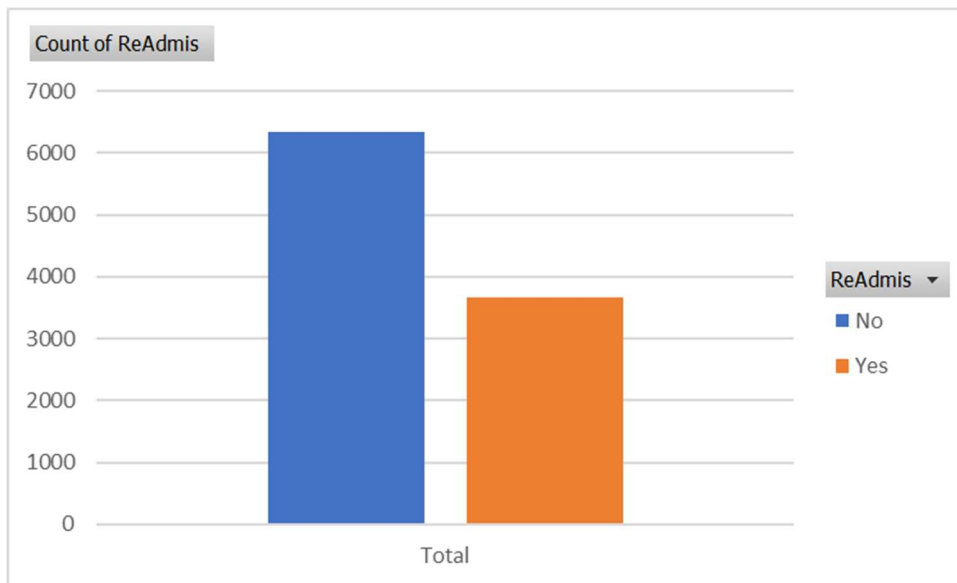
Column Labels <input type="button" value="v"/>			
	No	Yes	Grand Total
Count of Asthma	7107	2893	10000

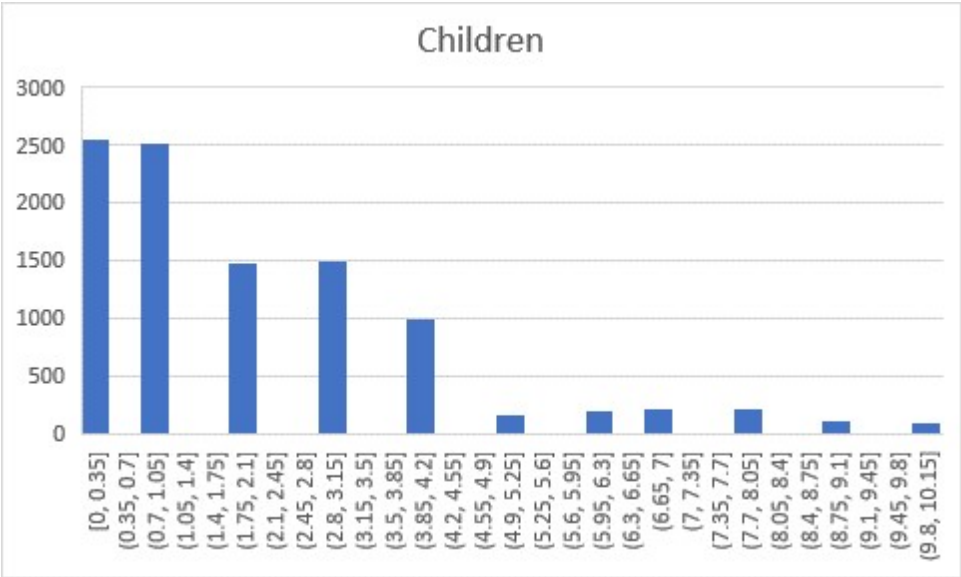
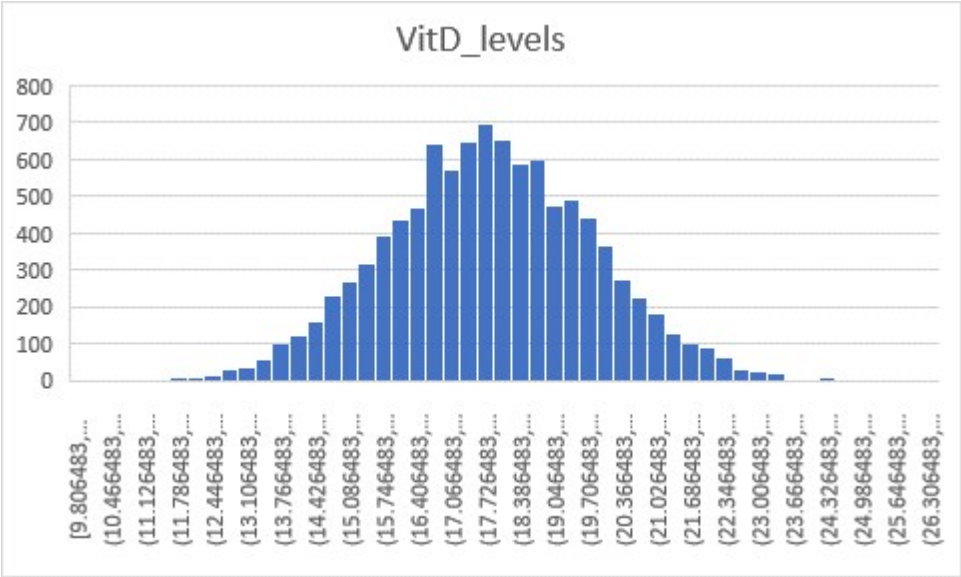
Summary statistics for quantitative independent variables

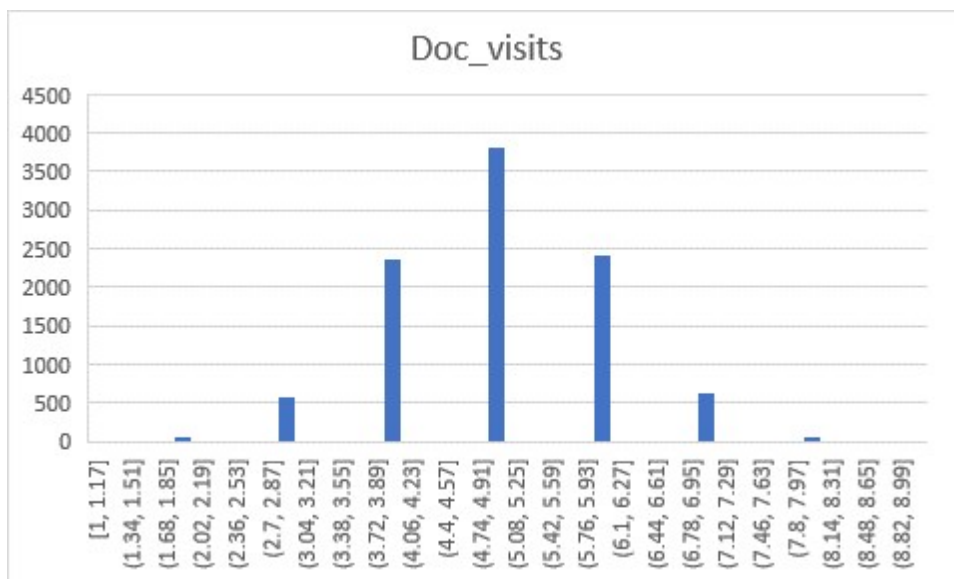
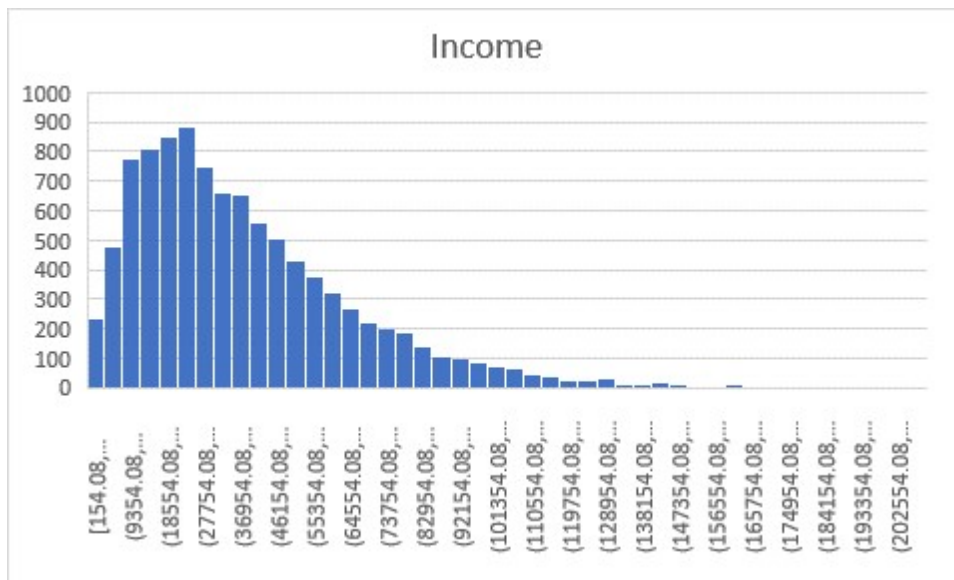
```
> # Summary statistics for independent quantitative variables
> summary(medical$Children)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.000  0.000   1.000   2.097   3.000  10.000
> summary(medical$Age)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 18.00  36.00  53.00  53.51  71.00  89.00
> summary(medical$Income)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 154.1 19598.8 33768.4 40490.5 54296.4 207249.1
> summary(medical$vitD_levels)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 9.806 16.626 17.951 17.964 19.348 26.394
> summary(medical$Doc_visits)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 1.000  4.000  5.000  5.012  6.000  9.000
> summary(medical$Full_meals_eaten)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.000  0.000  1.000  1.001  2.000  7.000
> summary(medical$vitD_supp)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 0.0000 0.0000  0.0000  0.3989  1.0000  5.0000
> summary(medical$Initial_days)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 1.002  7.896 35.836 34.455 61.161 71.981
> summary(medical$TotalCharge)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 1938  3179  5214  5312  7460  9181
> summary(medical$Additional_charges)
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 3126  7986 11574 12935 15626 30566
```

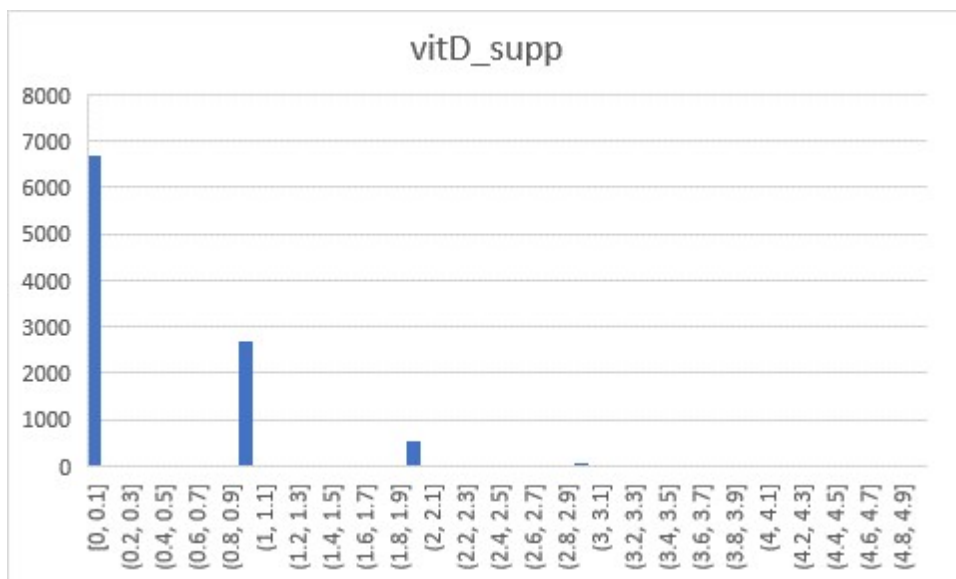
Part C3

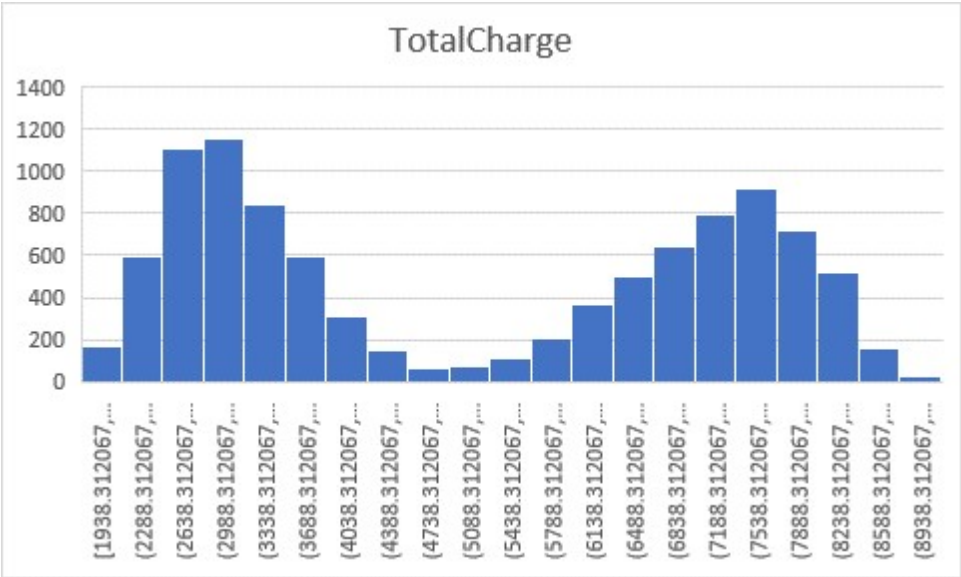
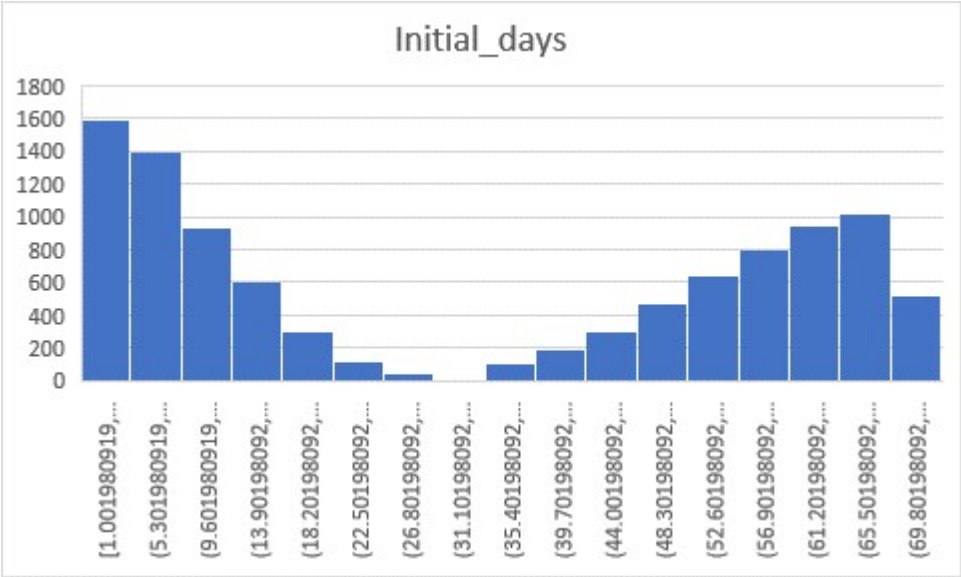
Univariate visualizations (Paula, 2020b)

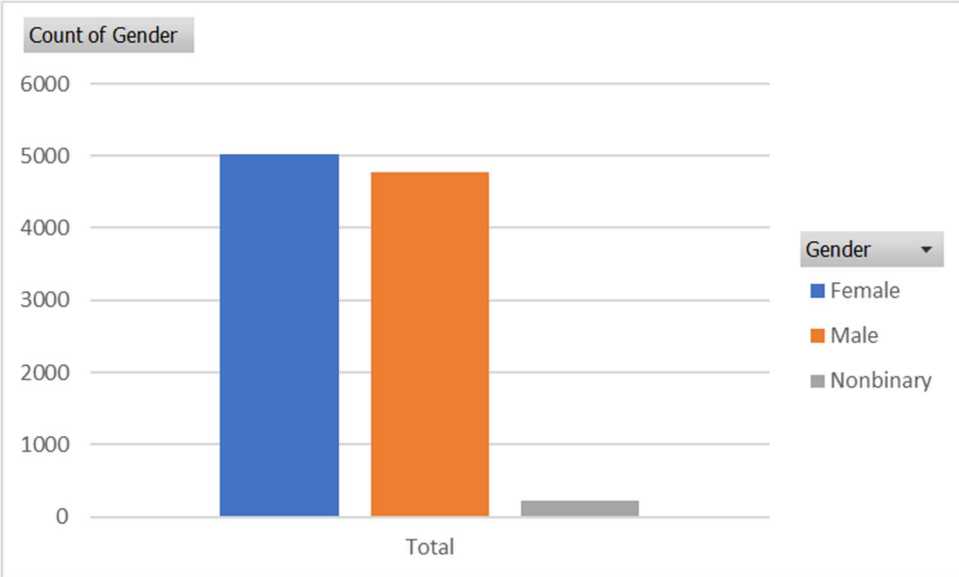
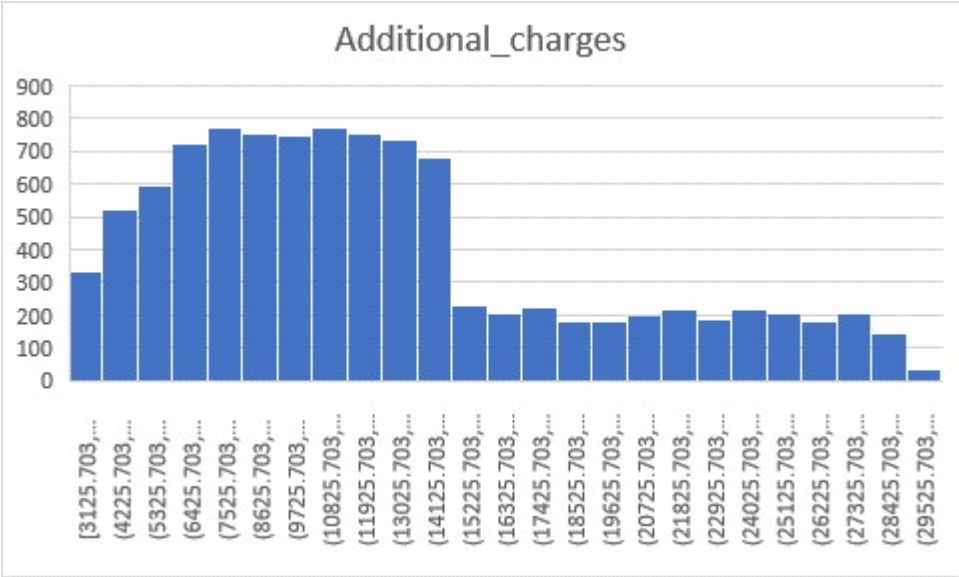


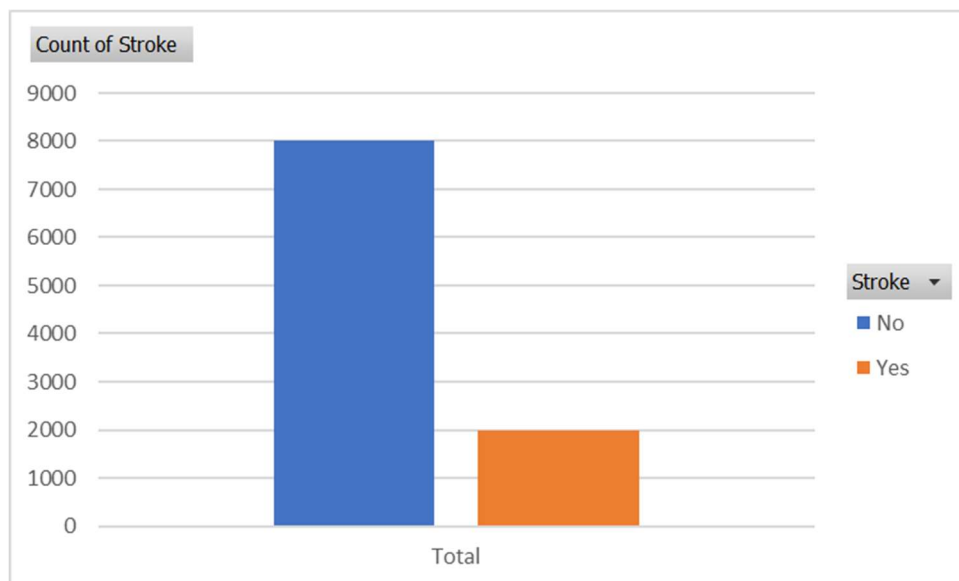
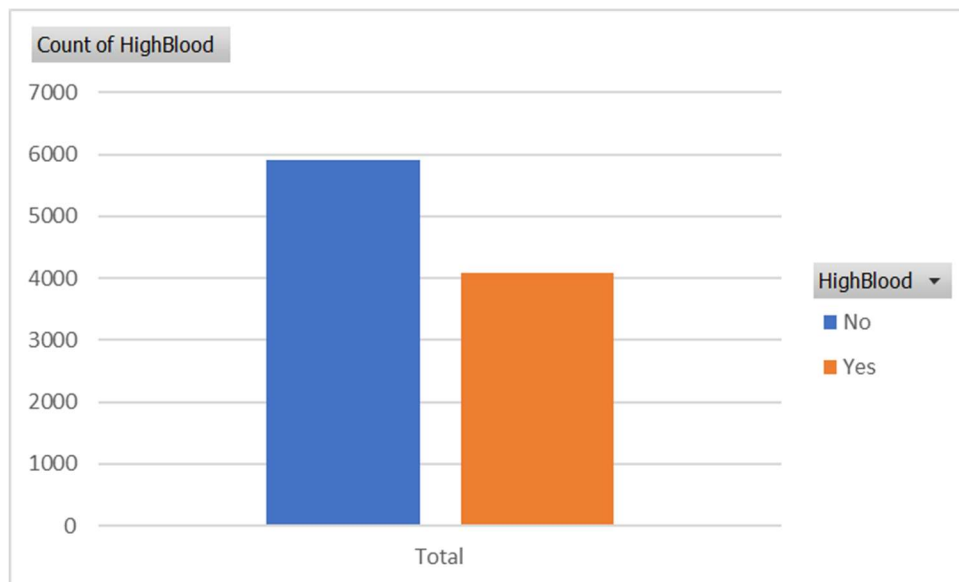


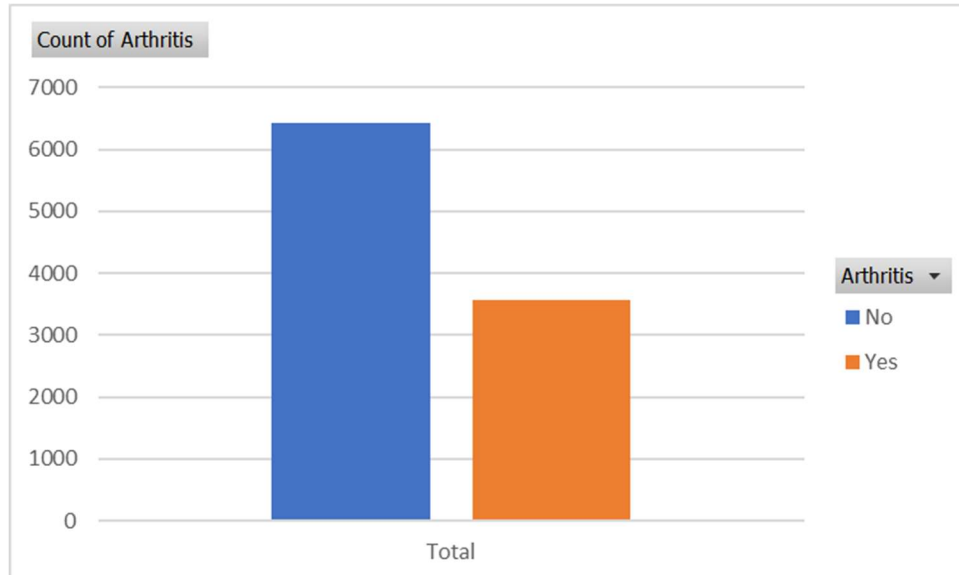
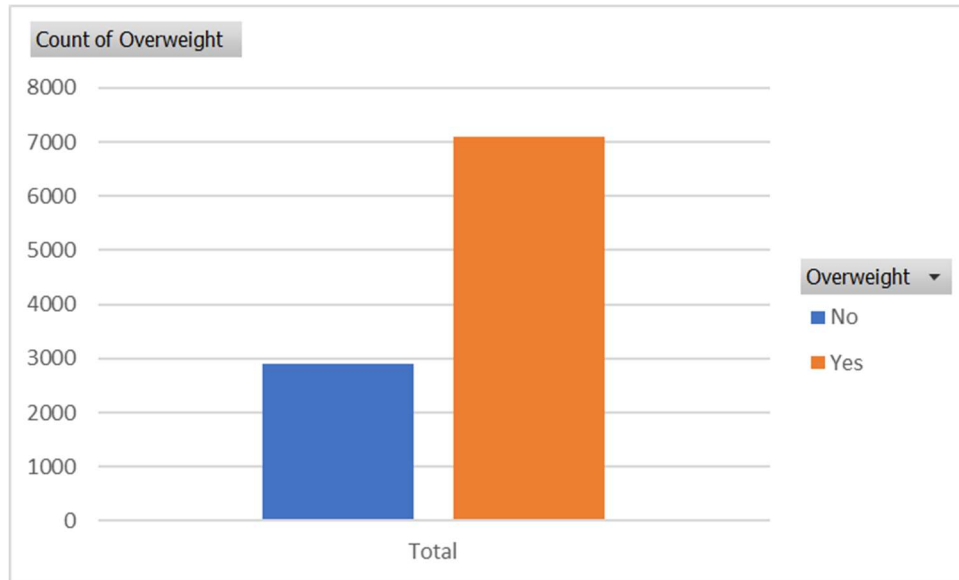


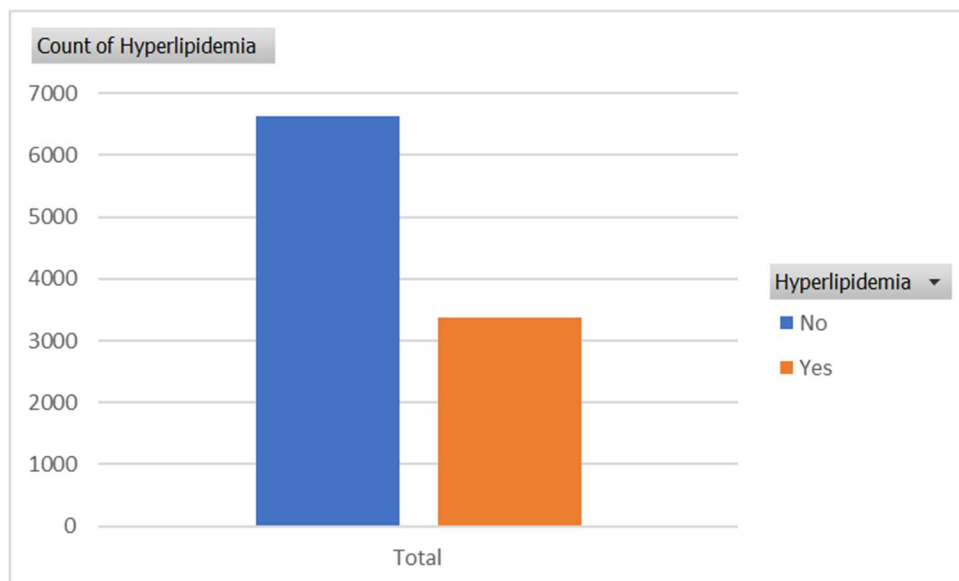
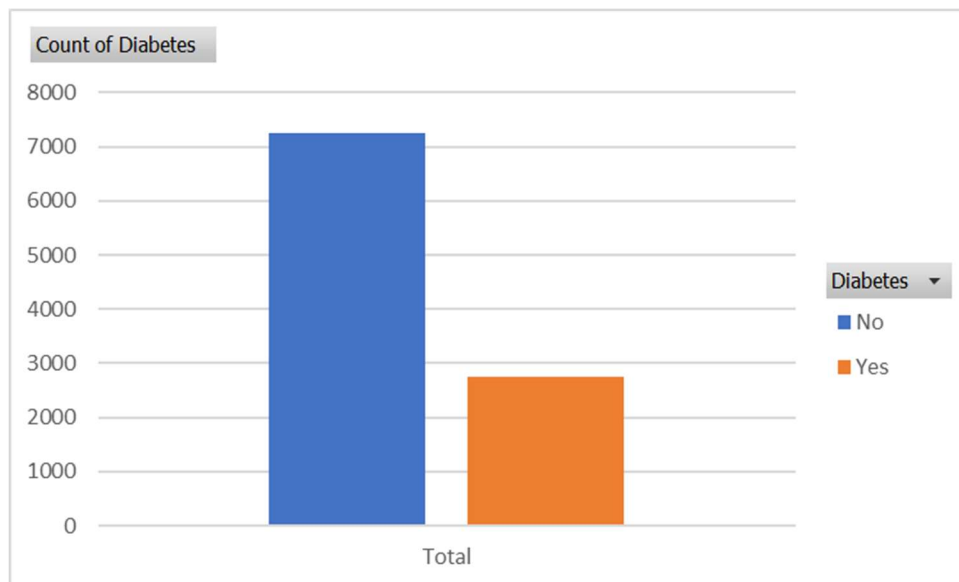


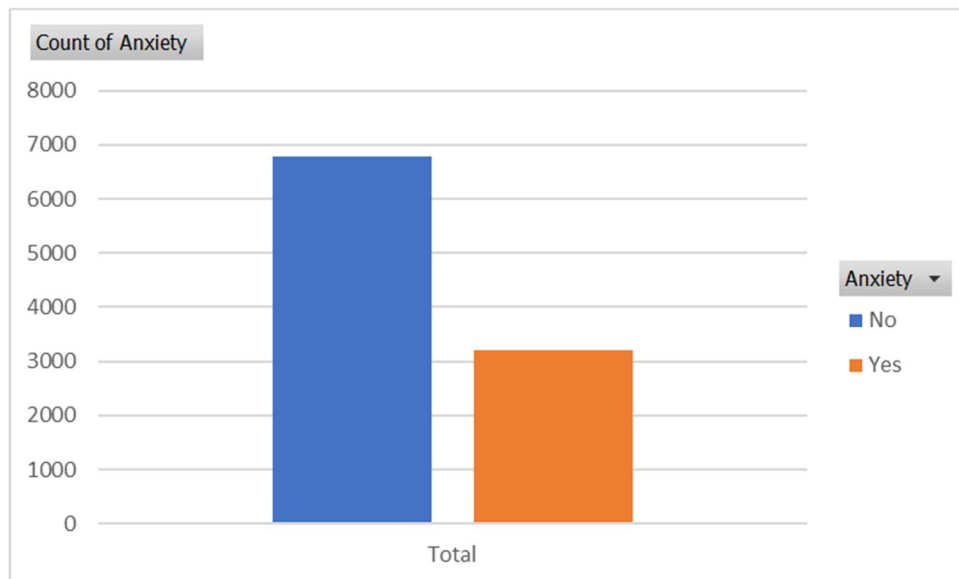
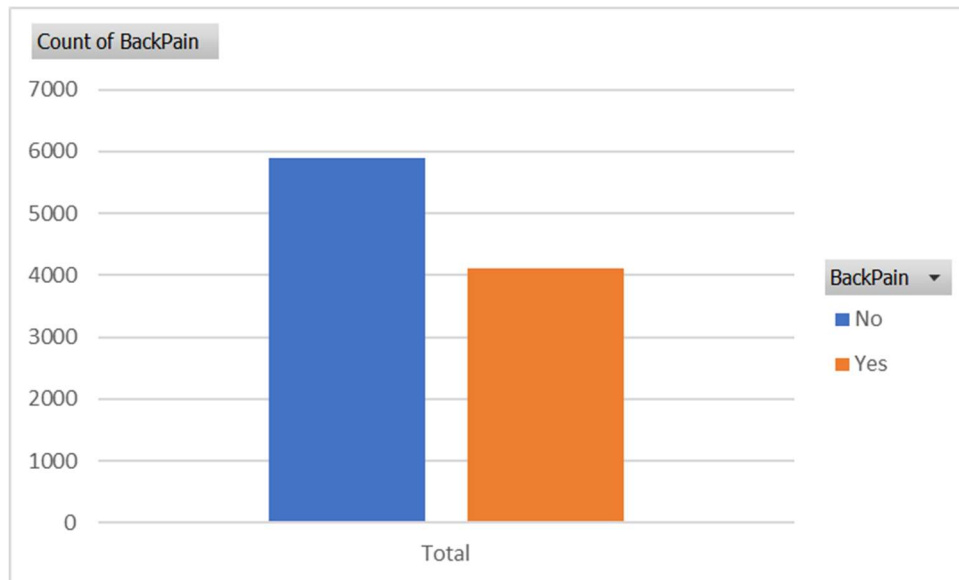


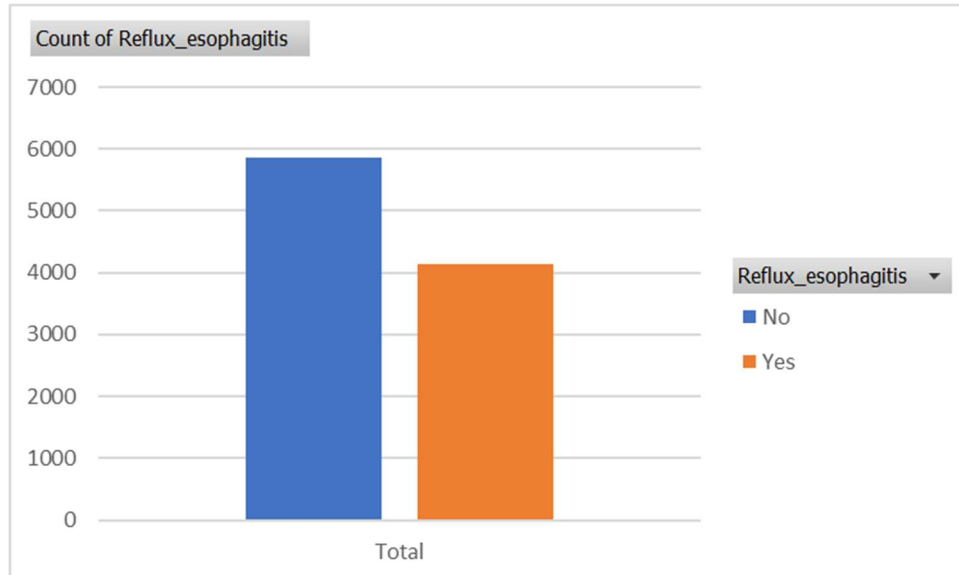
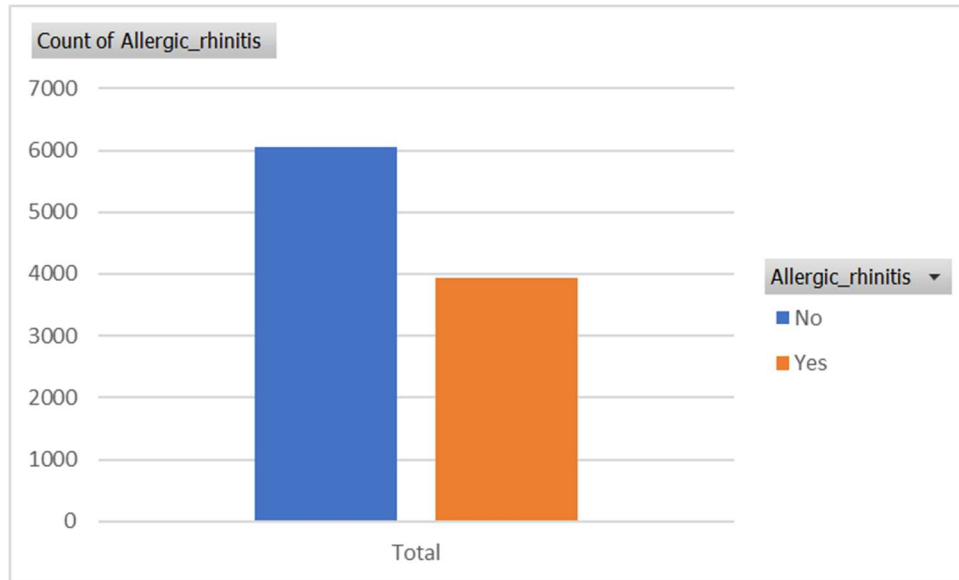


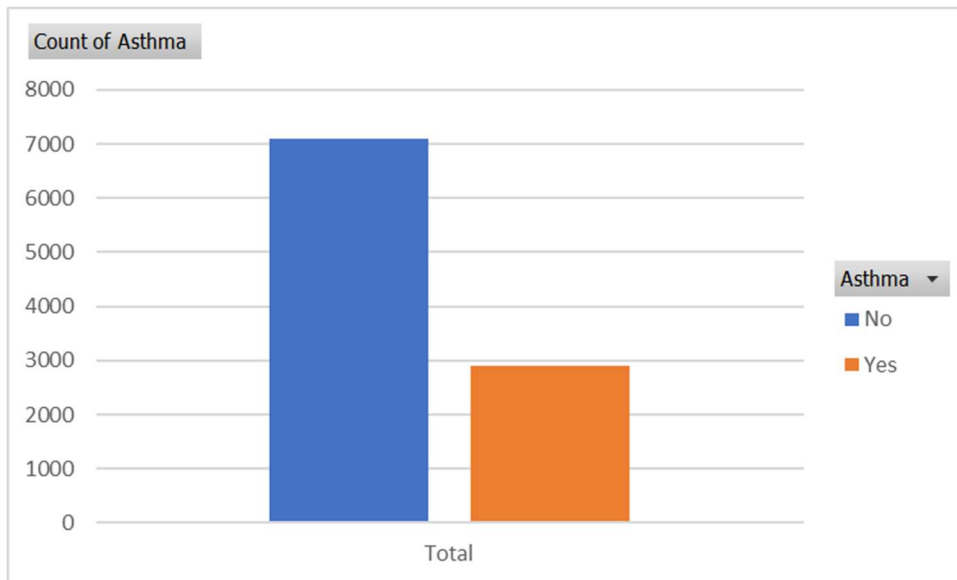




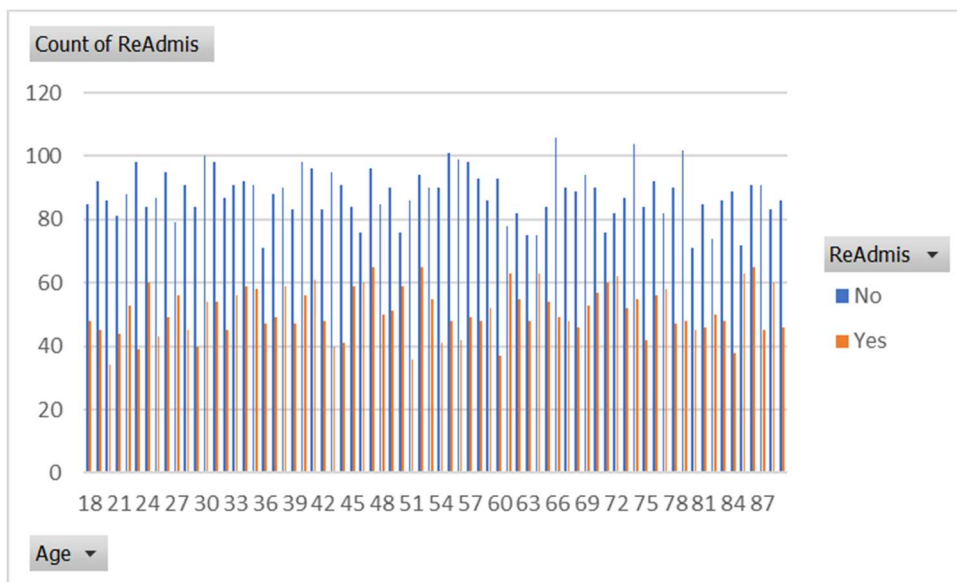


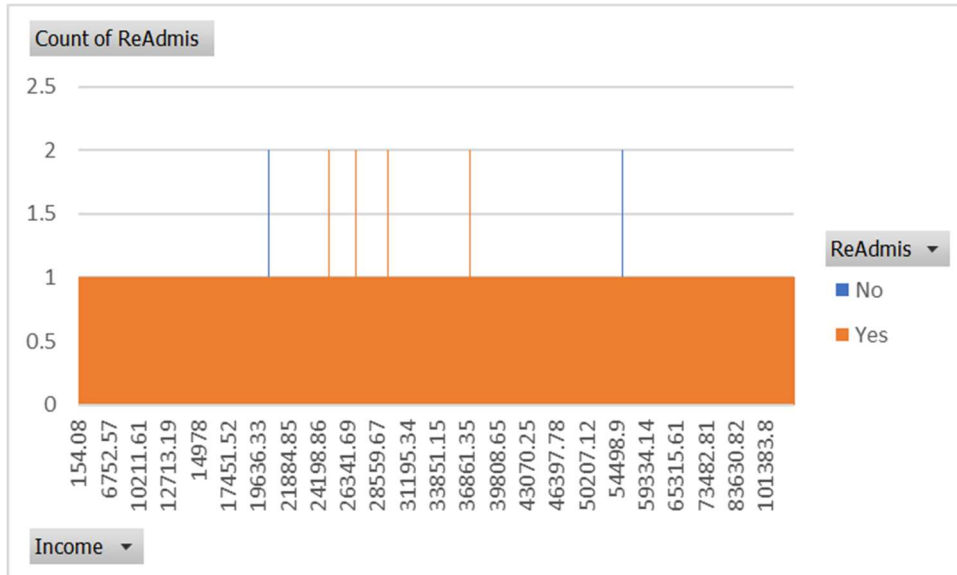
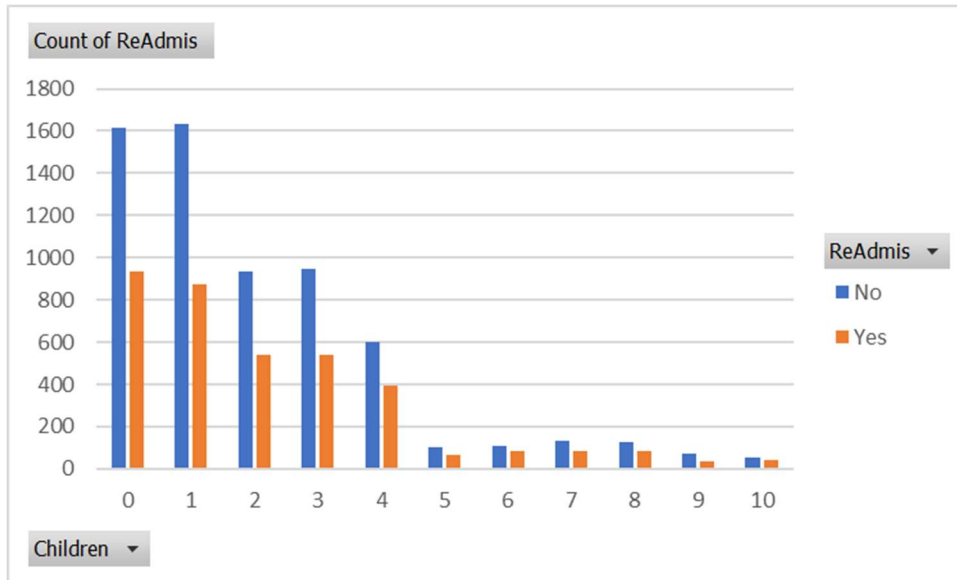


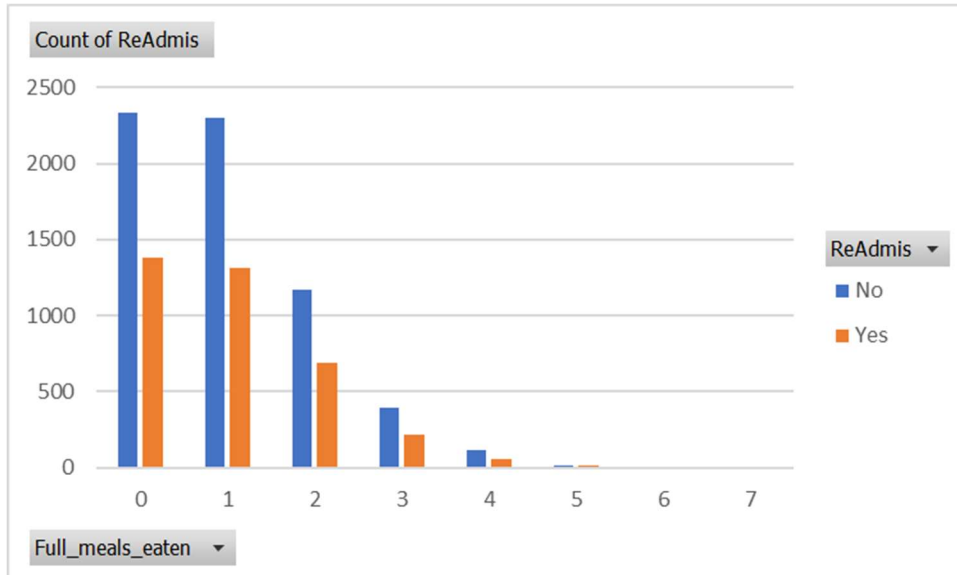
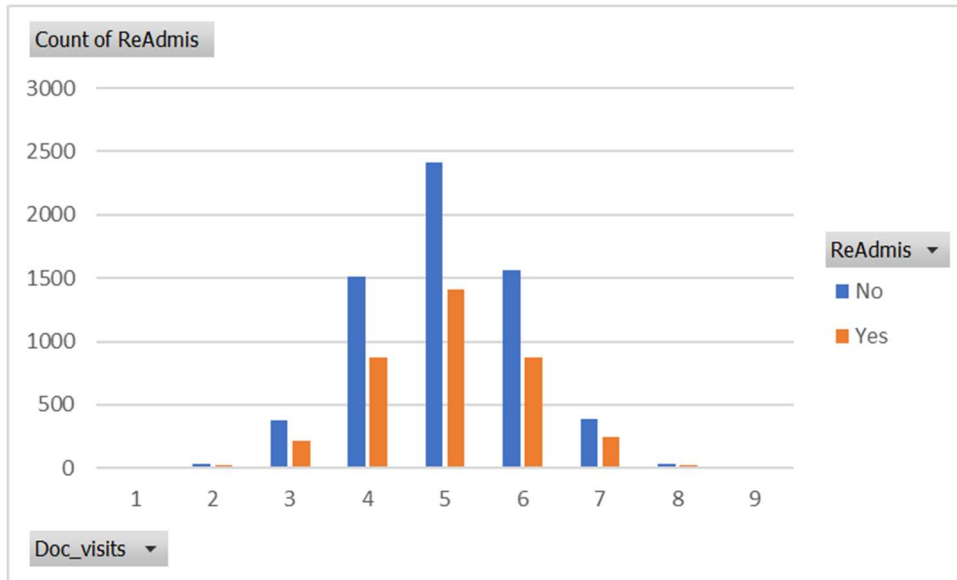


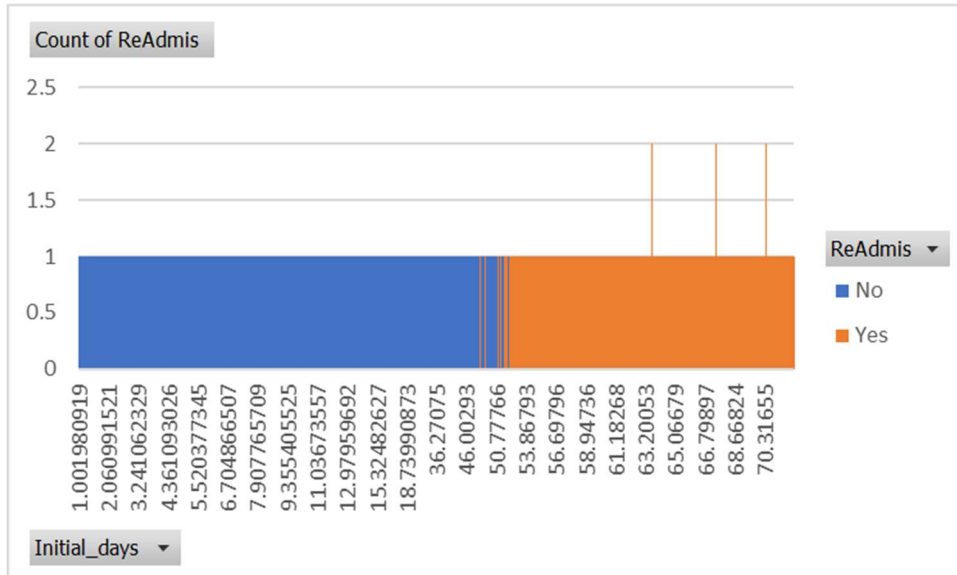
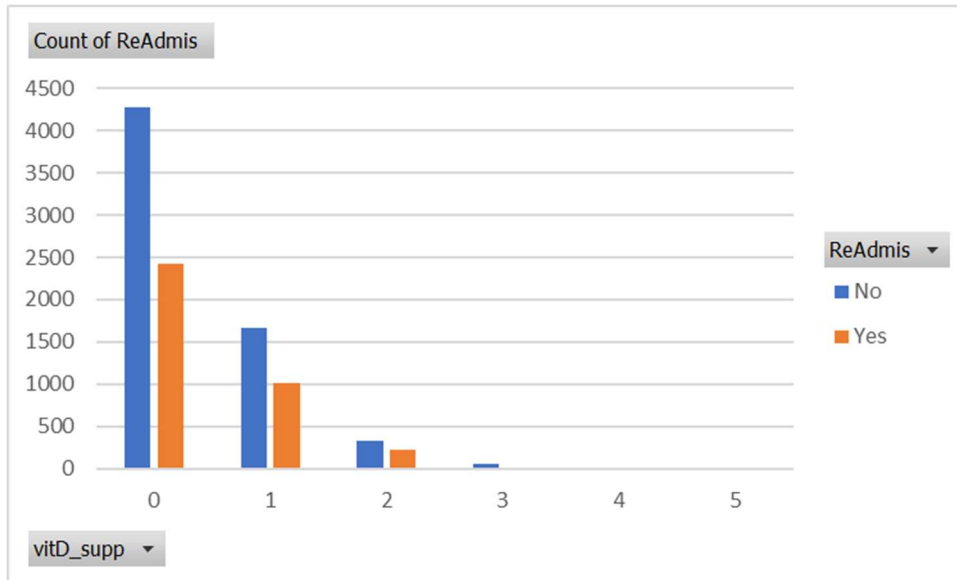


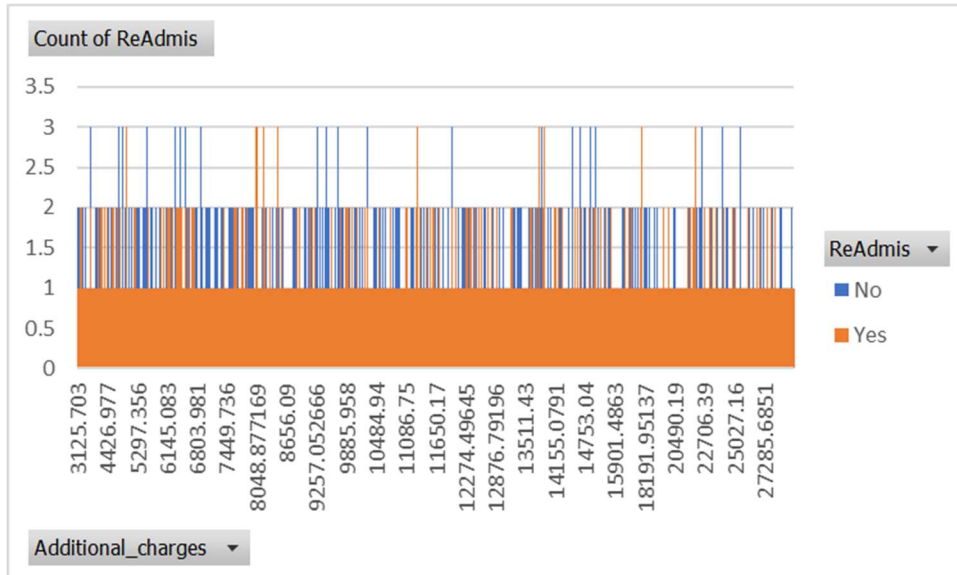
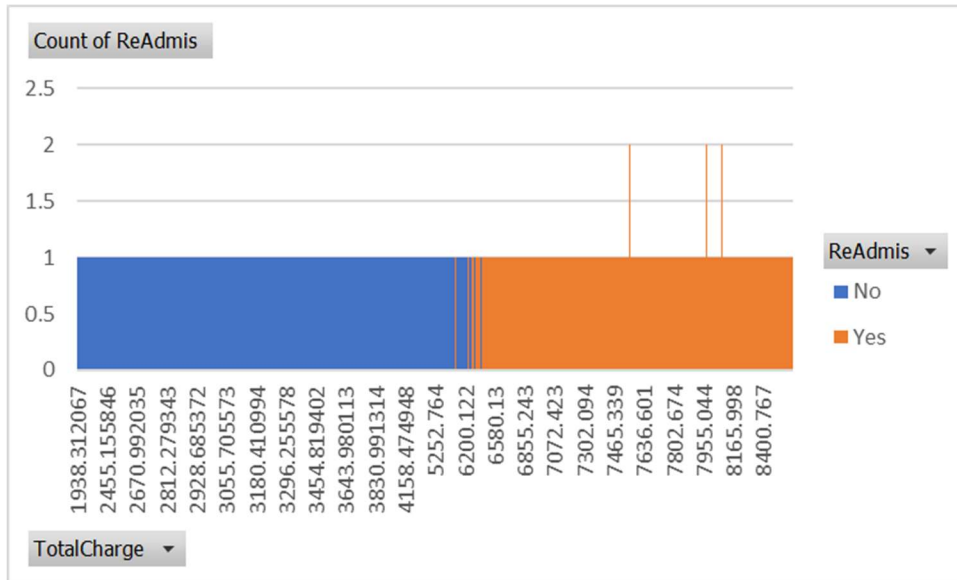
Bivariate visualizations (Paula, 2020b)

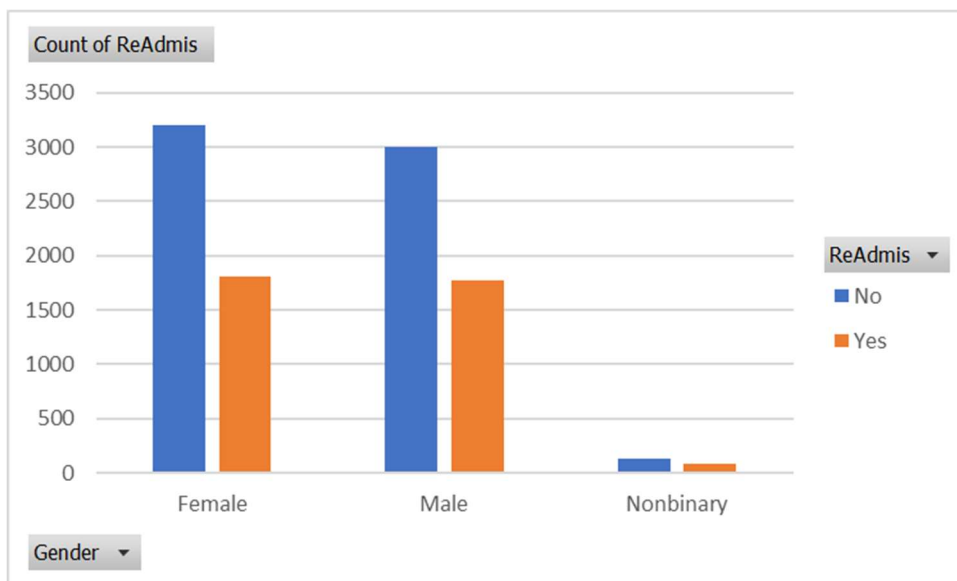
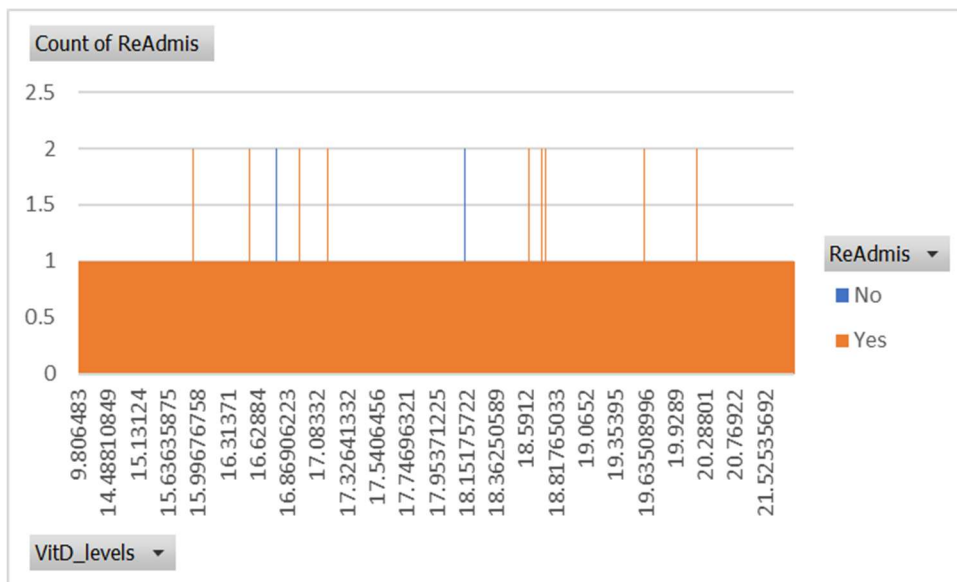


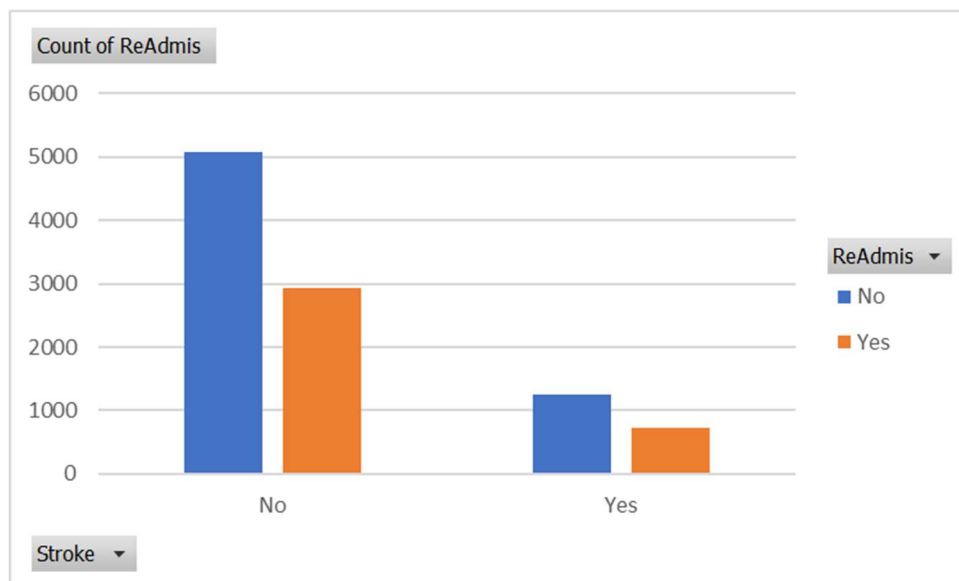
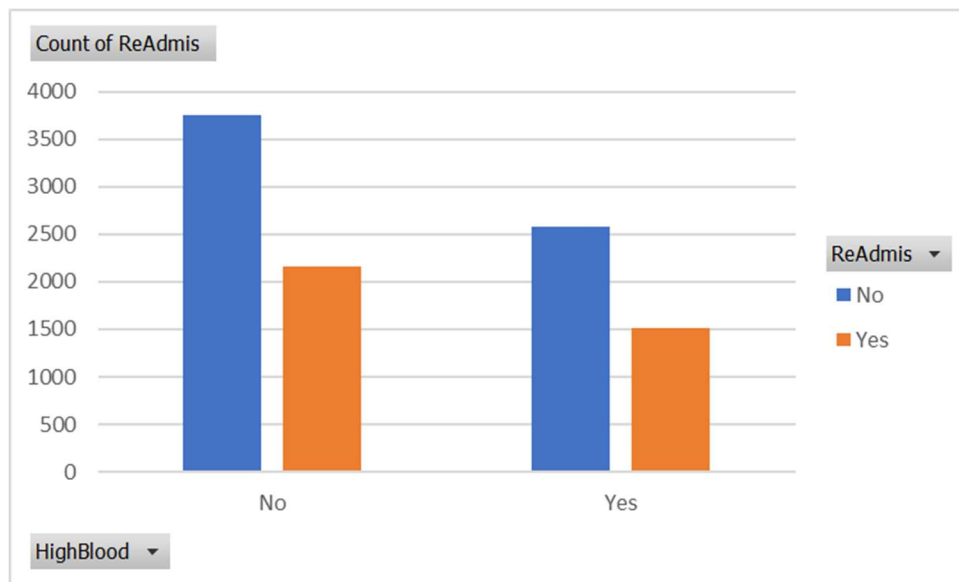


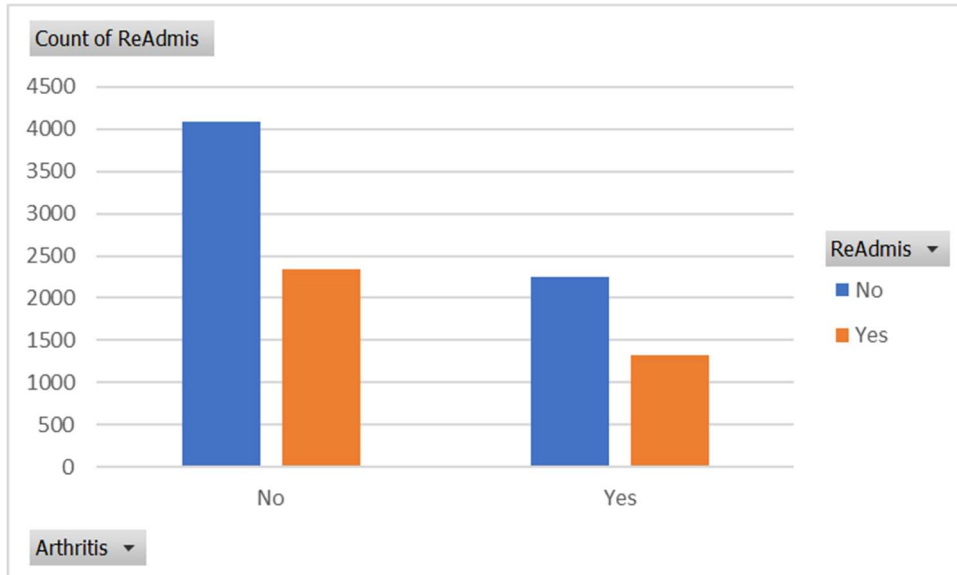
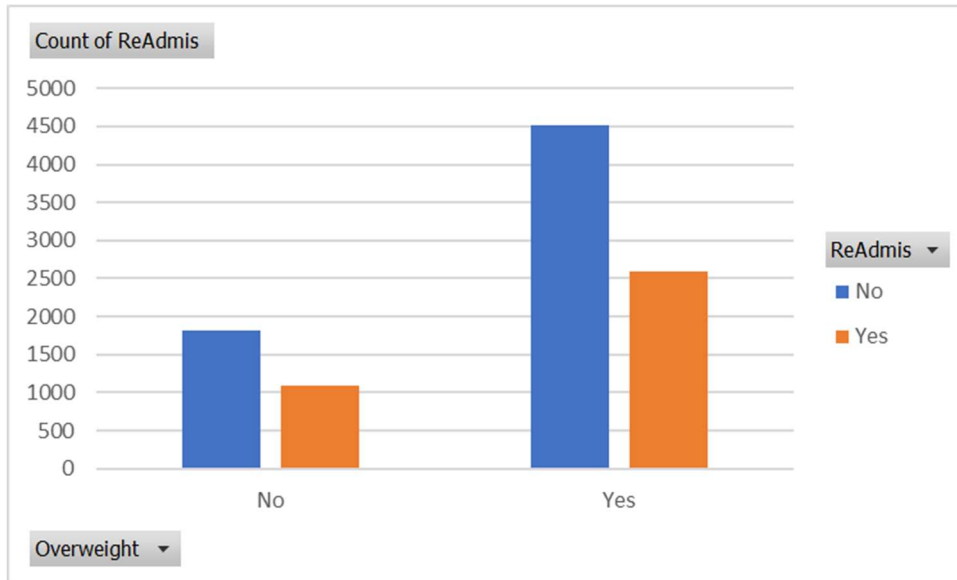


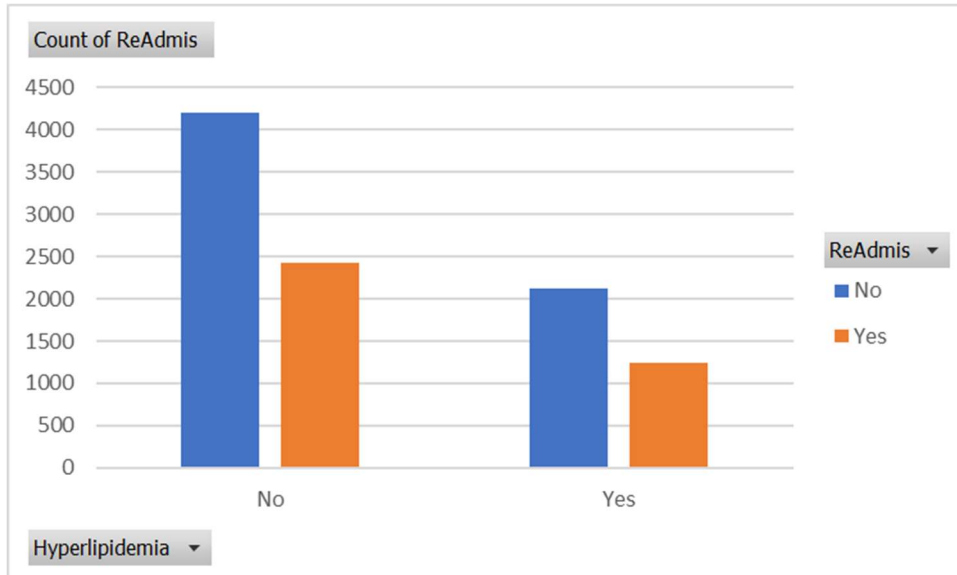
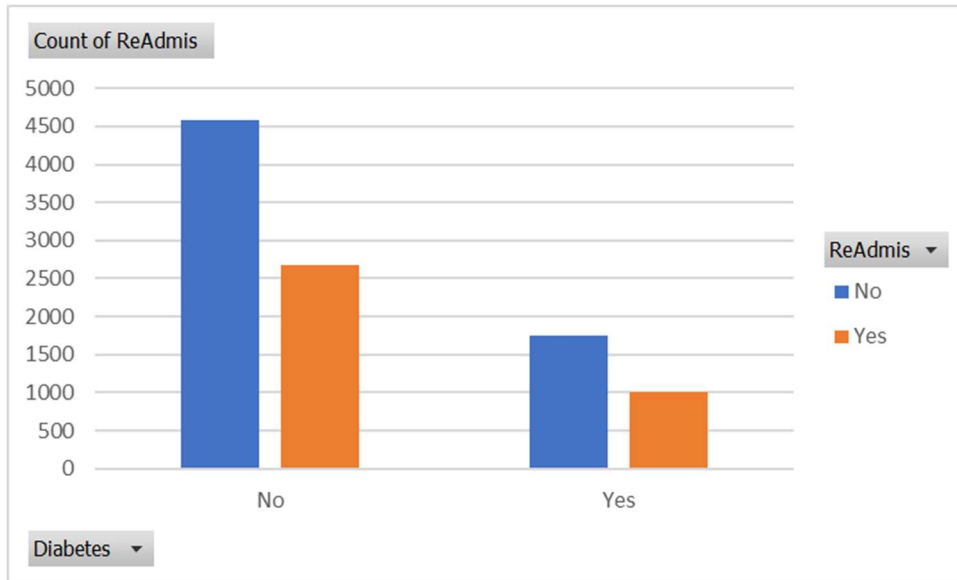


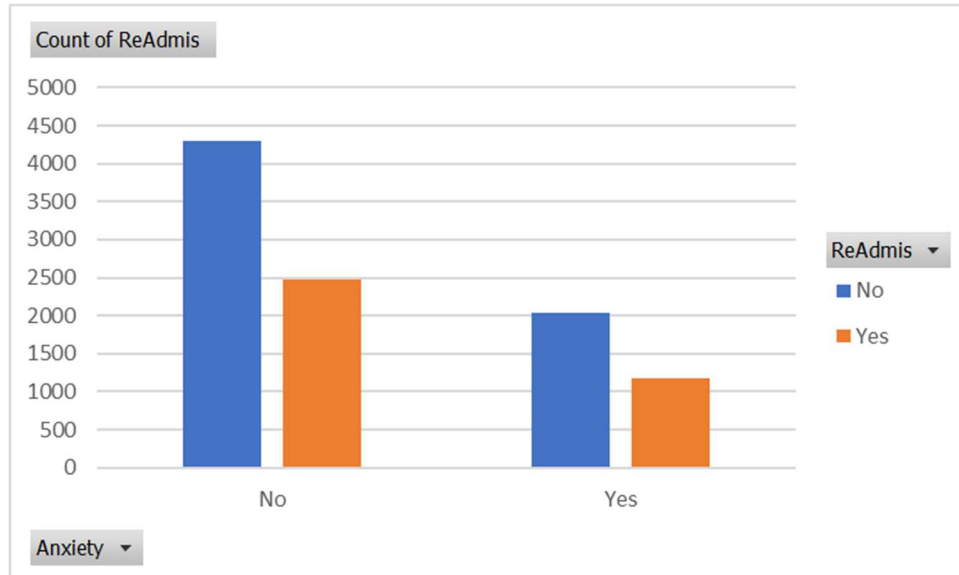
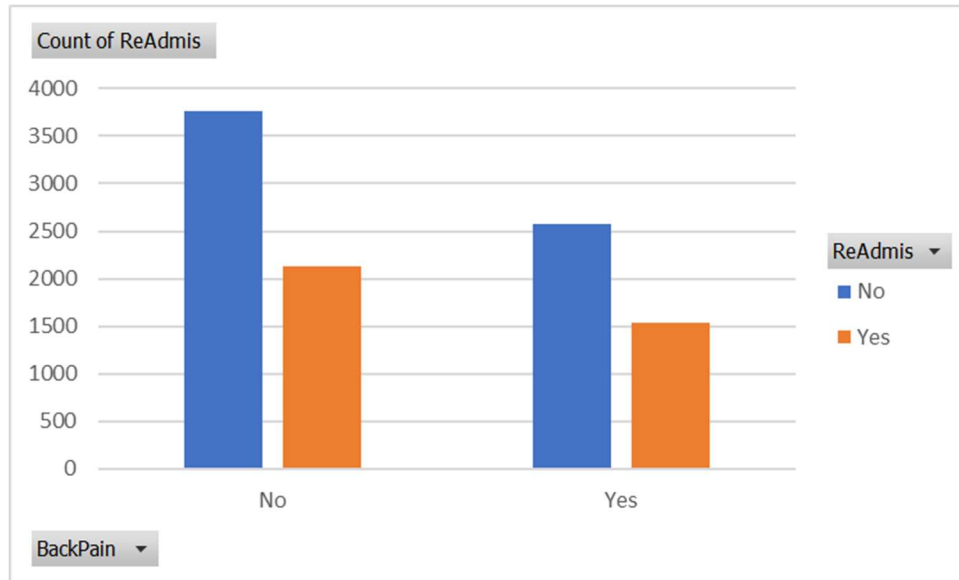


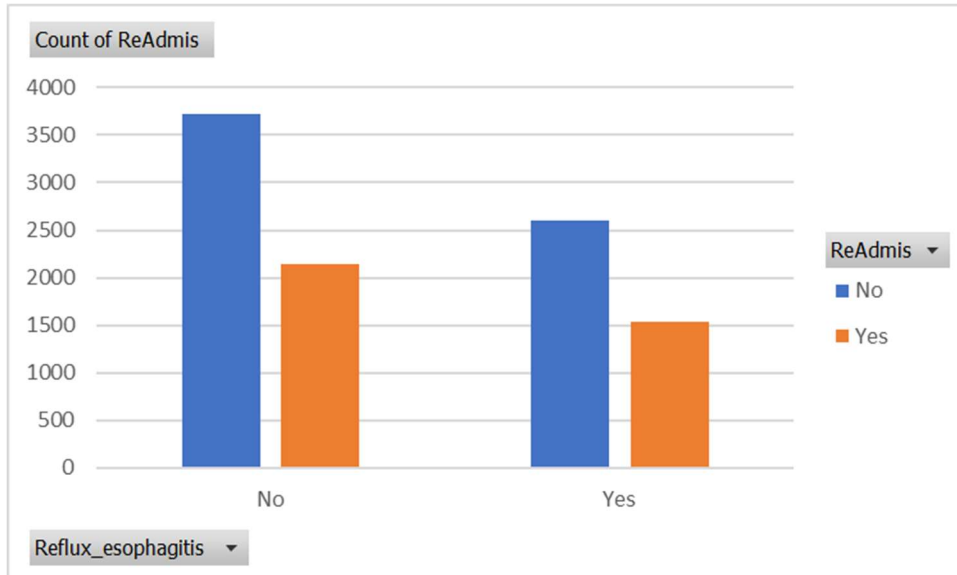
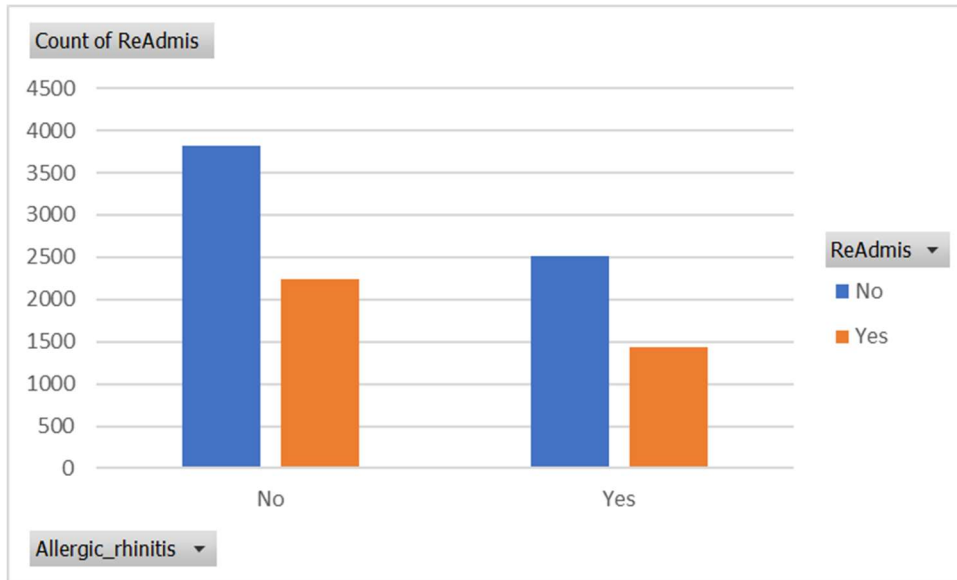


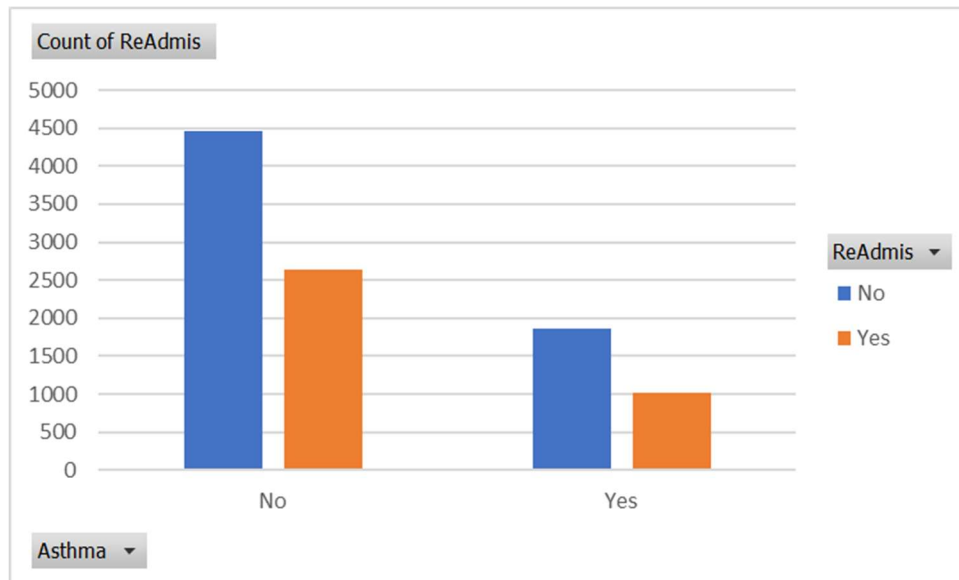












Part C4

Categorical variables to be used in the logistic regression model will need to be re-expressed. The Gender variable was re-expressed using the one-hot encoding method with the `dummyVars()` function. The remaining categorical variables were re-expressed using the label method with the `lapply()` and `revalue()` functions. See attached code. (Zach, 2021a)

Part C5

See attached file.

Part D1

The initial logistic regression model is:

$$\ln(p/(1-p)) = (-7.647e+01 - 1.845e-02(\text{Age}) - 5.412e-01(\text{GenderFemale}) - 4.460e-01(\text{GenderMale}) + 4.118e-02(\text{VitD_levels}) - 1.946e-01(\text{HighBlood}) + 1.523e+00(\text{Stroke}) - 2.556e-01(\text{Overweight}) - 1.339e+00(\text{Arthritis}) + 2.082e-01(\text{Diabetes}) + 4.686e-02(\text{Hyperlipidemia}) + 1.043e-01(\text{BackPain}) - 1.117e+00(\text{Anxiety}) - 4.792e-01(\text{Allergic_rhinitis}) - 4.915e-01(\text{Reflux_esophagitis}) - 1.135e+00(\text{Asthma}) + 6.808e-02(\text{Children}) + 5.854e-07(\text{Income}) + 7.721e-03(\text{Doc_visits}) + 5.661e-02(\text{Full_meals_eaten}) - 1.115e-01(\text{vitD_supp}) + 1.070e+00(\text{Initial_days}) + 2.765e-03(\text{TotalCharge}) + 8.316e-05(\text{Additional_charges}))$$

```
> summary(logres_initial)
```

Call:

```
glm(formula = ReAdmis ~ Age + GenderFemale + GenderMale + GenderNonbinary +  
  vitD_levels + HighBlood + Stroke + Overweight + Arthritis +  
  Diabetes + Hyperlipidemia + BackPain + Anxiety + Allergic_rhinitis +  
  Reflux_esophagitis + Asthma + Children + Income + Doc_visits +  
  Full_meals_eaten + vitD_supp + Initial_days + TotalCharge +  
  Additional_charges, family = binomial, data = medical_encoded)
```

Coefficients: (1 not defined because of singularities)

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-7.647e+01	4.175e+00	-18.315	< 2e-16	***
Age	-1.845e-02	1.367e-02	-1.349	0.1772	
GenderFemale	-5.412e-01	6.509e-01	-0.831	0.4057	
GenderMale	-4.460e-01	6.520e-01	-0.684	0.4940	
GenderNonbinary	NA	NA	NA	NA	
vitD_levels	4.118e-02	4.528e-02	0.909	0.3631	
HighBlood	-1.946e-01	5.344e-01	-0.364	0.7157	
Stroke	1.523e+00	2.516e-01	6.052	1.43e-09	***
Overweight	-2.556e-01	2.118e-01	-1.207	0.2275	
Arthritis	-1.339e+00	2.136e-01	-6.268	3.65e-10	***
Diabetes	2.082e-01	2.146e-01	0.970	0.3321	
Hyperlipidemia	4.686e-02	2.044e-01	0.229	0.8186	
BackPain	1.043e-01	1.935e-01	0.539	0.5900	
Anxiety	-1.117e+00	2.133e-01	-5.239	1.62e-07	***
Allergic_rhinitis	-4.792e-01	1.973e-01	-2.429	0.0151	*
Reflux_esophagitis	-4.915e-01	2.002e-01	-2.455	0.0141	*
Asthma	-1.135e+00	2.143e-01	-5.297	1.18e-07	***
Children	6.808e-02	4.257e-02	1.599	0.1097	
Income	5.854e-07	3.363e-06	0.174	0.8618	
Doc_visits	7.721e-03	8.855e-02	0.087	0.9305	
Full_meals_eaten	5.661e-02	9.495e-02	0.596	0.5510	
vitD_supp	-1.115e-01	1.497e-01	-0.745	0.4564	
Initial_days	1.070e+00	6.221e-02	17.204	< 2e-16	***
TotalCharge	2.765e-03	3.292e-04	8.399	< 2e-16	***
Additional_charges	8.316e-05	5.828e-05	1.427	0.1536	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 13145.7 on 9999 degrees of freedom
Residual deviance: 751.8 on 9976 degrees of freedom
AIC: 799.8

Number of Fisher Scoring iterations: 12

Part D2

Backward Stepwise Elimination was used as a feature selection procedure to reduce the initial model. This procedure allowed for first evaluating all the possible explanatory variables, and then improving the performance of the model by removing least significant features based on their p-value. The cutoff p-value of 0.05 was used to determine whether an independent variable was statistically significant. This allowed for the model to be evaluated at multiple steps by removing variables with a p-value greater than 0.05, one at a time, until an acceptable model was achieved.

Part D3

The reduced logistic regression model is:

$$\ln(p/(1-p)) = (-7.556e+01 - 1.398e-02(\text{Age}) + 1.497e+00(\text{Stroke}) - 1.323e+00(\text{Arthritis}) \\ - 1.086e+00(\text{Anxiety}) - 4.823e-01(\text{Allergic_rhinitis}) - 4.738e-01(\text{Reflux_esophagitis}) \\ - 1.139e+00(\text{Asthma}) + 1.054e+00(\text{Initial_days}) + 2.815e-03(\text{TotalCharge}) \\ + 5.976e-05(\text{Additional_charges}))$$

```
> summary(logres_final)

Call:
glm(formula = ReAdmis ~ Age + Stroke + Arthritis + Anxiety +
     Allergic_rhinitis + Reflux_esophagitis + Asthma + Initial_days +
     Totalcharge + Additional_charges, family = binomial, data = medical_encoded)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  -7.556e+01  3.973e+00 -19.018  < 2e-16 ***
Age           -1.398e-02  6.625e-03  -2.110  0.03486 *
Stroke         1.497e+00  2.449e-01   6.111  9.88e-10 ***
Arthritis     -1.323e+00  2.102e-01  -6.293  3.11e-10 ***
Anxiety       -1.086e+00  2.086e-01  -5.206  1.93e-07 ***
Allergic_rhinitis -4.823e-01  1.934e-01  -2.494  0.01263 *
Reflux_esophagitis -4.738e-01  1.950e-01  -2.430  0.01511 *
Asthma        -1.139e+00  2.124e-01  -5.360  8.31e-08 ***
Initial_days   1.054e+00  6.064e-02  17.385  < 2e-16 ***
TotalCharge    2.815e-03  3.152e-04   8.928  < 2e-16 ***
Additional_charges 5.976e-05  2.144e-05   2.787  0.00531 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 13145.70  on 9999  degrees of freedom
Residual deviance:  760.89  on 9989  degrees of freedom
AIC: 782.89

Number of Fisher scoring iterations: 12
```


The initial and reduced regression models were evaluated using the AIC value. The AIC for the initial model is 799.8, while the AIC for the reduced model is 782.89. The AIC for the reduced model is lower than the AIC for the initial model, implying that the reduced model is a better fit for the data.

[illegible]

```
> # Convert values from "Yes" and "No" to 1's and 0's
> medical_encoded$ReAdmis <- as.factor(medical_encoded$ReAdmis)
> medical_encoded$ReAdmis
 [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[36] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[71] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[106] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[141] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[176] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[211] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[246] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[281] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[316] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[351] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[386] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[421] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[456] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[491] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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[596] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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[666] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[701] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[736] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[771] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[806] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[841] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[876] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[911] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[946] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[981] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
[ reached getoption("max.print") -- omitted 9000 entries ]
Levels: 0 1

> unique(medical_encoded$ReAdmis)
[1] 0 1
Levels: 0 1
```



```
> # Create confusion matrix
> confusionMatrix(medical_encoded$ReAdmis,predicted)
Confusion Matrix and Statistics
```

	Reference	
Prediction	0	1
0	6250	81
1	75	3594

Accuracy : 0.9844
 95% CI : (0.9818, 0.9867)
 No Information Rate : 0.6325
 P-Value [Acc > NIR] : <2e-16

 Kappa : 0.9664

 McNemar's Test P-Value : 0.6889

 Sensitivity : 0.9881
 Specificity : 0.9780
 Pos Pred Value : 0.9872
 Neg Pred Value : 0.9796
 Prevalence : 0.6325
 Detection Rate : 0.6250
 Detection Prevalence : 0.6331
 Balanced Accuracy : 0.9831

 'Positive' Class : 0

Part E3

See attached code.

Part F1

The regression equation for the reduced model is:

$$\ln(p/(1-p)) = (-7.556e+01 - 1.398e-02(\text{Age}) + 1.497e+00(\text{Stroke}) - 1.323e+00(\text{Arthritis}) - 1.086e+00(\text{Anxiety}) - 4.823e-01(\text{Allergic_rhinitis}) - 4.738e-01(\text{Reflux_esophagitis}) - 1.139e+00(\text{Asthma}) + 1.054e+00(\text{Initial_days}) + 2.815e-03(\text{TotalCharge}) + 5.976e-05(\text{Additional_charges}))$$

Interpretation of the coefficients is detailed in the following table.

Keeping all things constant,

<i>A one unit increase in</i>	<i>changes the log odds of ReAdmis by</i>
Age	-1.398e-02
Stroke	+1.497e+00
Arthritis	-1.323e+00
Anxiety	-1.086e+00
Allergic_rhinitis	-4.823e-01
Reflux_esophagitis	-4.738e-01
Asthma	-1.139e+00
Initial_days	+1.054e+00
TotalCharge	+2.815e-03
Additional_charges	+5.976e-05

In terms of statistical significance, Initial_days and TotalCharge are the most significant variables (having p-values less than $2e-16$), followed by Stroke, Arthritis, Anxiety, and Asthma. Allergic_rhinitis, Reflux_esophagitis, and Additional_charges are also statistically significant but less so than the previously mentioned variables.

In terms of practical significance, considering the magnitude of the coefficient for each variable, those variables with the larger absolute value coefficients (Additional_charges, Allergic_rhinitis, and Reflux_esophagitis) indicate a stronger effect on the log-odds of the patient being readmitted within a month of release.

The data analysis is limited by the initial selection of explanatory variables. Variables that were not included could have produced a more accurate model.

Part F2

Based on these results, my recommendation is to use this model to predict the likelihood of a patient being readmitted within a month of release. This information can guide treatment or intervention decisions.

Part G

The demonstration can be viewed at

<https://wgu.hosted.panopto.com/Panopto/Pages/Viewer.aspx?id=4304a653-99cc-40ca-b905-b09e0150a5f2>

Part H

Paula. (2020b). Tips for analyzing categorical data in Excel. The Excel Club.

<https://theexcelclub.com/tips-for-analyzing-categorical-data-in-excel/>

Zach. (2021). How to convert categorical variables to numeric in R. Statology.

<https://www.statology.org/convert-categorical-variable-to-numeric-r/>

Zach. (2021a). How to perform One-Hot encoding in R. Statology.

<https://www.statology.org/one-hot-encoding-in-r/>

Part I

None used.