Matthew Morgan
Student ID: 010471280
Data Mining II - 212
Task 2: Dimensionality Reduction Methods
Western Governor's University
Program Mentor: Mandy Rasmuson

Part I: Research Question

A. Describe the purpose of this data mining report by doing the following:

A1. Propose one question relevant to a real-world organizational situation that you will answer by using principal component analysis (PCA).

The purpose of this task is to try and use dimensionality reduction methods to help answer a research question. My research question for this project will be if we can help determine if patient re-admissions can be predicted through the use of a decision tree classifier after using principal component analysis (PCA) to reduce the dimensionality of the provided dataset.

A2. Define one goal of the data analysis. Ensure that your goal is reasonable within the scope of the scenario and is represented in the available data.

The ultimate goal of this performance assessment is to predict patient re-admissions. Based on the data dictionary this is the primary goal of the WGU Health Data as high re-admission rates result in fines. If we can find out how to reduce patient re-admissions not only will we be able to save money by avoiding fines we can then use that money towards prevention and provide better health outcomes for the patients.

Part II: Method Justification

B. Explain the reasons for using PCA by doing the following:

B1. Explain how PCA analyzes the selected data set. Include expected outcomes.

PCA is a way we can reduce dimensions within a dataset. This can be done through feature elimination or extraction. Elimination is just that, it removes features that are redundant or have no correlation to the dependent variable. Extraction involves combining multiple features into one datapoint. This new datapoint is then evaluated to determine how important it is by how it effecfts the variance within the dataset. If it meets the threshold that is defined it is then considered a "principal component" in the appropriate model.

The expected outcome is to hopefully find a number of principal components that allow us to predict patient re-admissions. This will be evaluated by using the explained_variance_ratio_ attribute. The ones that are most important to the model will be saved, and the other eliminated so we can reduce the dimensionality of the dataset.

B2. Summarize one assumption of PCA.

One assumption of PCA provided by Datacamp is that, "the principal components having the highest variance are more important than those which don't." (Keita, 2023) Because we'll be taking the variance scores of the different principal components we will be guided towards what to keep and what we can eliminate based on that assumption.

Part III: Data Preparation

C. Perform data preparation for the chosen dataset by doing the following:

C1. Identify the continuous dataset variables that you will need in order to answer the PCA question proposed in part A1.

Variable #	Continuous Variable Dictionary
1	Latitude
2	Longitude
3	Population
4	Number of Children in Household
5	Age
6	Income of Patient
7	Patient's Vit D Level
8	Number of Physician Visits
9	Number of full meals eaten
9	Number of Vit D Supplements
10	Length of initial stay
11	Average daily amount charged for hospitalization
12	Average daily amount charged for additional charges
13	Initial_Admin_Emergency_admission

C2. Standardize the continuous dataset variables identified in part C1. Include a copy of the cleaned dataset.

```
In [157]: #DataCleaning

          #Import Packages needed for data cleaning and PCA
          import pandas as pd
          import numpy as np
          import matplotlib.pyplot as plt
          import seaborn as sns

          from sklearn.preprocessing import StandardScaler
          from sklearn.decomposition import PCA
          from sklearn.model_selection import train_test_split

          from sklearn.tree import DecisionTreeClassifier

          from sklearn.metrics import confusion_matrix
          from sklearn.metrics import roc_auc_score
          from sklearn.metrics import accuracy_score

          #Loading the CSV of the default dataset, index_col to prevent duplicated column
          df = pd.read_csv(r'C:\Users\mmorg\WGU\D212\medical_clean.csv', index_col=0)
          #Get overiew of dataset such as # of columns, names, and size
          df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 10000 entries, 1 to 10000
Data columns (total 49 columns):
 #   Column              Non-Null Count  Dtype  
---  ------              --------------  -----  
 0   Customer_id         10000 non-null  object 
 1   Interaction         10000 non-null  object 
 2   UID                 10000 non-null  object 
 3   City                10000 non-null  object 
 4   State               10000 non-null  object 
 5   County              10000 non-null  object 
 6   Zip                 10000 non-null  int64  
 7   Lat                 10000 non-null  float64
 8   Lng                 10000 non-null  float64
 9   Population          10000 non-null  int64  
 10  Area                10000 non-null  object 
 11  TimeZone            10000 non-null  object 
 12  Job                 10000 non-null  object 
 13  Children            10000 non-null  int64  
 14  Age                 10000 non-null  int64  
 15  Income              10000 non-null  float64
 16  Marital             10000 non-null  object 
 17  Gender              10000 non-null  object 
 18  ReAdmis             10000 non-null  object 
 19  VitD_levels         10000 non-null  float64
 20  Doc_visits          10000 non-null  int64  
 21  Full_meals_eaten    10000 non-null  int64  
 22  vitD_supp           10000 non-null  int64  
 23  Soft_drink          10000 non-null  object 
 24  Initial_admin       10000 non-null  object 
 25  HighBlood           10000 non-null  object 
 26  Stroke              10000 non-null  object 
 27  Complication_risk   10000 non-null  object 
 28  Overweight          10000 non-null  object 
 29  Arthritis           10000 non-null  object 
 30  Diabetes            10000 non-null  object 
 31  Hyperlipidemia      10000 non-null  object 
 32  BackPain            10000 non-null  object 
 33  Anxiety             10000 non-null  object 
 34  Allergic_rhinitis   10000 non-null  object 
 35  Reflux_esophagitis  10000 non-null  object 
 36  Asthma              10000 non-null  object 
 37  Services            10000 non-null  object 
 38  Initial_days        10000 non-null  float64
 39  TotalCharge         10000 non-null  float64
 40  Additional_charges  10000 non-null  float64
 41  Item1               10000 non-null  int64
 42  Item2               10000 non-null  int64
 43  Item3               10000 non-null  int64
 44  Item4               10000 non-null  int64
 45  Item5               10000 non-null  int64
 46  Item6               10000 non-null  int64
 47  Item7               10000 non-null  int64
 48  Item8               10000 non-null  int64
dtypes: float64(7), int64(15), object(27)
memory usage: 3.8+ MB
```

In [158]:
```
# More exploration to spot any potential problems with the dataset and what might need cleaned up
pd.set_option("display.max_columns", None)
df.head(5)
```

Out[158]:

	Customer_id	Interaction	UID	City	State	County	Zip	Lat	Lng	Po
CaseOrder										
1	C412403	8cd49b13-f45a-4b47-a2bd-173ffa932c2f	3a83ddb66e2ae73798bdf1d705dc0932	Eva	AL	Morgan	35621	34.34960	-86.72508	
2	Z919181	d2450b70-0337-4406-bdbb-bc1037f1734c	176354c5eef714957d486009feabf195	Marianna	FL	Jackson	32446	30.84513	-85.22907	
3	F995323	a2057123-abf5-4a2c-abad-8ffe33512562	e19a0fa00aeda885b8a436757e889bc9	Sioux Falls	SD	Minnehaha	57110	43.54321	-96.63772	
4	A879973	1dec528d-eb34-4079-adce-0d7a40e82205	cd17d7b6d152cb6f23957346d11c3f07	New Richland	MN	Waseca	56072	43.89744	-93.51479	
5	C544523	5885f56b-d6da-43a3-8760-83583af94266	d2f0425877b10ed6bb381f3e2579424a	West Point	VA	King William	23181	37.59894	-76.88958	

In [159]:
```
#Because we are only using continuous variables, not much cleaning needs to be done and we can remove columns
#that are categorical or don't apply to the PCA

# Assign all continuous variables for PCA to X variable
X = df[["Lat", "Lng", "Population", "Children", "Age", "Income", "VitD_levels", "Doc_visits",
        "Full_meals_eaten", "vitD_supp",  "Initial_days", "TotalCharge", "Additional_charges"]].copy()
# Define list of column headers
X_columns = list(X.columns)
# Assign patient re-admissions column to y variable
y = df["ReAdmis"]
```

In [160]:
```
# Standardize X by instantiating the StandardScaler(), then fitting and transforming to X
X_stand = StandardScaler().fit_transform(df[["Lat", "Lng", "Population", "Children", "Age", "Income", "VitD_le
        "Full_meals_eaten", "vitD_supp",  "Initial_days", "TotalCharge", "Additional_charges"]].copy())
# New dataframe with standardized values for verification
X_stand_df = pd.DataFrame(X_stand, columns=X_columns)
```

In [161]:
```
#Verifying the means of each column, should be 0 to confirm standardization
X_stand_means = X_stand_df.agg(['mean']).round(2)

print(X_std_means)
```

```
      Lat  Lng  Population  Children  Age  Income  VitD_levels  Doc_visits  \
mean -0.0  0.0        -0.0      -0.0  0.0     0.0         -0.0         0.0

      Full_meals_eaten  vitD_supp  Initial_days  Additional_charges
mean               0.0       -0.0          -0.0                -0.0
```

In [162]:
```
#Verifying the standard deviation of each column, should be 1 to confirm standardization
X_stand_stddv = X_stand_df.agg(['std']).round(2)

print(X_stand_stddv)
```

```
     Lat  Lng  Population  Children  Age  Income  VitD_levels  Doc_visits  \
std  1.0  1.0         1.0       1.0  1.0     1.0          1.0         1.0   

     Full_meals_eaten  vitD_supp  Initial_days  TotalCharge  \
std               1.0        1.0           1.0          1.0   

     Additional_charges  
std                 1.0  
```

In [163]:
```
#Checking correlations to determine redundant components
X_stand_df.corr()
```

Out[163]:

	Lat	Lng	Population	Children	Age	Income	VitD_levels	Doc_visits	Full_meals_eaten	vitD_sup
Lat	1.000000	-0.112348	-0.207572	0.006373	-0.007270	-0.019369	0.001493	0.008380	0.003401	0.00128
Lng	-0.112348	1.000000	-0.031979	-0.014114	0.007493	-0.006665	-0.006389	0.000754	-0.014231	-0.00196
Population	-0.207572	-0.031979	1.000000	0.002462	-0.018987	0.005426	0.002651	0.012646	-0.025608	0.00978
Children	0.006373	-0.014114	0.002462	1.000000	0.009836	0.007176	0.009487	-0.002292	0.003835	-0.00431
Age	-0.007270	0.007493	-0.018987	0.009836	1.000000	-0.012228	0.010315	0.006898	0.008555	0.01001
Income	-0.019369	-0.006665	0.005426	0.007176	-0.012228	1.000000	-0.013115	0.013464	-0.011365	0.00125
VitD_levels	0.001493	-0.006389	0.002651	0.009487	0.010315	-0.013115	1.000000	0.010210	0.023223	-0.00720
Doc_visits	0.008380	0.000754	0.012646	-0.002292	0.006898	0.013464	0.010210	1.000000	-0.002767	0.00568
Full_meals_eaten	0.003401	-0.014231	-0.025608	0.003835	0.008555	-0.011365	0.023223	-0.002767	1.000000	-0.01998
vitD_supp	0.001285	-0.001961	0.009781	-0.004319	0.010014	0.001253	-0.007203	0.005681	-0.019980	1.00000
Initial_days	-0.008820	-0.009292	0.017469	0.022467	0.016264	-0.012465	-0.003642	-0.006754	-0.017267	0.01597
TotalCharge	-0.010759	-0.008830	0.019188	0.024100	0.016876	-0.014345	-0.001403	-0.005043	-0.014306	0.01692
Additional_charges	-0.002283	0.000079	-0.004820	0.013548	0.716854	-0.009825	0.008290	0.008072	0.018763	0.01032

In [164]:
```
#As shown Initial_days and TotalCharge are highly correlated and redundant.
#As I have done in previous classes, I dropped TotalCharge as they both basically represent the same data.
#Longer stays lead to more initial charges.

#Re-creating X variable and X_columns with this in mind
X = df[["Lat", "Lng", "Population", "Children", "Age", "Income", "VitD_levels", "Doc_visits",
        "Full_meals_eaten", "vitD_supp",  "Initial_days", "Additional_charges"]].copy()
# Define list of column headers
X_columns = list(X.columns)
# Standardize X by instantiating the StandardScaler(), then fitting and transforming to X
X_stand = StandardScaler().fit_transform(df[["Lat", "Lng", "Population", "Children", "Age", "Income", "VitD_le
        "Full_meals_eaten", "vitD_supp",  "Initial_days", "Additional_charges"]].copy())
# New dataframe with standardized values for verification
X_stand_df = pd.DataFrame(X_stand, columns=X_columns)
```

In [165]:
```
#Verifying the means of each column, should be 0 to confirm standardization
X_stand_means = X_stand_df.agg(['mean']).round(2)

print(X_stand_means)
```

```
      Lat  Lng  Population  Children  Age  Income  VitD_levels  Doc_visits  \
mean -0.0  0.0        -0.0      -0.0  0.0     0.0         -0.0         0.0

      Full_meals_eaten  vitD_supp  Initial_days  Additional_charges
mean               0.0       -0.0          -0.0                -0.0
```

In [166]:
```
#Verifying the standard deviation of each column, should be 1 to confirm standardization
X_stand_stddv = X_stand_df.agg(['std']).round(2)

print(X_stand_stddv)
```

```
     Lat  Lng  Population  Children  Age  Income  VitD_levels  Doc_visits  \
std  1.0  1.0         1.0       1.0  1.0     1.0          1.0         1.0

     Full_meals_eaten  vitD_supp  Initial_days  Additional_charges
std               1.0        1.0           1.0                 1.0
```

```
In [167]: # Provide a copy of the cleaned Data Set, index=False prevents the creation of an additional column
          X_stand_df.to_csv(r'C:\Users\mmorg\WGU\D212\Cleaned212Task2data.csv', index=False)
```

Part IV: Analysis

D. Perform PCA by doing the following:

D1. Determine the matrix of all the principal components.

Now that the data is standardized, we can use PCA to reduce dimensionality. We can use fit_transform() to combine both of these steps into one function.

After creating the matrix we can examine what weight each feature contributes to each of the principal components generated. For example PC1 is primarily based on Initial_days, whereas PC2 is influenced by Longitude and Initial_days. The higher the numbers on this matrix mean that those observations have a higher influence on those principle componets and we can start working on dimensionality reduction in the next step.

```
In [168]: # Instantiating data
          pca = PCA(n_components = 12, random_state = 0)
          # Fit and transform the PCA to X_stand
          X_pca = pca.fit_transform(X_stand)
          # Create PCA Matrix, shows the weight that a feature contributes to each Principal Component
          X_pca_matrix = pd.DataFrame(pca.components_,
                                      columns = ["PC1", "PC2", "PC3", "PC4", "PC5", "PC6",
                                                 "PC7", "PC8", "PC9", "PC10", "PC11", "PC12"])
          X_pca_matrix
```

Out[168]:

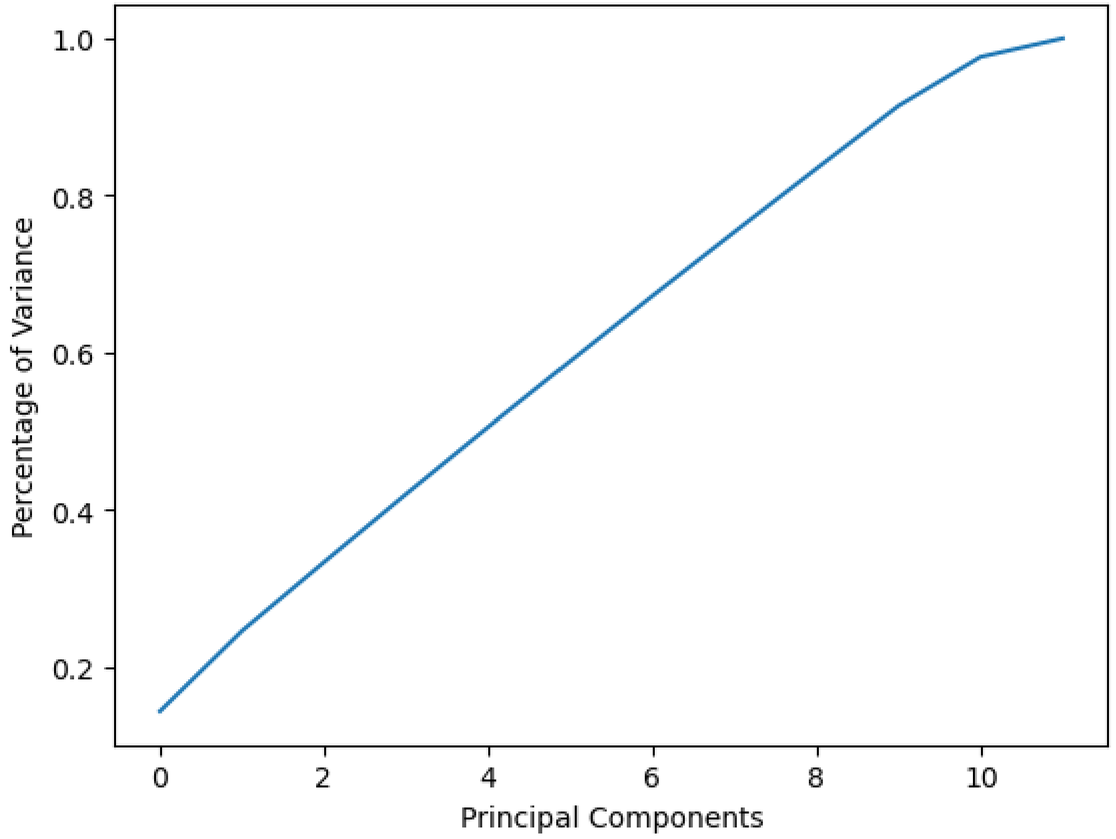
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
0	-0.003058	0.007652	-0.022811	0.023338	0.705901	-0.022410	0.019598	0.013893	0.027481	0.019038	0.020315	0.705664
1	-0.712542	0.265927	0.629684	-0.023013	0.008656	0.069845	-0.021974	0.013776	-0.111319	0.037972	0.070488	0.010325
2	0.129259	-0.564164	0.253543	0.350595	-0.003164	0.088519	-0.080655	0.053630	-0.299785	0.338816	0.505879	-0.001590
3	-0.064795	-0.343004	0.234772	0.291952	-0.022226	-0.137444	0.560328	0.048673	0.531893	-0.343571	-0.032595	-0.007786
4	0.041323	-0.235515	0.102756	-0.120302	0.009154	0.617901	-0.011810	0.586993	-0.028745	0.007754	-0.435667	0.022723
5	-0.042849	0.001443	-0.052169	0.448856	0.013231	0.477300	-0.391113	-0.420891	0.033011	-0.483289	-0.030242	0.016962
6	0.007356	-0.528847	0.273410	-0.545779	0.017394	-0.128018	-0.297966	-0.412969	0.118341	-0.039959	-0.234668	0.030821
7	-0.057235	0.073339	-0.067841	0.135775	-0.014133	0.326654	0.193909	-0.411312	0.351625	0.698886	-0.206142	-0.007117
8	-0.052112	0.052695	-0.008722	0.068395	-0.020392	-0.129952	-0.592420	0.354429	0.655825	0.142106	0.213063	-0.013102
9	-0.002282	0.049267	-0.111711	-0.503772	0.006684	0.463827	0.219518	-0.064247	0.196984	-0.145438	0.635462	-0.006324
10	0.679482	0.384103	0.614897	-0.006411	-0.001120	0.056180	-0.003230	-0.056510	0.074130	-0.018554	0.003061	0.020499
11	0.008854	-0.005042	0.016922	0.003751	0.707038	0.002297	-0.002533	0.000685	0.010346	0.000585	-0.011905	-0.706705

D2. Identify the total number of principal components using the elbow rule or the Kaiser criterion.

Now that we have our 12 principal components we can start working on reducing those that have little influence. To do this we can create a plot and use the elbow rule. Below you can see the elbow plot and it starts to level out around 10 on the x-axis. Because it starts at 0, and the 0 is referring to PC1, this means that we want to keep 11 principal components heading forward.

The plot from this dataset isn't one of the most clear or definitive plots I've seen in previous coursework. However, there is a clear leveling out of the line after PC11, so we will drop our number of components down to 11 from here on out.

```
In [169]: # Use a scree plot to visualize the contribution of each PC to the whole of variance
          # Scree plot
          plt.plot(np.cumsum(pca.explained_variance_ratio_))
          plt.xlabel("Principal Components")
          plt.ylabel("Percentage of Variance")
          plt.show();
```



```
D3.  Identify the variance of each of the principal components identified in part D2.

To identify the variance of each PCA identified in D2 we have to run the PCA again with only 11 components
and produce a new matrix. Once we have the PCA created we can then assign the explained_variance_ratio_
attribute. The numbers provided are percentage of variation of each principal component in decimal format.
```

In [170]:
```
# Instantiating data
reduced_pca = PCA(n_components = 11, random_state = 0)
# Fit and transform the PCA to X_stand
reduced_pca.fit(X_stand)
final_pca = reduced_pca.transform(X_stand)
# Create PCA Matrix, shows the weight that a feature contributes to each Principal Component
final_pca_matrix = pd.DataFrame(reduced_pca.components_.T,
                              columns = ["PC1", "PC2", "PC3", "PC4", "PC5", "PC6",
                                        "PC7", "PC8", "PC9", "PC10", "PC11"])
final_pca_matrix
```

Out[170]:

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
0	-0.003058	-0.712542	0.129259	-0.064795	0.041323	-0.042849	0.007356	-0.057235	-0.052112	-0.002282	0.679482
1	0.007652	0.265927	-0.564164	-0.343004	-0.235515	0.001443	-0.528847	0.073339	0.052695	0.049267	0.384103
2	-0.022811	0.629684	0.253543	0.234772	0.102756	-0.052169	0.273410	-0.067841	-0.008722	-0.111711	0.614897
3	0.023338	-0.023013	0.350595	0.291952	-0.120302	0.448856	-0.545779	0.135775	0.068395	-0.503772	-0.006411
4	0.705901	0.008656	-0.003164	-0.022226	0.009154	0.013231	0.017394	-0.014133	-0.020392	0.006684	-0.001120
5	-0.022410	0.069845	0.088519	-0.137444	0.617901	0.477300	-0.128018	0.326654	-0.129952	0.463827	0.056180
6	0.019598	-0.021974	-0.080655	0.560328	-0.011810	-0.391113	-0.297966	0.193909	-0.592420	0.219518	-0.003230
7	0.013893	0.013776	0.053630	0.048673	0.586993	-0.420891	-0.412969	-0.411312	0.354429	-0.064247	-0.056510
8	0.027481	-0.111319	-0.299785	0.531893	-0.028745	0.033011	0.118341	0.351625	0.655825	0.196984	0.074130
9	0.019038	0.037972	0.338816	-0.343571	0.007754	-0.483289	-0.039959	0.698886	0.142106	-0.145438	-0.018554
10	0.020315	0.070488	0.505879	-0.032595	-0.435667	-0.030242	-0.234668	-0.206142	0.213063	0.635462	0.003061
11	0.705664	0.010325	-0.001590	-0.007786	0.022723	0.016962	0.030821	-0.007117	-0.013102	-0.006324	0.020499

In [171]:
```
list(reduced_pca.explained_variance_ratio_)
```

Out[171]:
```
[0.14329551589301778,
 0.10240073568553085,
 0.08757786111482174,
 0.08667044956990438,
 0.08521515256145173,
 0.08373292555920939,
 0.0831305698317373,
 0.08150602610684196,
 0.0807104238018291,
 0.07998956523163969,
 0.06221023077235041]
```

D4. Identify the total variance captured by the principal components identified in part D2.

Provided below is a running total of the variance of each principal component. This shows that the 11 principal components are responsible for 97.6% of total variance.

In [172]:
```
list(reduced_pca.explained_variance_ratio_.cumsum())
```

Out[172]:
```
[0.14329551589301778,
 0.24569625157854863,
 0.3332741126933704,
 0.41994456226327476,
 0.5051597148247264,
 0.5888926403839359,
 0.6720232102156731,
 0.7535292363225151,
 0.8342396601243443,
 0.9142292253559839,
 0.9764394561283344]
```

D5. Summarize the results of your data analysis.

Now that we've successfully performed our PCA, we can try to make some predictions and see how good of a job we did. We will now use a Decision Tree Classifier to try and classify patients based on our 11 remaining principal components and predict whether they will be re-admitted.

In [173]:
```
# Create train and test sets from our final pca, which was already been fit and transformed
X_train, X_test, y_train, y_test = train_test_split(final_pca, y, train_size = 0.7, test_size=0.3, random_stat
# Confirm that our train and test datasets are shaped correctly
print(X_train.shape)
print(X_test.shape)
```

```
(7000, 11)
(3000, 11)
```

In [174]:
```
# Instantiate DecisionTreeClassifier
classification_model = DecisionTreeClassifier(random_state=0).fit(X_train, y_train)
y_predicted = classification_model.predict(X_test)
# Check accuracy score
test_accuracy = accuracy_score(y_test, y_predicted)
print("The accuracy of the model")
print(test_accuracy)
# Predict probabilities of the positive class
y_predicted_probability = classification_model.predict_proba(X_test)[:,1]
# Create confusion matrix
final_matrix = confusion_matrix(y_test, y_predicted)
# Print confusion matrix
print("\nThe confusion matrix for the Decision Tree Classifier")
print(final_matrix)
#Generate AUC score
print("\nThe Area Under the Curve (AUC) for the Decision Tree Classifier:")
#Print AUC score
print(roc_auc_score(y_test, y_predicted_probability))
```

```
The accuracy of the model
0.8873333333333333

The confusion matrix for the Decision Tree Classifier
[[1731  180]
 [ 158  931]]

The Area Under the Curve (AUC) for the Decision Tree Classifier:
0.880360620620361
```

After confirming that our train and test datasets are correct in shape we can continue forward with our model. Once we create the model we check the accuracy score and find that it is 88.7% accurate.

To see how it performs with raw numbers we create a confusion matrix. The read this matrix we have to understand what the four numbers mean. The left side numbers (1,731 and 158) refer to predictions of no re-admission. The right side numbers (180 and 931) refer to predictions of re-admission. The top row numbers (1,731 and 180) are actual patient results of no re-admission while the bottom row numbers (158 and 931) are actual patient results of re-admission.

So from reading this matrix we can see that of the 3,000 patients predicted, 2,662 (1,731 + 931) were predicted correctly while the remaining 338 (180 + 158) were incorrectly predicted.

Finally, our Area Under the Curve score can be looked at for even more evidence of our model's strength in predicting patient re-admissions. Our score here is 88% which is a great score and provides evidence that our model is strong.

In conclusion, I am somewhat shocked at these results. I have ran other prediction models on this dataset with similar accuracies. However, those analyses were using categorical data like health conditions and why the patient was hospitalized, in contrast to the continuous data of this dataset that for the most part seemingly should have no bearing on patient re-admission. Who would think that latitude and longitude could be used to predict patient re-admissions in this context? If there was something about where that person was living I would have to assume that it would result in one of the health conditions I mentioned as part of the categorical data analysis.

This definitely makes me think about a possible next step for this dataset and predicting patient re-admissions with even higher accuracy. If we could analyze this dataset with continuous and categorical data we could probably design a very accurate model that would outperform this model with an 89% accuracy score and 88% AUC score.

Part V: Attachments

E. Record the web sources used to acquire data or segments of third-party code to support the analysis. Ensure the web sources are reliable.

I used information from the Datacamp modules, and my previous submissions in D206 and D212 Task 1 to help complete the coding in this assignment.

F. Acknowledge sources, using in-text citations and references, for content that is quoted, paraphrased, or summarized.

Keita, Z. (2023). Principal Component Analysis in R Tutorial. https://datacamp.com/tutorial/pca-analysis-r