MONKEYPOX PREDICTION

1. BUSINESS UNDERSTANDING

Overview

Monkeypox, according to the Centers for Disease Control and Prevention, is an uncommon disease caused by infection with the monkeypox virus. Monkeypox virus is part of the same family of viruses as variola virus, the virus that causes smallpox. Monkeypox symptoms are similar to smallpox symptoms, but milder, and monkeypox is rarely fatal. Monkeypox was discovered in 1958 when two outbreaks of a pox-like disease occurred in colonies of monkeys kept for research. Despite being named “monkeypox,” the source of the disease remains unknown. However, African rodents and non-human primates (like monkeys) might harbor the virus and infect people.

The first human case of monkeypox was recorded in 1970. Prior to the 2022 outbreak in May, monkeypox had been reported in people in several central and western African countries. Previously, almost all monkeypox cases in people outside of Africa were linked to international travel to countries where the disease commonly occurs or through imported animals. These cases occurred on multiple continents.

`Transmission` : Monkeypox is a viral zoonosis (virus transmitted to humans from animals)It is transmitted through close contact with an infected person or animal, body fluids, respiratory droplets and contaminated materials such as bedding.

Problem Statement

As more cases of monkeypox emerge, the world becomes increasingly concerned, as they do not want a repeat of what happened not too long ago, when the infamous Covid-19 broke out and altered the world as we know it. Faced with the reality that such viral diseases can actually shut down the planet, the organization must develop ways to reduce the spread of this disease, enter the Health authorities in the United Kingdom, they have established an incident management team to coordinate the extensive contact tracing in regards to how quickly the virus can be transferred and, worse, mutate into a more lethal variant.

On July 23, the World Health Organization declared the outbreak “a public health emergency of international concern.” Another thing you should know about monkeypox is that it is extremely unpleasant. The current strain has a 1% mortality rate, and as of this writing, there have been three deaths reported in outbreaks outside of Africa, and five deaths in African countries where the

disease is endemic, since the beginning of the year. The West African strain of the monkeypox virus is associated with milder disease and fewer deaths than the Central African strain.

Even if the chances of death are low, patients with monkeypox have reported how painful and debilitating the disease is. "People may experience flu-like symptoms at first, such as fever and headache, but as the disease progresses, you get a multi-stage rash, lesions can develop in your mouth, feet, and genital region, and these develop into pus-filled blisters."Symptoms can appear between five and 21 days after infection, though the average incubation period is 6 to 13 days. For the first few days, there are headaches, fever, muscle aches, and fatigue.

As students of the Incident Management team we have been tasked to create a model to accurately identify potential infected persons in order to make contact tracing faster and more efficient, thereby halting the spread.

Proposed Solution

One proposed solution is to cultivate the use of data in attempting to predict whether or not a person has monkeypox in order to make contact tracing easier.

Specific Objectives

- To predict whether a patient is negative or positive for monkeypox based on the symptoms they exhibit
- To analyze the various variables such as Sore Throat,Penile Oedema, Oral Lesions ,Systemic illness and STIs and know their relationship with monkeypox

Research Questions

- Which model best predicts monkeypox disease?
- Which symptom has the highest correlation to monkeypox?
- Which symptom has the lowest correlation to monkeypox?

Success Criteria

Tentatively, the study will be judged a success if, we build a model to predict monkeypox with a

Importing Libraries

Libraries to enhance data manipulation.

These comprises of;

> **NumPy**

NumPy is an open source project aiming to enable numerical computing with Python.

> **pandas**

pandas is a fast, powerful, flexible and easy to use open source data analysis and manipulation tool, built on top of the Python programming language.

```
import pandas as pd
import numpy as np
```

Libraries for visualization;

> **Seaborn**

Seaborn is a Python data visualization library based on matplotlib. It provides a high-level interface for drawing attractive and informative statistical graphics.

> **Matplotlib**

Matplotlib is a comprehensive library for creating static, animated, and interactive visualizations in Python.

```
import seaborn as sns
# setting the theme
sns.set_style("darkgrid")

import matplotlib.pyplot as plt
```

Libraries for modelling tasks;

> **scikit-learn**

Simple and efficient tools for predictive data analysis, accessible to everybody, and reusable in various contexts built on NumPy, SciPy, and matplotlib

```
from sklearn.linear_model import Ridge, Lasso, LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.pipeline import Pipeline
from sklearn.metrics import recall_score, precision_score ,accuracy_score, plot_confusion_mat
from sklearn.model_selection import cross_val_score, GridSearchCV, train_test_split
from imblearn.over_sampling import SMOTE, ADASYN
```

Library for saving our final model

```
import joblib
```

Library for ignoring deprecation warnings

```
import warnings
warnings.simplefilter(action='ignore', category=FutureWarning)
warnings.filterwarnings('ignore')
```

Defining relevant Functions.

```
# function to display the values on the graph
def show_values(axs, orient="v", space=.01):
    def _single(ax):
        if orient == "v":
            for p in ax.patches:
                _x = p.get_x() + p.get_width() / 2
                _y = p.get_y() + p.get_height() + (p.get_height()*0.01)
                value = '{:.1f}'.format(p.get_height())
                ax.text(_x, _y, value, ha="center")
        elif orient == "h":
            for p in ax.patches:
                _x = p.get_x() + p.get_width() + float(space)
                _y = p.get_y() + p.get_height() - (p.get_height()*0.5)
                value = '{:.1f}'.format(p.get_width())
                ax.text(_x, _y, value, ha="left")

    if isinstance(axs, np.ndarray):
        for idx, ax in np.ndenumerate(axs):
            _single(ax)
    else:
        _single(axs)

# function to plot the pie charts
def univariate(name):
    """ Function to plot the pie charts """

    figure = plt.pie(mp[name].value_counts(), labels = mp[name].unique(),
             startangle = 90, shadow = True, autopct = "%2.1f%%")
    plt.title(name)
    return figure

#function to train model and return the score
def model_trainer(model, X_tr, y_tr, X_te, y_te):
    model.fit(X_tr, y_tr)
```

```
    pre = model.predict(X_te)
    precision =precision_score(y_te, pre)
    recall =recall_score(y_te, pre)
    accuracy =accuracy_score(y_te, pre)
    f1 = f1_score(y_te, pre)

    return {'precision':precision,
            'recall_score':recall,
            'accuracy_score':accuracy,
            'f1_score':f1}

#function to tune the model and find best parameters for the DecisionTreeClassifier using gri
def grid_search(model, parms, X_tr, y_tr):
    gs_tree = GridSearchCV(model, parms, cv=3)
    gs_tree.fit(X_tr, y_tr)

    return gs_tree.best_params_
```

Loading Data

```
# Loading the data using pandas into mp {Monkey Pox}

# Index_col sets the index to be the patient id as there is no need to have more than one uni

mp = pd.read_csv('DATA.csv')
```

2. DATA UNDERSTANDING

Overview

We are using a SYNTHETIC dataset generated from a study published by the British Medical Journal. It is a description of the clinical features and novel presentations of human monkeypox during the outbreak of 2022 in central London.

The data has already been loaded in the above code cell.

```
# preview of the first 5 rows
mp.head()
```

	Patient_ID	Systemic Illness	Rectal Pain	Sore Throat	Penile Oedema	Oral Lesions	Solitary Lesion	Swollen Tonsils	HIV Infection
0	P0	None	False	True	True	True	False	True	False

```
# Checking the summary of the data

mp.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 25000 entries, 0 to 24999
Data columns (total 11 columns):
 #   Column                          Non-Null Count  Dtype 
---  ------                          --------------  ----- 
 0   Patient_ID                      25000 non-null  object
 1   Systemic Illness                25000 non-null  object
 2   Rectal Pain                     25000 non-null  bool  
 3   Sore Throat                     25000 non-null  bool  
 4   Penile Oedema                   25000 non-null  bool  
 5   Oral Lesions                    25000 non-null  bool  
 6   Solitary Lesion                 25000 non-null  bool  
 7   Swollen Tonsils                 25000 non-null  bool  
 8   HIV Infection                   25000 non-null  bool  
 9   Sexually Transmitted Infection  25000 non-null  bool  
 10  MonkeyPox                       25000 non-null  object
dtypes: bool(8), object(3)
memory usage: 781.4+ KB
```

```
# checking for duplicates using the index as a guide as the index is the personal id
mp.duplicated().sum()
```

```
0
```

```
# viewing the column names of the dataset

mp.columns
```

```
Index(['Patient_ID', 'Systemic Illness', 'Rectal Pain', 'Sore Throat',
       'Penile Oedema', 'Oral Lesions', 'Solitary Lesion', 'Swollen Tonsils',
       'HIV Infection', 'Sexually Transmitted Infection', 'MonkeyPox'],
      dtype='object')
```

```
# checking the summary statistics of the data
mp.describe()
```

Patient_ID	Systemic Illness	Rectal Pain	Sore Throat	Penile Oedema	Oral Lesions	Solitary Lesion	Swollen Tonsils	Infec

```
# shape of the data
mp.shape
```

```
(25000, 11)
```

```
# Checking on the uniue value counts in Systemic Illness
mp['Systemic Illness'].value_counts()
```

```
Fever                   6382
Swollen Lymph Nodes     6252
None                    6216
Muscle Aches and Pain   6150
Name: Systemic Illness, dtype: int64
```

```
# Reducing ambiguity in the systemic illness column we change none to No systemic Illness

mp['Systemic Illness'].replace(to_replace= 'None',value= 'No_Systemic_Illness',inplace= True)
```

```
# confirming
mp['Systemic Illness'].value_counts()
```

```
Fever                   6382
Swollen Lymph Nodes     6252
No_Systemic_Illness     6216
Muscle Aches and Pain   6150
Name: Systemic Illness, dtype: int64
```

Summary

- Our data has 25,000 rows and 11 columns
- The data has 8 columns of dtype `Bool` and 2 columns of dtype `object`.
- There are no missing columns in the data.
- There are no duplicates in the data.
- One column in particular will be dropped `Patient_ID` as the patient id wont be helpful in the modeling as it will only add noise for the machine.
- Uniformity of column names will also be done to reduce ambiguity.
- The following are the relevant columns in our data;
    - Systemic Illness
    - Rectal Pain
    - Sore Throat
    - Penile Oedema

- Oral Lesions
- Solitary Lesion
- Swollen Tonsils
- HIV Infection
- Sexually Transmitted Infection
- MonkeyPox

Systemic illness has the most value counts after Patient_ID with 4.

data cleaning will be relatievly easy as the data has no missing values and no duplicates.

Since the data has no duplicates and missing values, we can go ahead and perfom column name uniforminty, type casting. and drop the `Patient_ID` before starting on Exploratory Data Analysis to gain more insights from the data.

Dropping Patient ID

```
# dropping the patient id
mp.drop(columns=['Patient_ID'],axis = 1, inplace=True)
mp.head(3)
```

	Systemic Illness	Rectal Pain	Sore Throat	Penile Oedema	Oral Lesions	Solitary Lesion	Swollen Tonsils	HIV Infection	Tr
0	No_Systemic_Illness	False	True	True	True	False	True	False	
1	Fever	True	False	True	True	False	False	True	

Uniformity of Column names

```
# replacing the names
mp.rename(columns={'Systemic Illness':'Systemic_Illness',
                   'Rectal Pain':'Rectal_Pain',
                   'Sore Throat':'Sore_Throat',
                   'Penile Oedema':'Penile_Oedema',
                   'Oral Lesions':'Oral_Lesions',
                   'Solitary Lesion':'Solitary_Leision',
                   'Swollen Tonsils':'Swollen_Tonsils',
                   'HIV Infection':'HIV_Infection',
                   'Sexually Transmitted Infection':'STI',
                   'MonkeyPox':'Target'},inplace=True)
mp.head(3)
```

	Systemic_Illness	Rectal_Pain	Sore_Throat	Penile_Oedema	Oral_Lesions	Solitary_L
0	No_Systemic_Illness	False	True	True	True	
1	Fever	True	False	True	True	

Type casting Objects to Categorical data types

```
# For loop to get all object types in the data frame
col_obj = []
for x in list(mp.columns):
    if mp[x].dtypes == object:
        col_obj.append(x)
col_obj
```

```
['Systemic_Illness', 'Target']
```

```
# type_casting object to categorical

mp[col_obj] = mp[col_obj].astype('category')

# confirming
mp.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 25000 entries, 0 to 24999
Data columns (total 10 columns):
 #   Column            Non-Null Count  Dtype
---  ------            --------------  -----
 0   Systemic_Illness  25000 non-null  category
 1   Rectal_Pain       25000 non-null  bool
 2   Sore_Throat       25000 non-null  bool
 3   Penile_Oedema     25000 non-null  bool
 4   Oral_Lesions      25000 non-null  bool
 5   Solitary_Leision  25000 non-null  bool
 6   Swollen_Tonsils   25000 non-null  bool
 7   HIV_Infection     25000 non-null  bool
 8   STI               25000 non-null  bool
 9   Target            25000 non-null  category
dtypes: bool(8), category(2)
memory usage: 244.6 KB
```

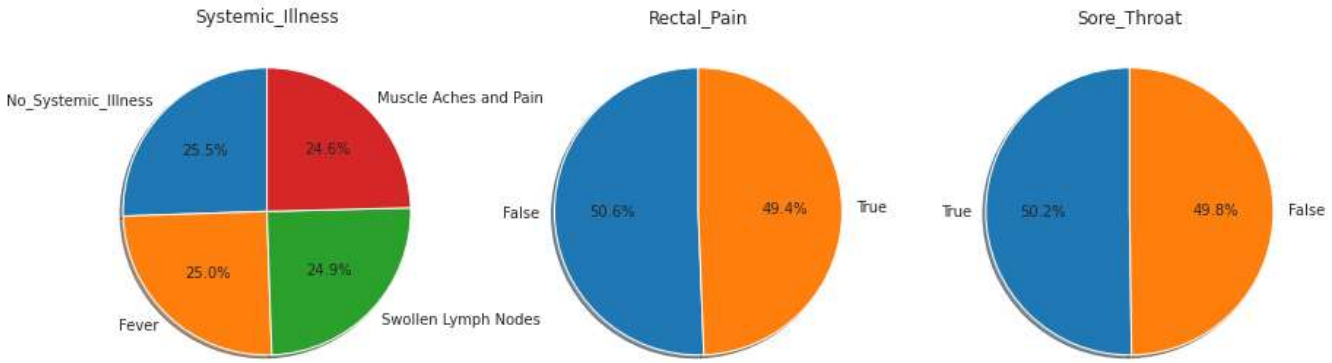
Exploratory Data Analysis

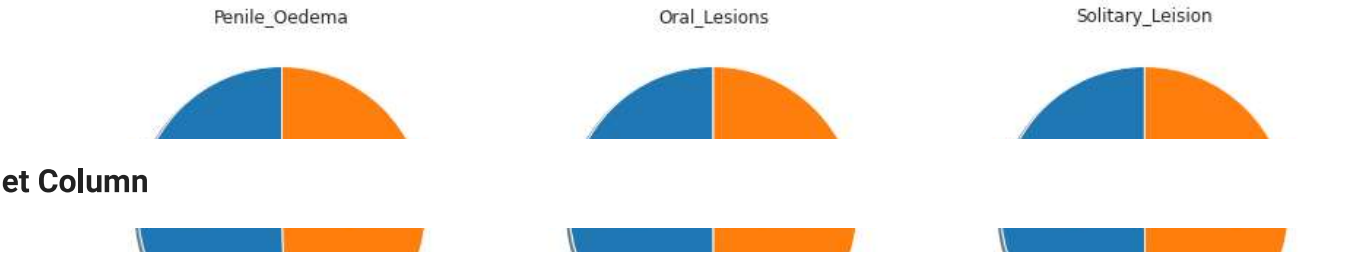
UNIVARIATE ANALYSIS

Feature columns

In univariate analysis, we will investigate the distribution of symptoms using pie charts.

```
# Making a list of column names to use in the notebook
col = list(mp.columns)


# columns to use when plotting the pie charts
columns =  col[:-1]

# plotting the pie charts
plt.figure(figsize = (15, 20))
for i in enumerate(columns):
    plt.subplot(3, 3, i[0] + 1)
    univariate(i[1])
```





Target Column

```
univariate("Target");
```

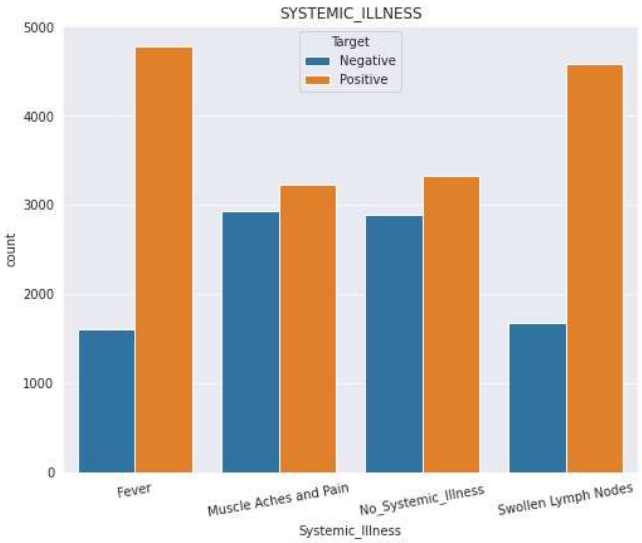
Univariate Analysis summary

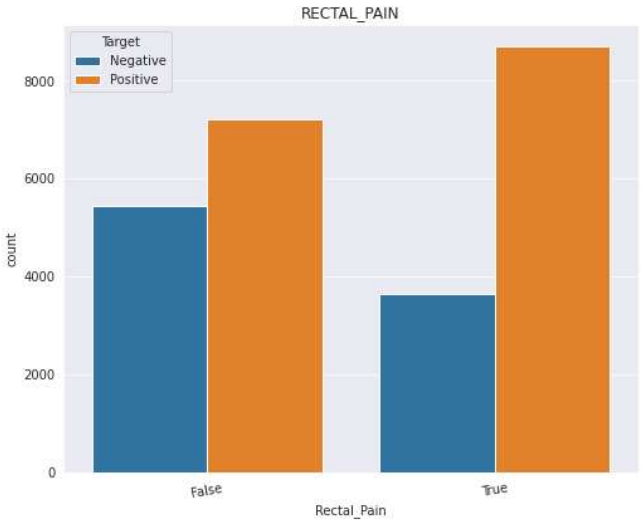
- From the above, all symptoms have an almost uniform distribution based on whether it is true or false.
- For the target column, 63.6% of the data consists of those who are monkeypox negative and 36.4% are those who are monkeypox positive therefore there is a class imbalance in our target column.

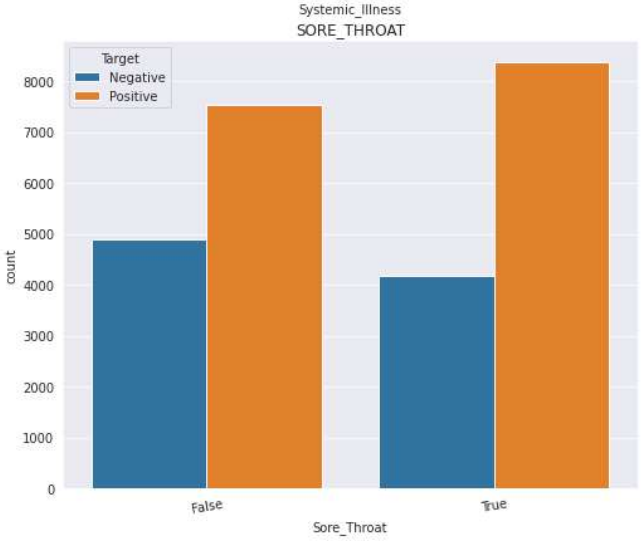
BIVARIATE ANALYSIS

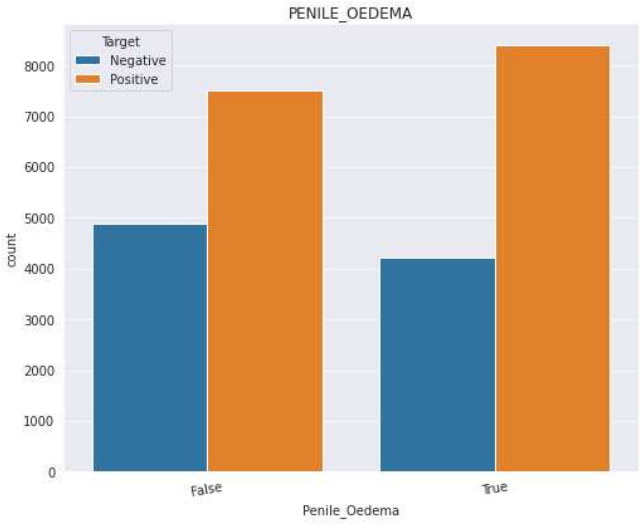
In Bivariate analysis, we will compare the feature columns to our target variable to see the relationship between the two. This will be achieved by plotting side by side bar charts to see the relationship.

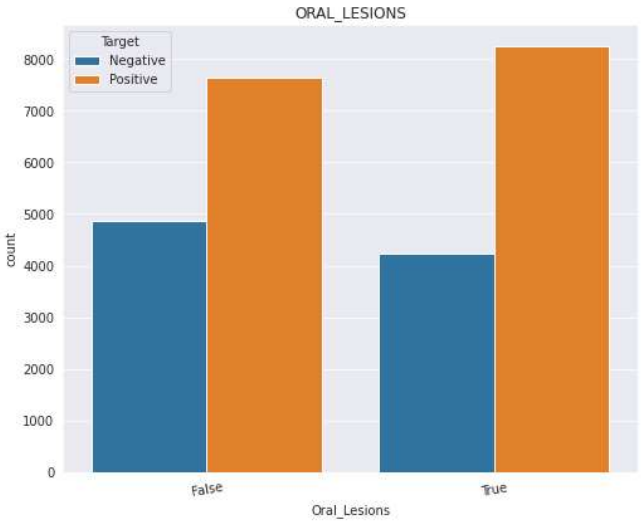
```
# Plotting side by side graphs for the bivariate analysis

features = col[:-1]
plt.figure(figsize = (18, 38))
for idx,val in enumerate(features):
    plt.subplot(5, 2, idx + 1)
    sns.countplot(x = val, hue = "Target", data = mp )
    plt.xticks(rotation = 10)
    plt.title(val.upper())
```

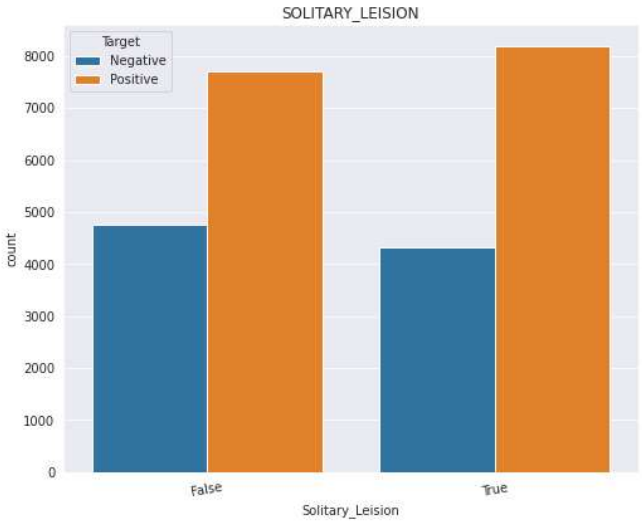

SYSTEMIC_ILLNESS
Target
Negative
Positive
count
Fever
Muscle Aches and Pain
No_Systemic_Illness
Swollen Lymph Nodes
Systemic_Illness

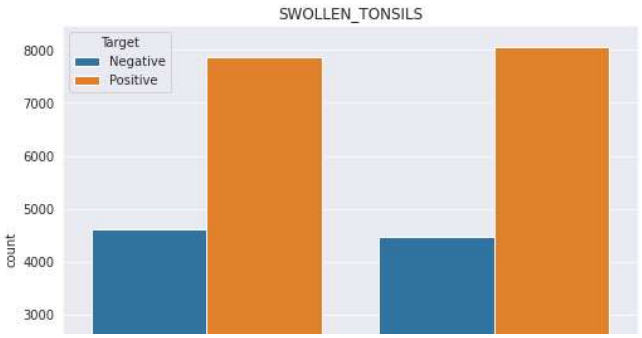

RECTAL_PAIN
Target
Negative
Positive
count
False
True
Rectal_Pain

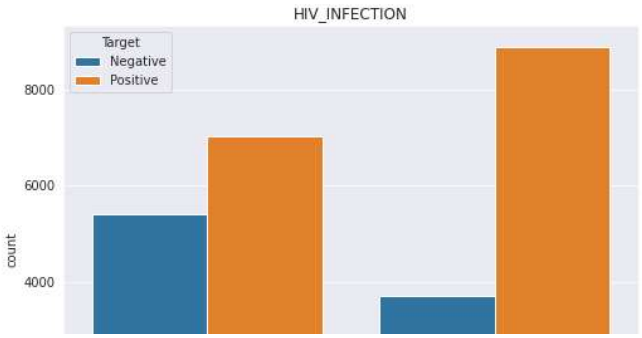

SORE_THROAT
Target
Negative
Positive
count
False
True
Sore_Throat

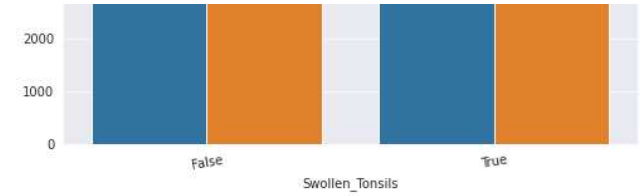

PENILE_OEDEMA
Target
Negative
Positive
count
False
True
Penile_Oedema

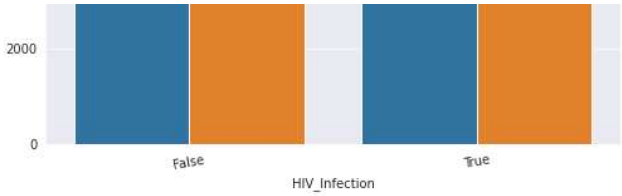

ORAL_LESIONS
Target
Negative
Positive
count
False
True
Oral_Lesions

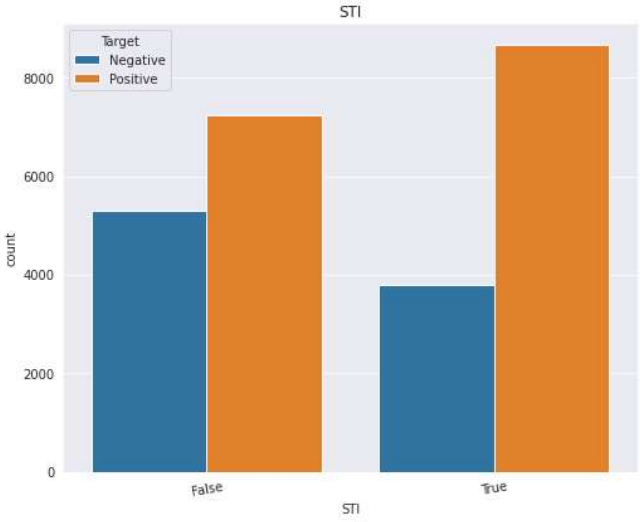

SOLITARY_LEISION
Target
Negative
Positive
count
False
True
Solitary_Leision


SWOLLEN_TONSILS
Target
Negative
Positive
count


HIV_INFECTION
Target
Negative
Positive
count





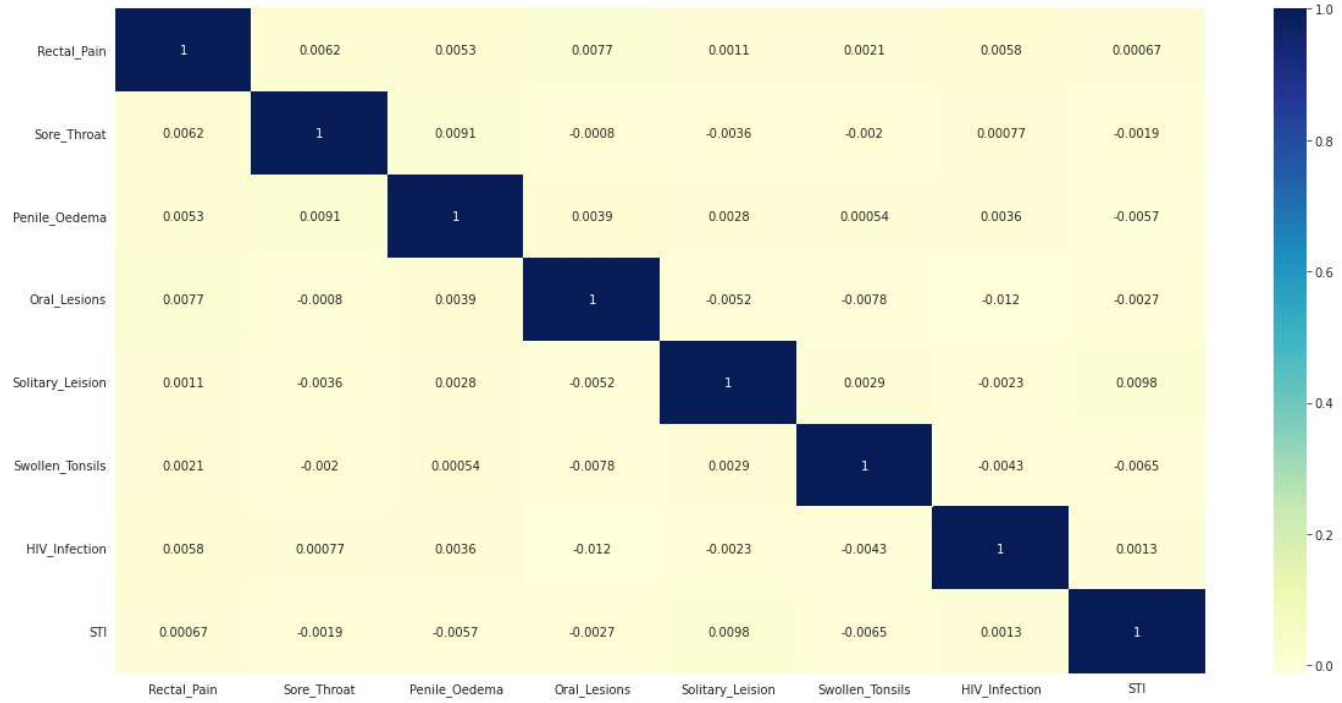


Bivariate Analysis Summary

- For the systemic illness symptoms, people with `fever` and `swollen lymph nodes` have a high chance of being MonkeyPox positive.
- People with the symptoms of `HIV Infection`, `Rectal Pain` and `Sexually Transmitted Infection` also have a high chance of being MonkeyPox positive.
- They all

INVESTIGATING CORRELATION

```
plt.figure(figsize = (20, 10))
var = mp.corr()
sns.heatmap(var, annot = True, cmap = "YlGnBu");
```



No high correlation was observed in the dataset.

3. DATA PREPARATION

Now that we have finished with EDa. We should prepare the data `mp` for modeling by one hot encoding to get binary column.

```
col
```

```
['Systemic_Illness',
 'Rectal_Pain',
 'Sore_Throat',
 'Penile_Oedema',
 'Oral_Lesions',
 'Solitary_Leision',
 'Swollen_Tonsils',
 'HIV_Infection',
 'STI',
 'Target']
```

```
# type casting Systemic illness by using get dummies
df = pd.get_dummies(data= mp, columns= ['Systemic_Illness'],drop_first= False)
```

```
# dropping every other column to isolate the systemic illness ...will concat later.
df_Systemic = df.drop(columns= col[1:],axis = 1)
# df_Systemic = df_Systemic.drop(columns= ['Systemic Illness_No Systemic Illness'],axis = 1)
df_Systemic
```

	Systemic_Illness_Fever	Systemic_Illness_Muscle Aches and Pain	Systemic_Illness_No_Systemic_I
0	0	0	
1	1	0	
2	1	0	
3	0	0	
4	0	0	
...	...	...	
24995	0	0	
24996	1	0	
24997	0	0	
24998	0	0	
24999	0	0	

```
# drop_first is set to true to reduce on multicoliniearity
df_d = pd.get_dummies(data = mp, columns= col[1:], drop_first= True)
df_d
```

	Systemic_Illness	Rectal_Pain_True	Sore_Throat_True	Penile_Oedema_True	Oral_
0	No_Systemic_Illness	0	1	1	
1	Fever	1	0	1	
4	Swollen Lymph	1	1	1	

```
# Dropping Systemic illness as its already dummied out

df_d.drop(axis = 1, columns= ['Systemic_Illness'] ,inplace = True)
```

```
# Column names will have to be changed but that can be done in one go
# first we finish up on converting the column data types t a usable state.
df_d.head()
```

	Rectal_Pain_True	Sore_Throat_True	Penile_Oedema_True	Oral_Lesions_True	Solitary_
0	0	1	1	1	
1	1	0	1	1	
2	0	1	1	0	
3	1	0	0	0	
4	1	1	1	0	

```
df_clean = pd.concat([df_Systemic,df_d], axis = 1,join= 'inner')
df_clean
```

	Systemic_Illness_Fever	Systemic_Illness_Muscle Aches and Pain	Systemic_Illness_No_Systemic_I
0	0	0	
1	1	0	

```
# Rechecking the multicolinearity to ensure that data preparation has not introduced any
plt.figure(figsize = (20, 10))
var = df_clean.corr()
sns.heatmap(var, annot = True, cmap = "YlGnBu");
```

```
list(df_clean.columns)
```

```
['Systemic_Illness_Fever',
 'Systemic_Illness_Muscle Aches and Pain',
 'Systemic_Illness_No_Systemic_Illness',
 'Systemic_Illness_Swollen Lymph Nodes',
 'Rectal_Pain_True',
 'Sore_Throat_True',
 'Penile_Oedema_True',
 'Oral_Lesions_True',
 'Solitary_Leision_True',
 'Swollen_Tonsils_True',
 'HIV_Infection_True',
 'STI_True',
 'Target_Positive']
```

```
df_clean.rename(columns={'Systemic_Illness_Fever':'SI_Fever',
                         'Systemic_Illness_Muscle Aches and Pain':'SI_Muscle_Aches&Pain',
                         'Systemic_Illness_Swollen Lymph Nodes':'SI_Swollen_Lymph_Nodes',
                         'Rectal_Pain_True':'Rectal_Pain',
                         'Sore_Throat_True':'Sore_Throat',
                         'Penile_Oedema_True':'Penile_Oedema',
                         'Oral_Lesions_True':'Oral_Lesions',
                         'Solitary_Lesion_True':'Solitary_Leision',
                         'Swollen_Tonsils_True':'Swollen_Tonsils',
                         'HIV_Infection_True':'HIV_Infection',
                         'STI_True':'STI',
                         'Target_Positive':'Target'},inplace=True)
```

```
df_clean.head()
```

	SI_Fever	SI_Muscle_Aches&Pain	Systemic_Illness_No_Systemic_Illness	SI_Swollen_Lyr
0	0	0	1	
1	1	0	0	
2	1	0	0	
3	0	0	1	
4	0	0	0	

```
# splitting the data into X [predictors] and y [target]
X = df_clean.drop(columns= ['Target'],axis = 1)
y = df_clean['Target']
```

```
# Random state for reapetability, test size of 30% as it is the optimum
# Stratify is used to ensure the test and train data have the same ratio

X_train, X_test, y_train, y_test = train_test_split(X,y,random_state=0,test_size= 0.3,stratif
```

4. MODELLING

```
#checking class balance in the training target variable
print(y_train.value_counts())
print('\n')

#checking class balance in the training target variable
print(y_test.value_counts())
```

```
1    11136
0     6364
Name: Target, dtype: int64


1    4773
0    2727
Name: Target, dtype: int64
```

An imbalance between positive and negative is observed

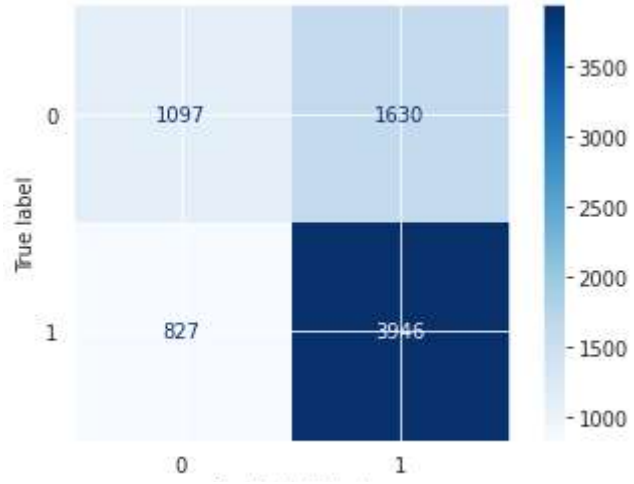
Base Model DecisionTreeClassifier

```
#train and get the score of the base model without handling the imbalance in the class and se
base_tree =  DecisionTreeClassifier()
model_trainer(base_tree, X_train, y_train,X_test,y_test)
```

```
{'precision': 0.7076757532281205,
 'recall_score': 0.8267337104546407,
 'accuracy_score': 0.6724,
 'f1_score': 0.7625857570779785}
```

A recall of 82 % and precision of 71% is a good start now lets tune it to look for improvements.

```
#visualize the confusion matrix
cnf_matrix  = plot_confusion_matrix(base_tree, X_test, y_test, cmap=plt.cm.Blues)
```




```
#balance the training classes and see the effect on the model using SMOTE
X_train_smote, y_train_smote = SMOTE().fit_resample(X_train, y_train)

print(y_train_smote.value_counts())
```

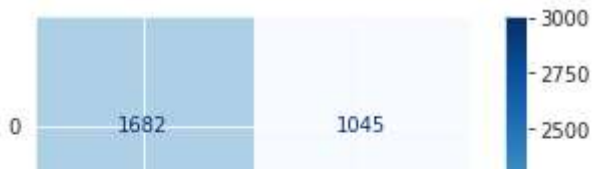
```
0    11136
1    11136
Name: Target, dtype: int64
```

```
#retrain the model with the model with the balanced classes
base_tree_smote = DecisionTreeClassifier()

Basemodel_balanced = model_trainer(base_tree_smote, X_train_smote, y_train_smote,X_test,y_tes

Basemodel_balanced
```

```
{'precision': 0.7417840375586855,
 'recall_score': 0.6289545359312801,
 'accuracy_score': 0.6245333333333334,
 'f1_score': 0.6807256235827666}
```

Precision has increased to 74% which is good, but the recal has reduced to 63%.

```
#visualize the confusion matrix
cnf_matrix  = plot_confusion_matrix(base_tree_smote, X_test, y_test, cmap=plt.cm.Blues)
```



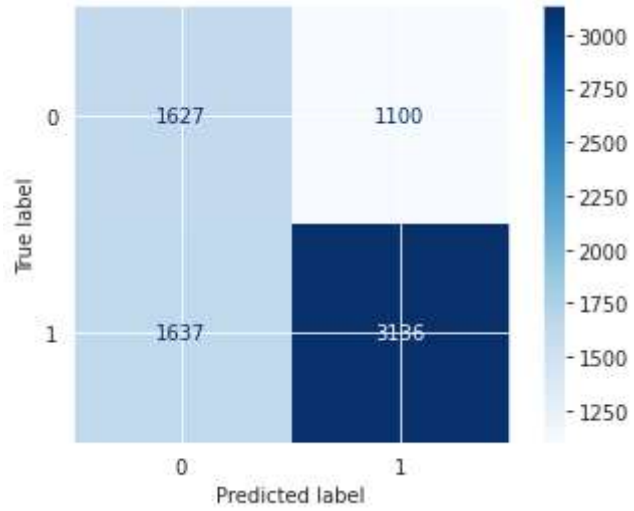

```
#balanced class best perameters
param_grid = {
    'criterion': ['gini', 'entropy'],
    'max_depth': [5, 10, 15, 20],
    'min_samples_split': [1, 5, 10, 20],
    'min_samples_leaf': [1, 2, 3, 4, 5, 6]
  }
grid_search(DecisionTreeClassifier(),param_grid, X_train_smote, y_train_smote)
```

```
{'criterion': 'entropy',
 'max_depth': 10,
 'min_samples_leaf': 1,
 'min_samples_split': 20}
```

```
#  Using the best parameters.
dtree_par =  DecisionTreeClassifier(criterion= 'gini', max_depth = 15, min_samples_split= 5,m
DecisionTree = model_trainer(dtree_par, X_train_smote,y_train_smote, X_test,y_test)
DecisionTree
```

```
{'precision': 0.7403210576015109,
 'recall_score': 0.6570291221454012,
 'accuracy_score': 0.6350666666666667,
 'f1_score': 0.6961926961926962}
```

```
cnf_matrix  = plot_confusion_matrix(dtree_par, X_test, y_test, cmap=plt.cm.Blues)
```



The model recall score increased to 64% meaning more positive patients were identified but there are still many wrongly classified patients

Whereas the precision score maintained at 74% , dropped by 0.003 when decimal places are

LogisticRegression and KNeighborsClassifier

```
#evaluating the two more models and see if they perform better then the DecisionTreeClassifie
# these two are LogisticRegression() and KNeighborsClassifier()

logreg = LogisticRegression()
knn = KNeighborsClassifier()

models = [logreg,knn]
scores=[]
recall=[]
scores_2 = []
precision_=[]

for i in models:
    estimator=Pipeline([
        ('model',i)])
    Prec_ =cross_val_score(estimator,X_train_smote,y_train_smote,cv=3,scoring='precision')
    recall_scre=cross_val_score(estimator,X_train_smote,y_train_smote,cv=3,scoring='recall')
    scores.append(recall_scre)
    scores_2.append(Prec_)
    recall.append(recall_scre.mean())
    precision_.append(Prec_.mean())


pd.DataFrame({'model':['Logistic Regression','KNN'],'Precision score':precision_,'Recall Scor
```

model	Precision score	Recall Score
KNN	0.579220	0.817619
Logistic Regression	0.628075	0.589260

recall score shoots up to 82% but Precision score drops to 58%

KNeighbors

```
#plot the KNN and virtualize the confussion matrix

kn_base =  KNeighborsClassifier()
model_trainer(kn_base, X_train_smote, y_train_smote,X_test,y_test)
```

```
{'precision': 0.7001890359168242,
 'recall_score': 0.7760318457992876,
 'accuracy_score': 0.646,
 'f1_score': 0.7361621782768559}
```

precision score at 70% while recall score at 77%

```
#tune the the KNN
knn_gridSearch = KNeighborsClassifier()

parameters = {'n_neighbors':[10,15,22,30],
              'leaf_size':[3,4,5,8,10],
              'algorithm':['auto', 'kd_tree'],
              'n_jobs':[-1]}
grid_search(knn_gridSearch, parameters, X_train_smote, y_train_smote)
```

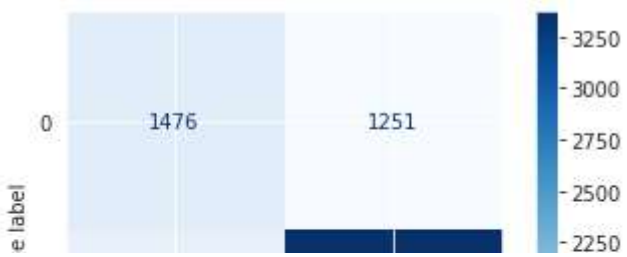
```
{'algorithm': 'auto', 'leaf_size': 4, 'n_jobs': -1, 'n_neighbors': 22}
```

```
# Using the best parameters
knn_improved = KNeighborsClassifier(algorithm = 'auto', leaf_size = 3, n_jobs = -1, n_neighbc
KNeighbors = model_trainer(knn_improved, X_train_smote,y_train_smote, X_test,y_test)
KNeighbors
```

```
{'precision': 0.7293964957819598,
 'recall_score': 0.7064739157762414,
 'accuracy_score': 0.6464,
 'f1_score': 0.7177522349936143}
```

Precision raises to 73% while recall drops to 71%

```
cnf_matrix  = plot_confusion_matrix(knn_improved, X_test, y_test, cmap=plt.cm.Blues)
```



The KNN Model has improved our recall significantly and this means our model will be able to identify more people with the virus

Logistic Regression

```
#final model the logisticRegressor
base_logrig = LogisticRegression()
model_trainer(base_logrig, X_train_smote, y_train_smote,X_test,y_test)
```

```
{'precision': 0.7422434367541766,
 'recall_score': 0.5864236329352609,
 'accuracy_score': 0.6072,
 'f1_score': 0.6551966292134832}
```

precision score is 74 % while recall is at an unacceptable low of 59%

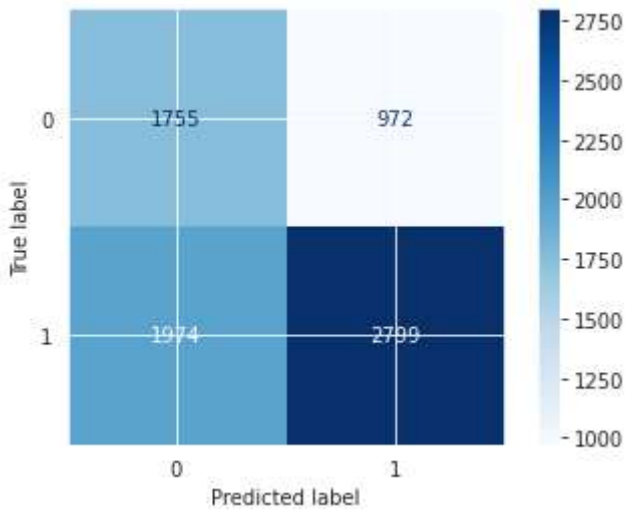
```
#performing hyper perameter tuning on the model
logR_improved = LogisticRegression()

parameters = { 'C': np.logspace(-4, 4, 50),
                'penalty' : ['l1', 'l2'],}
grid_search(logR_improved, parameters, X_train_smote, y_train_smote)
```

```
{'C': 0.0004498432668969444, 'penalty': 'l2'}
```

```
# Using the best parameters
logR = LogisticRegression(C = 0.0004498432668969444, penalty ='l2')
LogisticReg = model_trainer(logR, X_train_smote, y_train_smote,X_test,y_test)
LogisticReg
```

```
{'precision': 0.7422434367541766,
 'recall_score': 0.5864236329352609,
 'accuracy_score': 0.6072,
 'f1_score': 0.6551966292134832}
```

```
cnf_matrix  = plot_confusion_matrix(logR, X_test, y_test, cmap=plt.cm.Blues)
```



Precision score and recall score have not changed

Random Forest Classifier

```
pipe = Pipeline([
                    ('Rfc',RandomForestClassifier(random_state=0,))

                ])
min_range = list(np.arange(0.08,0.14,0.02))
grid_params = [{
               'Rfc__n_estimators':[50,100],
               'Rfc__min_samples_leaf':min_range,
               'Rfc__max_features':['sqrt','log2'],
               'Rfc__max_leaf_nodes':[12,13],
               'Rfc__bootstrap':[True,False]
               }]

gs = GridSearchCV(estimator= pipe, param_grid= grid_params, cv= 10,scoring='precision')

gs.fit(X_train,y_train)

# Best accuracy
print('Best precision: %.3f' % gs.best_score_)
print('_________')
# Best params
print('\nBest params:\n', gs.best_params_)
print('_________')

y_pred = gs.predict(X_test)

print('_________')

print(precision_score(y_true= y_test,y_pred= y_pred))
```

```
Best precision: 0.669
_________

Best params:
 {'Rfc__bootstrap': False, 'Rfc__max_features': 'sqrt', 'Rfc__max_leaf_nodes': 12, 'Rfc
_________

_________
0.6720953904318744
```

```
# Using the best parameters
RandomForest = RandomForestClassifier(bootstrap = False, max_features = 'sqrt',max_leaf_nodes
                                      min_samples_leaf= 0.08,n_estimators= 50)
RandomForestClass = model_trainer(RandomForest, X_train_smote, y_train_smote,X_test,y_test)
RandomForestClass
```

```
{'precision': 0.7468000930882011,
 'recall_score': 0.6723234862769747,
 'accuracy_score': 0.6464,
 'f1_score': 0.7076074972436605}
```

```
scores = [LogisticReg, Basemodel_balanced, DecisionTree,KNeighbors,RandomForestClass ]
column_name = ['LogisticReg','Basemodel', 'DecisionTree','KNeighbors','RandomForestClassifier
```

```
df = pd.DataFrame(columns = column_name)
df.LogisticReg =LogisticReg.values()
df.Basemodel = Basemodel_balanced.values()
df.DecisionTree = DecisionTree.values()
df.KNeighbors = KNeighbors.values()
df.RandomForestClassifier = RandomForestClass.values()
df.index = ['precision', 'recall_score','accuracy_score','f1_score']
df
```

	LogisticReg	Basemodel	DecisionTree	KNeighbors	RandomForestClassifie
precision	0.742243	0.741784	0.740321	0.729396	0.74680
recall_score	0.586424	0.628955	0.657029	0.706474	0.67232
accuracy_score	0.607200	0.624533	0.635067	0.646400	0.64640
f1_score	0.655197	0.680726	0.696193	0.717752	0.70760

The KNeighborsClassifier had the best sores and since this model will be used in detecting MonkeyPox viruses a high recall is needed then precision since this will prevent the number of false positives making more positive cases to be identified and treated in advance

```
#develop a final pipline that will be used to train the model on the whole dataset and make t
```

```
#Balance the whole dataset using smote
X_smote, y_smote = SMOTE().fit_resample(X, y)
y_smote.value_counts()
```

```
0    15909
1    15909
Name: Target, dtype: int64
```

```
pipeline = Pipeline([('KNN', KNeighborsClassifier(algorithm = 'auto', leaf_size = 4, n_jobs =
pipeline.fit(X_smote,y_smote)
```

```
Pipeline(steps=[('KNN',
                 KNeighborsClassifier(leaf_size=4, n_jobs=-1, n_neighbors=8))])
```

```
#model performance after training on the whole data
model_trainer(pipeline, X_smote, y_smote,X_test,y_test)
```

```
{'precision': 0.7313642756680732,
 'recall_score': 0.7626230882044835,
 'accuracy_score': 0.6706666666666666,
 'f1_score': 0.7466666666666666}
```

```
#save our model into a pickle
with open('model.pkl', 'wb') as f:
  joblib.dump(pipeline, f)
```

5. EVALUATION

```
df = pd.DataFrame(columns = column_name)
df.LogisticReg =LogisticReg.values()
df.Basemodel = Basemodel_balanced.values()
df.DecisionTree = DecisionTree.values()
df.KNeighbors = KNeighbors.values()

df.index = ['precision', 'recall_score','accuracy_score','f1_score']
df
```

	LogisticReg	Basemodel	DecisionTree	KNeighbors	RandomForestClassifie
precision	0.742243	0.741784	0.740321	0.729396	Na
recall_score	0.586424	0.628955	0.657029	0.706474	Na
accuracy_score	0.607200	0.624533	0.635067	0.646400	Na
f1_score	0.655197	0.680726	0.696193	0.717752	Na

The differences in accuracy are low thus other evaluation metrics are required. In this case, we shall use recall to evaluate the various models and decide on the best one. Based on the recall scores, The KNeighbors model displays both high precision meaning it produces correct positive predictions about 71.74% percent of the time. It also displays a comparatively high recall score which means it does not produce a lot of false negatives.

```
log_prediction =base_logrig.predict(X_test)
knn_prediction =knn_improved.predict(X_test)
```

```
#evaluating the scores for prediction
from sklearn.metrics import classification_report

print ("CLassification report - Logistic Regression\n",
       classification_report(y_test, log_prediction, target_names = [ "FRAUD","VALID"]))
print ("CLassification report - KNN Classifier\n",
       classification_report(y_test, knn_prediction, target_names = ["FRAUD","VALID"]))
```

```
     CLassification report - Logistic Regression
                   precision    recall  f1-score   support

            FRAUD       0.47      0.64      0.54      2727
            VALID       0.74      0.59      0.66      4773

         accuracy                           0.61      7500
        macro avg       0.61      0.61      0.60      7500
     weighted avg       0.64      0.61      0.61      7500

     CLassification report - KNN Classifier
                   precision    recall  f1-score   support

            FRAUD       0.51      0.54      0.53      2727
            VALID       0.73      0.71      0.72      4773

         accuracy                           0.65      7500
        macro avg       0.62      0.62      0.62      7500
     weighted avg       0.65      0.65      0.65      7500
```

```
#previously defined scores for the training for comparison with the previous cell
KNeighbors
```

```
     {'precision': 0.7293964957819598,
      'recall_score': 0.7064739157762414,
      'accuracy_score': 0.6464,
      'f1_score': 0.7177522349936143}
```

Using the classification report library we can see that our model performs equally as well in the prediction. This means that it was well fitted.The consistency in precision and recall in the KNN