STATS 3DA3

Homework Assignment 6

Charlotte Bentley (400331595)

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```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import matplotlib.cm as cm
import seaborn as sns

from sklearn.cluster import KMeans
from sklearn.decomposition import PCA
from sklearn.model_selection import train_test_split
from sklearn import neighbors
from sklearn import metrics
from sklearn.preprocessing import scale
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, classification_report, roc_curve, roc_auc_score
import statsmodels.api as sm
```

```
Data = pd.read_csv('kidney_disease.csv')
```

1. Classification Problem Identification

Based on this dataset, our goal is to create a classification model to accurately predict whether a patient has early-stage chronic kidney disease (CKD). Using demographics and clinical results, we will assess paterns in CKD patients, and using machine learning, identify individuals with early-stage CKD.

2. Variable Transformation

```
Data = Data.drop(columns = 'id')
```

As of this step in our analysis, the only transformations used will be removing the id. Other transformations will be implemented further on. The types of transformations we will be making will involve removing incomplete observations and splitting the data set.

3. Dataset Overview

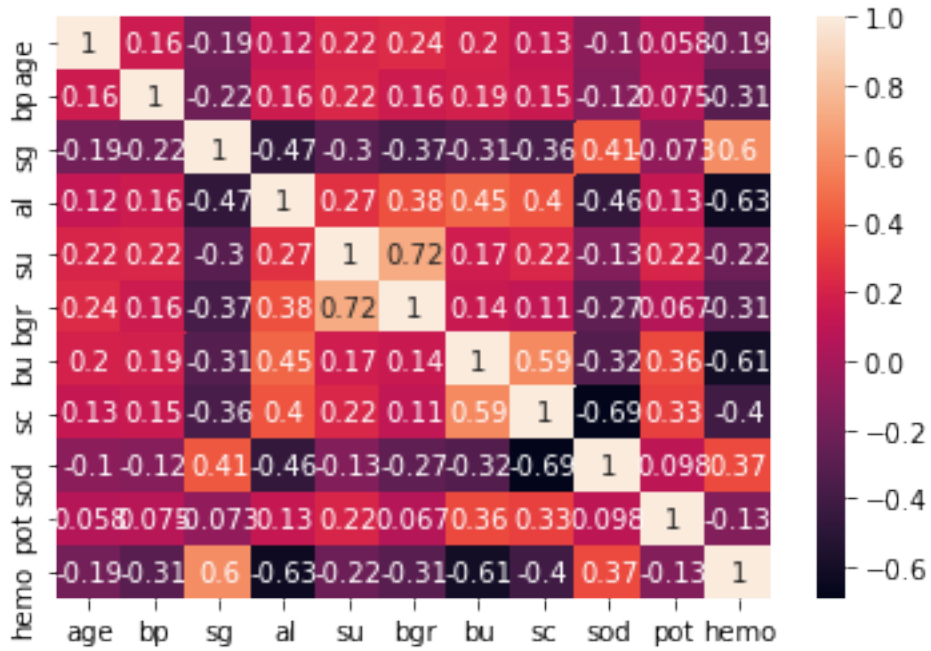
```
Data.describe()
```

	age	bp	sg	al	su	bgr	bu	sc
count	391.000000	388.000000	353.000000	354.000000	351.000000	356.000000	381.000000	383.000000
mean	51.483376	76.469072	1.017408	1.016949	0.450142	148.036517	57.425722	3.072454
std	17.169714	13.683637	0.005717	1.352679	1.099191	79.281714	50.503006	5.741126
min	2.000000	50.000000	1.005000	0.000000	0.000000	22.000000	1.500000	0.400000
25%	42.000000	70.000000	1.010000	0.000000	0.000000	99.000000	27.000000	0.900000
50%	55.000000	80.000000	1.020000	0.000000	0.000000	121.000000	42.000000	1.300000
75%	64.500000	80.000000	1.020000	2.000000	0.000000	163.000000	66.000000	2.800000
max	90.000000	180.000000	1.025000	5.000000	5.000000	490.000000	391.000000	76.000000

This dataset originally contains 25 various variables with 400 observations. 11 of which are numeric and 14 are nominal. We can see from the counts of all our variables that some observations are missing values. Since this information is important to our analysis, in future steps we will be removing any incomplete observations. In variables like blood urea and blood glucose random, we see a very high distribution for our results. Considering we have both patients and controls in our dataset, this means that extreme high or low levels may be an indicator for diagnosis.

4. Association Between Variables

```
sns.heatmap(Data.corr(), annot=True)
```



Loooking at our heatmap of the association between variables we see there is not a lot of direct correlation between variables. Our most direct relationship is between blood glucose random and sugar at 0.72. This also makes the most sense considering blood gluclose is the main sugar found in your blood, hence why the two are correlated. Another direct relationship is between serum creatinine and blood urea at 0.59. Again, this correlation makes sense as elevated levels in either of these indicates the kidneys are not working. Because of this we would definitely want serum creatine and blood urea for our feature selection as they not only have a good association, but are good at predicting chronic kidney disease.

5. Missing Value Analysis and Handling.

```
DF = Data.dropna()
DF
```

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wc
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	117.0	...	32	6700
9	53.0	90.0	1.020	2.0	0.0	abnormal	abnormal	present	notpresent	70.0	...	29	12100
11	63.0	70.0	1.010	3.0	0.0	abnormal	abnormal	present	notpresent	380.0	...	32	4500
14	68.0	80.0	1.010	3.0	2.0	normal	abnormal	present	present	157.0	...	16	11000

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wc
20	61.0	80.0	1.015	2.0	0.0	abnormal	abnormal	notpresent	notpresent	173.0	...	24	9200
...	...	...	...	...	...	...	...	...	...	...	...	...	...
395	55.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	140.0	...	47	6700
396	42.0	70.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	75.0	...	54	7800
397	12.0	80.0	1.020	0.0	0.0	normal	normal	notpresent	notpresent	100.0	...	49	6600
398	17.0	60.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	114.0	...	51	7200
399	58.0	80.0	1.025	0.0	0.0	normal	normal	notpresent	notpresent	131.0	...	53	6800

We have chosen to remove all incomplete observations since the inclusion of said values may affect our statistical anlyses.

6. Outlier Analysis

We have decided to skip our outlier analysis since we are more focused on pattern recognition and many of our variables are nominal.

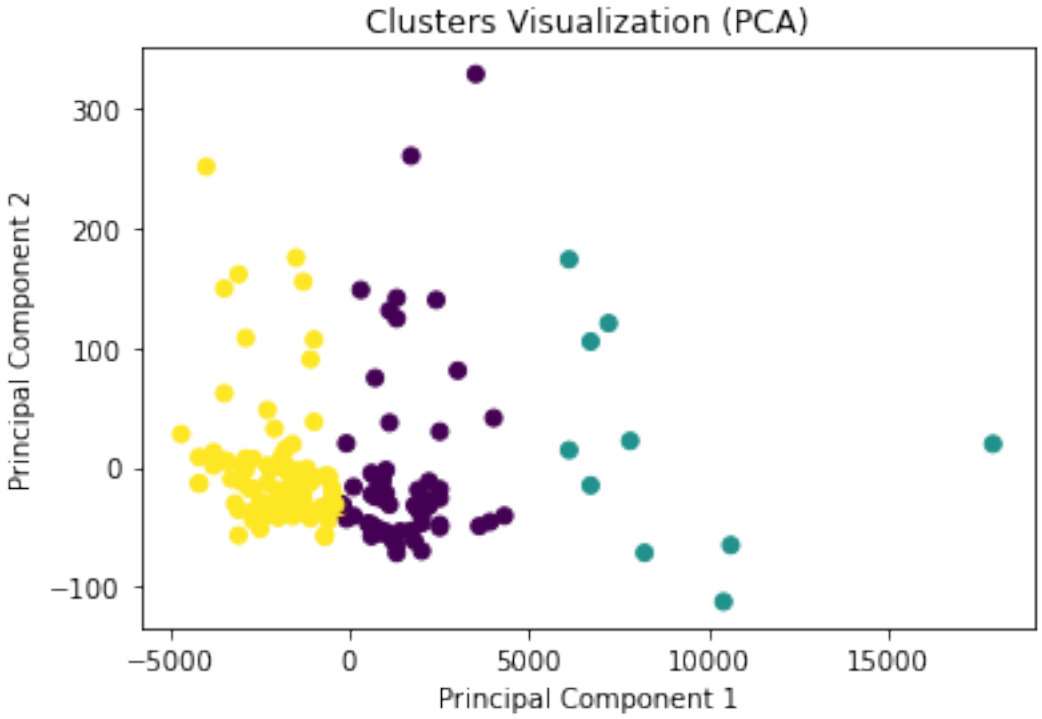
7. Sub-group Analysis

```
Y = DF['class'].map({'ckd':1 , 'notckd':0})
X = DF.drop(columns=['class','sg','rbc','pc','pcc','ba','htn','dm','cad','pe','ane','appet'])
```

```
# K-means clustering
kmeans = KMeans(n_clusters=3)
clusters = kmeans.fit_predict(X)


# Visualization
pca = PCA(n_components=2)
data_pca = pca.fit_transform(X)
plt.scatter(data_pca[:, 0], data_pca[:, 1], c=clusters)
plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.title('Clusters Visualization (PCA)')
```

```
plt.show()
cluster_labels = kmeans.fit_predict(X)
print(cluster_labels)
```

```
/Users/charlotte/opt/anaconda3/lib/python3.8/site-packages/sklearn/cluster/_kmeans.py:1416: Fu
  super()._check_params_vs_input(X, default_n_init=10)
/Users/charlotte/opt/anaconda3/lib/python3.8/site-packages/sklearn/cluster/_kmeans.py:1416: Fu
  super()._check_params_vs_input(X, default_n_init=10)
```




```
[1 0 1 0 0 1 0 2 1 2 1 1 1 0 0 1 1 2 1 2 0 0 2 2 1 0 0 0 2 1 2 0 2 0 0 1 0
 1 2 0 1 0 1 0 0 0 1 0 0 0 0 0 0 1 0 1 1 0 1 0 1 0 1 1 0 1 1 1 0 1 0 1 1 1 0
 1 1 0 1 0 0 1 1 0 1 1 1 0 1 1 0 1 1 0 0 1 1 0 0 1 1 1 0 1 1 1 1 1 1 1 1 1
 1 1 0 1 1 1 1 1 0 1 1 1 1 0 0 0 1 0 0 0 1 0 0 1 0 0 1 1 1 1 1 0 1 1 1 0 1
 1 1 1 1 0 1 1 1 1 1]
```

8. Data Splitting

```
x_train, x_test, y_train, y_test = train_test_split(
    X,
    Y,
    train_size=0.7,
    random_state=1,
    stratify=Y
    )
```

9. Classifier Choices

For this dataset we have chosen to use the K Nearest Neighbours (KNN) classification and the Logistic Regression classification. We have chosen KNN for multiple reasons; for starters, it is strong against outliers. Considering we chose not to continue with outlier analysis, outliers having less influence in this model is definitely a valuable tool. Not only is it effective with outliers, it can handle nonlinear relationships effectively. As for Logistic Regression, it is highly efficient and interpretable which is something we see as valuable in our analysis.

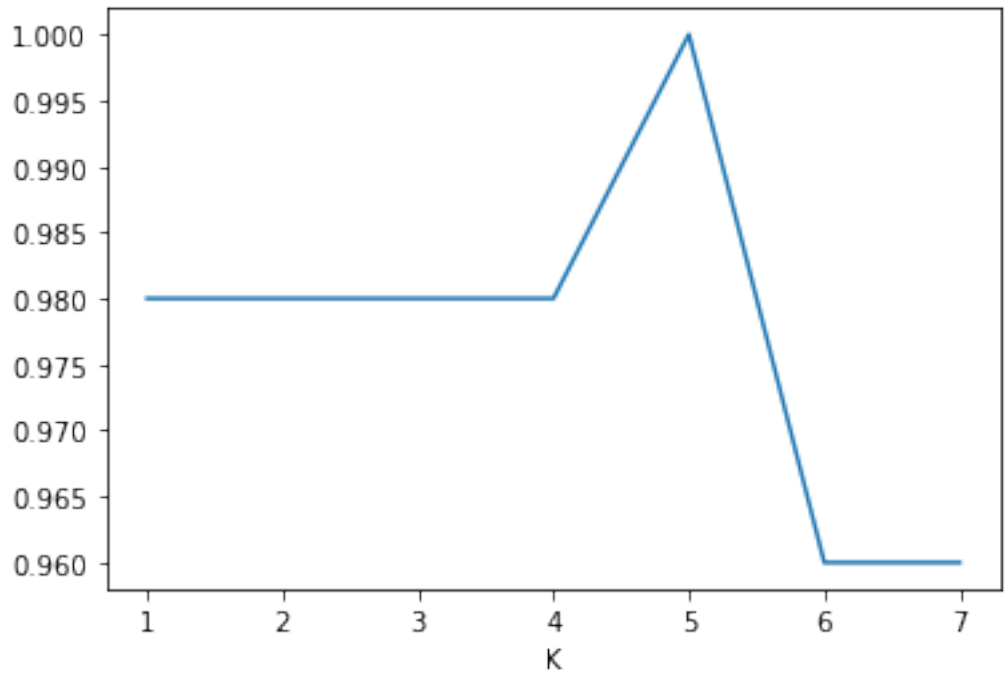
10. Performance Metrics

For our data set, we will be focusing on sensitivity and specificity for comparing the performance of our classifiers. We have chosen these 2 as they both evaluate the accuracy of the model in predicting an individual with disease as possitive (sensitivity), and predicting an individual without a disease as negative. From this we can then evaluate our false positive and negative rates to help us create a more accurate model.

11. Feature Selection/Extraction

```
X = scale(X, axis=0)


x_train, x_test, y_train, y_test = train_test_split(
    X,
    Y,
    train_size=0.7,
    random_state=1,
```

```
    stratify=Y
    )
k_range = range(1, 8)
scores = []

for k in k_range:
    knn = neighbors.KNeighborsClassifier(n_neighbors=k)
    knn.fit(x_train, y_train)
    y_pred = knn.predict(x_test)
    scores.append(round(metrics.accuracy_score(y_test, y_pred),2))

plt.plot(k_range, scores)
plt.xlabel('K')
plt.xticks(range(1,8))
plt.show()
```

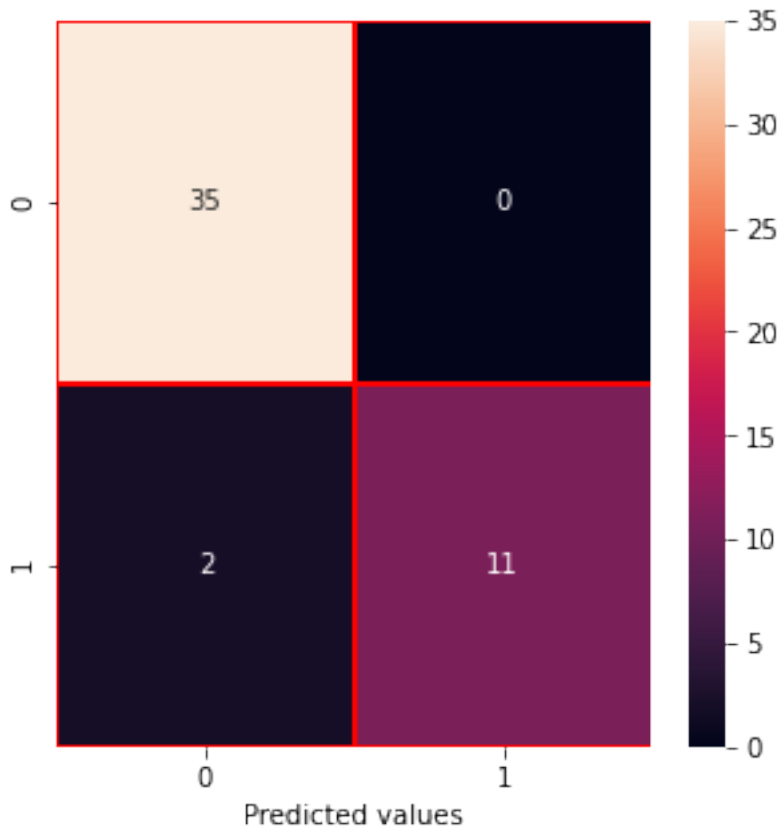


Since we have not scaled our data thus far, there is a chance that one of our variables is dominating our analysis. By scaling, we are ensuring all variables are equally taken into account. To further improve the performance of KNN we have plotted K against accuracy to determine the optimal

number of clusters in our analysis. Looking at our above graph we see our optimal K is 5 clusters with almost perfect accuracy of 95.83%.

12. Classifier Comparison

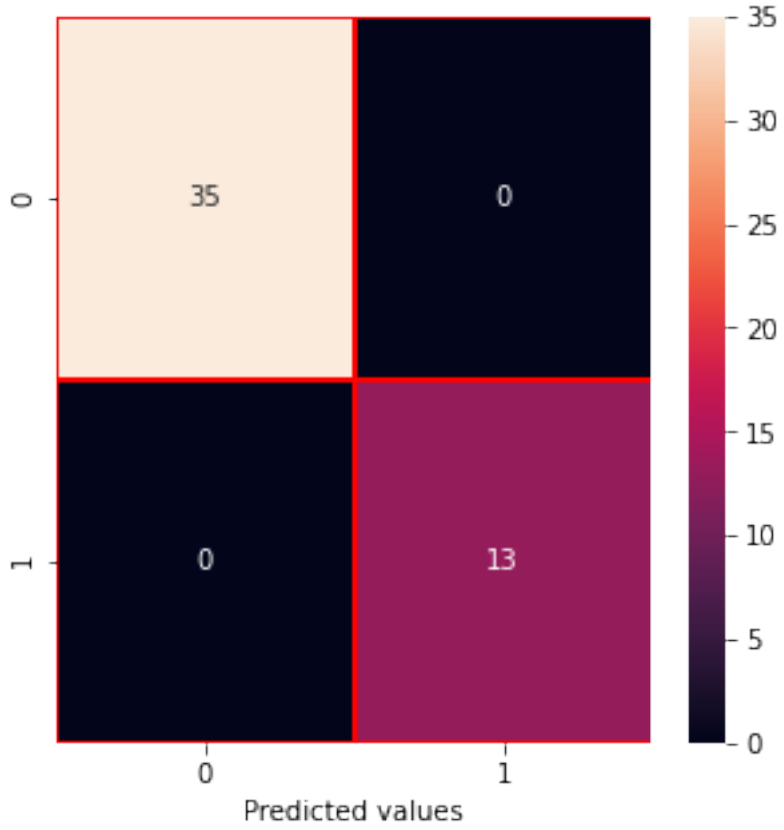
```
# KNN Classification
cm = confusion_matrix(y_test, y_pred)


f, ax =plt.subplots(figsize = (5,5))
sns.heatmap(cm,annot = True, linewidths= 0.5, linecolor="red", fmt=".0f", ax=ax)
plt.xlabel('Predicted values')
plt.show()


sensitivity = cm[1,1]/(cm[1,1]+cm[1,0])
print('Sensitivity : ', sensitivity )


specificity = cm[0,0]/(cm[0,0]+cm[0,1])
print('Specificity : ', specificity)
```




```
Sensitivity :  0.8461538461538461
Specificity :  1.0
```

```
# Logistic Regression
def_log = LogisticRegression()
def_log.fit(x_train, y_train)

pred_prob = def_log.predict_proba(x_test)

df = pd.DataFrame(
    data = {'prob0': pred_prob[:,1], 'y_test': y_test}
    )

df['y_test_pred'] = df.prob0.map(lambda x: 1 if x>0.5 else 0)
df.head()
```

```
cm = confusion_matrix(df.y_test, df.y_test_pred)

f, ax =plt.subplots(figsize = (5,5))
sns.heatmap(cm,annot = True, linewidths= 0.5, linecolor="red", fmt=".0f", ax=ax)
plt.xlabel('Predicted values')
plt.show()

sensitivity = cm[1,1]/(cm[1,1]+cm[1,0])
print('Sensitivity : ', sensitivity )

specificity = cm[0,0]/(cm[0,0]+cm[0,1])
print('Specificity : ', specificity)
```




```
Sensitivity :  1.0
Specificity :  1.0
```

Looking at our performance metrics for both of our classifiers, both show highly promising results. Our KNN Classifier shows a specificity of 1 and a sensitivity of 0.846. Meaning this classification method results in 100% of individuals without chronic kidney disease to be correctly identified and 84.6% of individuals with chronic kidney disease to be correctly diagnosed. As for Logistic regresssion, we find this to be even greater with a 100% sensitivity and specificity score. This means our model is 100% accurate in predicting those with chronic kidney disease and those without.

13. Interpretable Classifier Insight

```
y = DF['class'].map({'ckd':1 , 'notckd':0})
x = DF.drop(columns = 'class')
```

```
x['rbc'] = x['rbc'].map({'normal':1 , 'abnormal':0})
x['pc'] = x['pc'].map({'normal':1 , 'abnormal':0})
x['pcc'] = x['pcc'].map({'present':1 , 'notpresent':0})
x['ba'] = x['ba'].map({'present':1 , 'notpresent':0})
x['htn'] = x['htn'].map({'yes':1 , 'no':0})
x['dm'] = x['dm'].map({'yes':1 , 'no':0})
x['cad'] = x['cad'].map({'yes':1 , 'no':0})
x['appet'] = x['appet'].map({'good':1 , 'poor':0})
x['pe'] = x['pe'].map({'yes':1 , 'no':0})
x['ane'] = x['ane'].map({'yes':1 , 'no':0})
```

```
scaler = StandardScaler()
x = scaler.fit_transform(x)


x_train, x_test, y_train, y_test = train_test_split(
    x,
    y,
    train_size=0.70,
    random_state=0,
    stratify=y
    )
```

```
logit_model = sm.Logit(y_train, sm.add_constant(x_train))
logit_result = logit_model.fit()

print(logit_result.summary())
```

```
Warning: Maximum number of iterations has been exceeded.
         Current function value: 0.000000
         Iterations: 35
                           Logit Regression Results
==============================================================================
Dep. Variable:                  class   No. Observations:                  110
Model:                          Logit   Df Residuals:                       85
Method:                           MLE   Df Model:                           24
Date:                Fri, 12 Apr 2024   Pseudo R-squ.:                   1.000
Time:                        15:42:24   Log-Likelihood:            -1.7143e-05
converged:                      False   LL-Null:                       -64.455
Covariance Type:            nonrobust   LLR p-value:                 2.443e-16
==============================================================================
                 coef    std err          z      P>|z|      [0.025      0.975]
------------------------------------------------------------------------------
const        -10.1081   5.74e+05  -1.76e-05      1.000   -1.12e+06    1.12e+06
x1            -1.5228   1.78e+05  -8.54e-06      1.000    -3.5e+05     3.5e+05
x2            -0.0118   1.56e+05  -7.58e-08      1.000   -3.06e+05    3.06e+05
x3            -0.6778   3.12e+05  -2.18e-06      1.000   -6.11e+05    6.11e+05
x4             7.0316   2.41e+06   2.92e-06      1.000   -4.72e+06    4.72e+06
x5            -5.8034   3.39e+06  -1.71e-06      1.000   -6.65e+06    6.65e+06
x6            -5.4067   1.37e+06  -3.94e-06      1.000   -2.69e+06    2.69e+06
x7            -9.8944   2.81e+06  -3.52e-06      1.000    -5.5e+06     5.5e+06
x8             3.1513   1.15e+06   2.75e-06      1.000   -2.25e+06    2.25e+06
x9             1.3295   4.65e+05   2.86e-06      1.000   -9.11e+05    9.11e+05
x10            2.9695   5.42e+05   5.48e-06      1.000   -1.06e+06    1.06e+06
```

```
x11          -1.5169   6.01e+05  -2.53e-06      1.000   -1.18e+06    1.18e+06
x12           0.3956   1.45e+06   2.74e-07      1.000   -2.83e+06    2.83e+06
x13          -1.0302   1.81e+05  -5.69e-06      1.000   -3.55e+05    3.55e+05
x14          -8.9194   1.26e+06  -7.09e-06      1.000   -2.47e+06    2.47e+06
x15          -0.4296   4.72e+05   -9.1e-07      1.000   -9.25e+05    9.25e+05
x16          -0.2981   3.59e+05  -8.31e-07      1.000   -7.03e+05    7.03e+05
x17           1.6619   2.79e+05   5.96e-06      1.000   -5.46e+05    5.46e+05
x18           0.0360   2.65e+05   1.36e-07      1.000   -5.19e+05    5.19e+05
x19          18.1776   9.48e+05   1.92e-05      1.000   -1.86e+06    1.86e+06
x20           1.5681   1.53e+06   1.03e-06      1.000      -3e+06       3e+06
x21          -3.1426   3.46e+06  -9.08e-07      1.000   -6.79e+06    6.79e+06
x22          -4.5409    7.3e+05  -6.22e-06      1.000   -1.43e+06    1.43e+06
x23          -2.2927   1.48e+06  -1.55e-06      1.000    -2.9e+06     2.9e+06
x24          -6.7131    1.3e+06  -5.15e-06      1.000   -2.55e+06    2.55e+06
==============================================================================

Complete Separation: The results show that there iscomplete separation.
In this case the Maximum Likelihood Estimator does not exist and the parameters
are not identified.

/Users/charlotte/opt/anaconda3/lib/python3.8/site-packages/statsmodels/base/model.py:567: Conve
  warn("Maximum Likelihood optimization failed to converge. "
```

Looking at our summary above, our P column states that every variable is statistically significant. Looking at the absolute of our coefficient values, hypertension is our highest coefficient, or our most significant predictor variable for chronic kidney disease. Meaning, hypertension is our strongest indicator of whether a person has chronic kidney disease or not. On the other hand, our smallest coefficient is blood preasure. Meaning, blood pressure is our least significant variable in predicting chronic kidney disease.

14. [Bonus]

One way we can improve our classifier performance is to train each sub-group individually. We will train based on 5 groups considering that was our most optimal K value.

15. Team Contributions

All problems have been answered by myself.

16. Link

https://github.com/charloben/Asssignment-6.git