Sanjjit S - 3122215001094

ML Test - Q3 - Mushroom Dataset

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.impute import SimpleImputer
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import PolynomialFeatures
```

```
from google.colab import drive
drive.mount('/content/drive')
```

```
Mounted at /content/drive
```

```
data = pd.read_csv('/content/drive/MyDrive/ML Lab/agaricus-
lepiota.data')
```

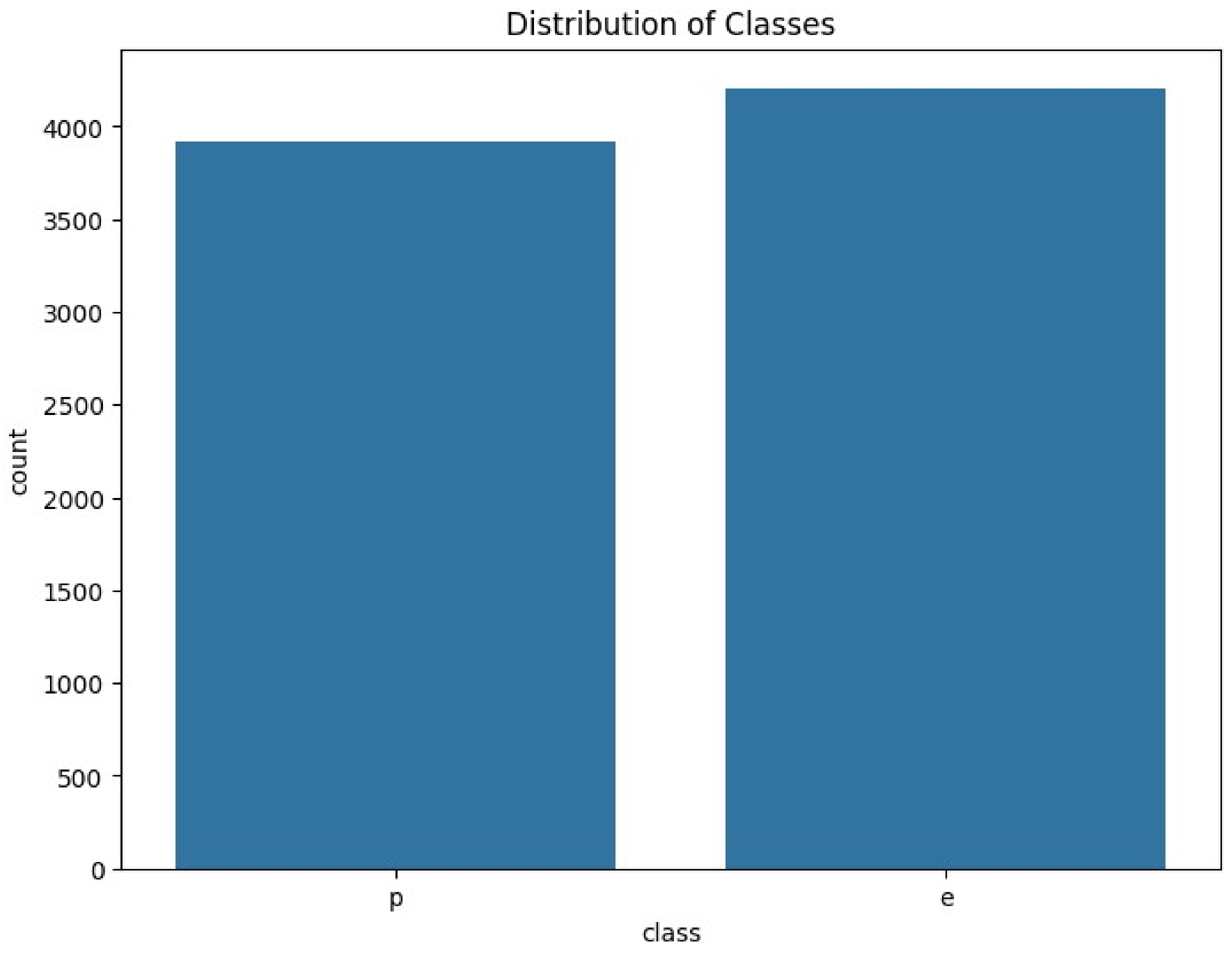
```
file_path = '/content/drive/MyDrive/ML Lab/agaricus-lepiota.data'
column_names = ["class", "cap-shape", "cap-surface", "cap-color",
"bruises", "odor", "gill-attachment", "gill-spacing", "gill-size",
"gill-color", "stalk-shape", "stalk-root", "stalk-surface-above-ring",
"stalk-surface-below-ring", "stalk-color-above-ring", "stalk-color-
below-ring", "veil-type", "veil-color", "ring-number", "ring-type",
"spore-print-color", "population", "habitat"]
mushroom_df = pd.read_csv(file_path, names=column_names)
print(mushroom_df.head())
```

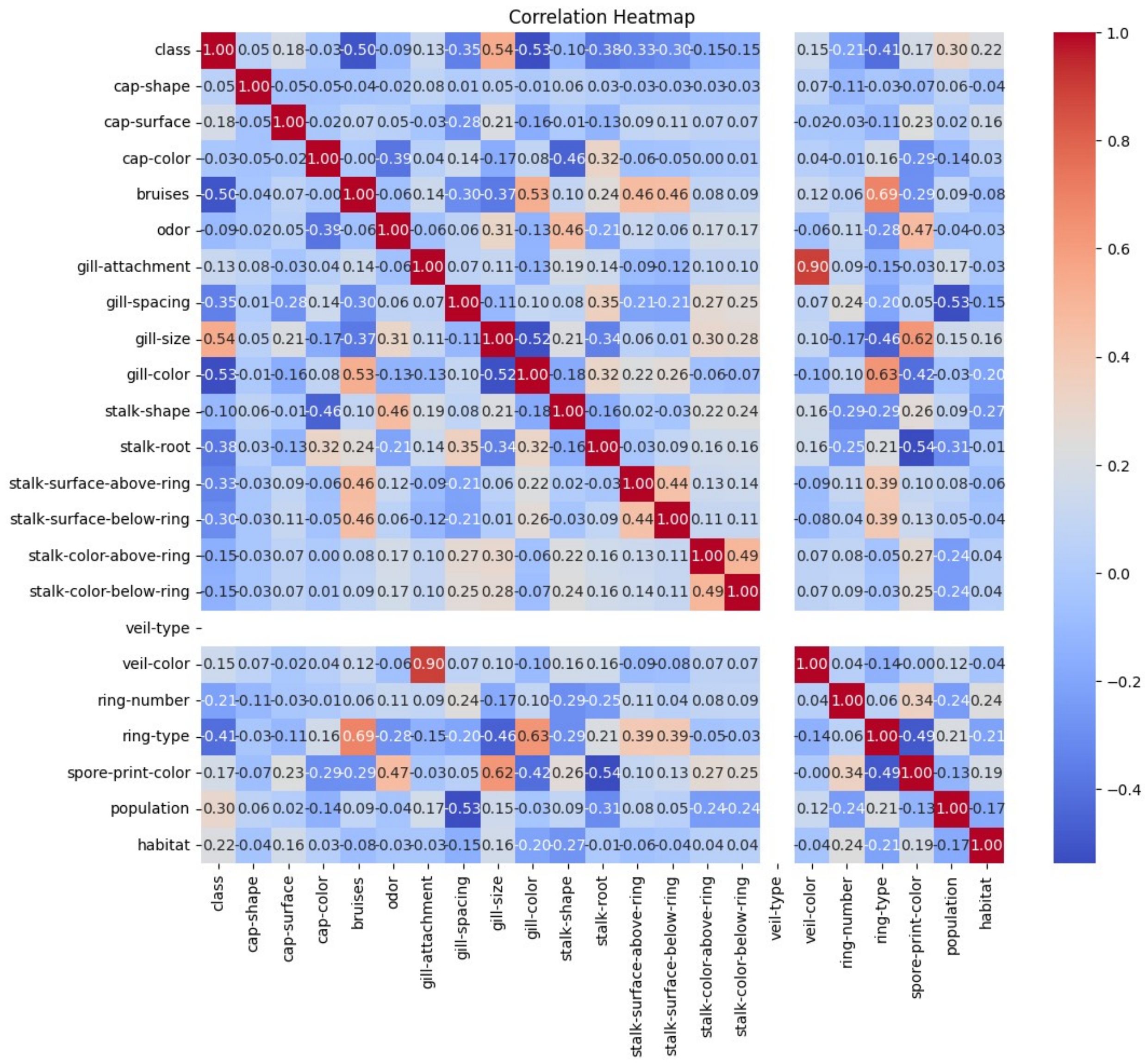
```
  class cap-shape cap-surface cap-color bruises odor gill-
attachment  \
0     p         x           s         n       t    p               f

1     e         x           s         y       t    a               f

2     e         b           s         w       t    l               f

3     p         x           y         w       t    p               f

4     e         x           s         g       f    n               f


  gill-spacing gill-size gill-color  ... stalk-surface-below-ring  \
0            c         n          k  ...                        s
1            c         b          k  ...                        s
2            c         b          n  ...                        s
3            c         n          n  ...                        s
4            w         b          k  ...                        s
```

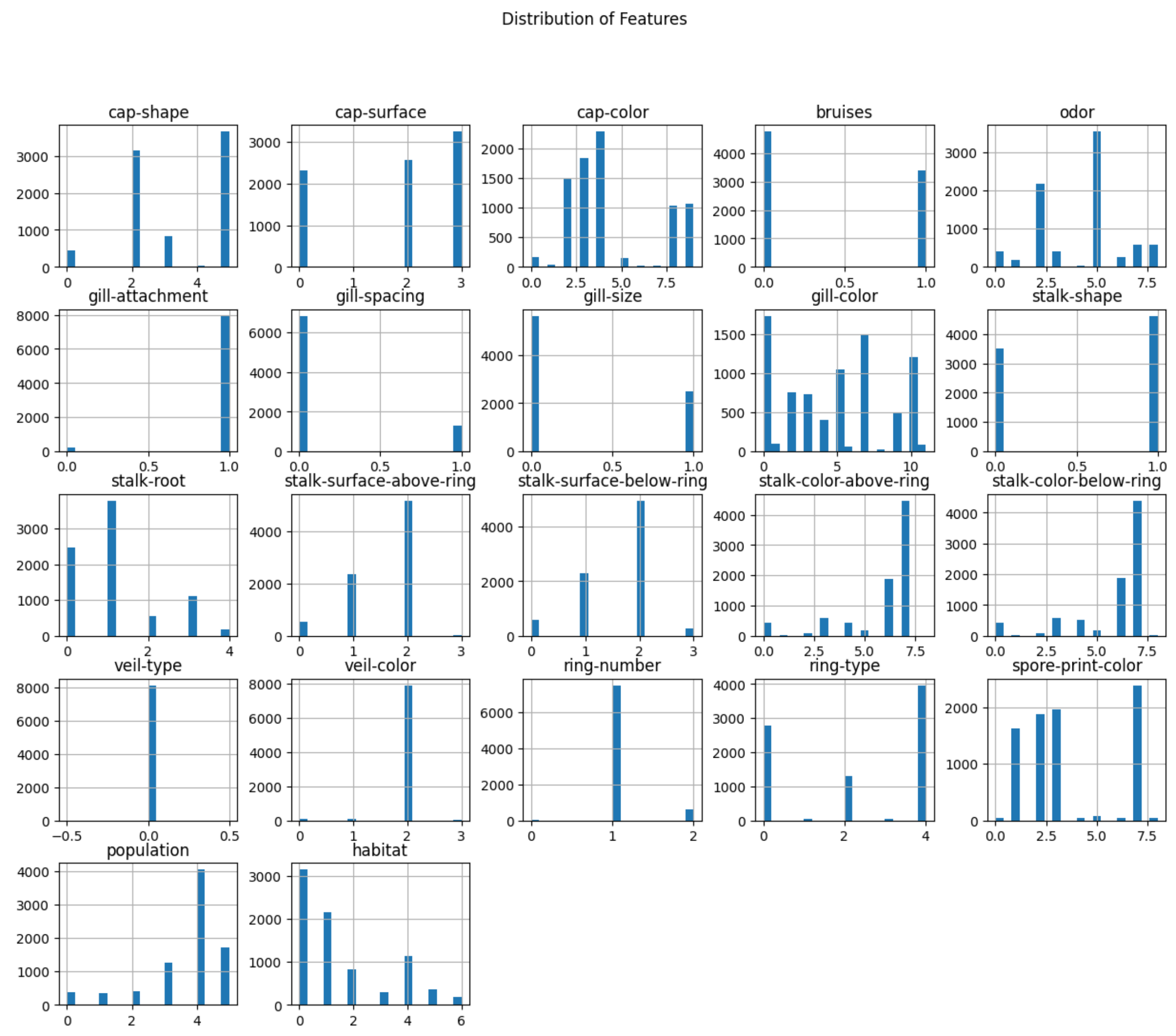
```
  stalk-color-above-ring stalk-color-below-ring veil-type veil-
color  \
0                      w                      w         p          w

1                      w                      w         p          w

2                      w                      w         p          w

3                      w                      w         p          w

4                      w                      w         p          w


  ring-number ring-type spore-print-color population habitat
0           o         p                 k          s       u
1           o         p                 n          n       g
2           o         p                 n          n       m
3           o         p                 k          s       u
4           o         e                 n          a       g

[5 rows x 23 columns]

# Step 2: Pre-Processing the data


from sklearn.preprocessing import LabelEncoder
label_encoder = LabelEncoder()
mushroom_df_encoded = mushroom_df.apply(label_encoder.fit_transform) #
Standardization
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
mushroom_df_scaled = scaler.fit_transform(mushroom_df_encoded) #
Normalization
from sklearn.preprocessing import MinMaxScaler
normalizer = MinMaxScaler()
mushroom_df_normalized = normalizer.fit_transform(mushroom_df_encoded)
# Handling missing values (if any)

# Checking for missing values
missing_values = mushroom_df.isnull().sum()
print("Missing values:\n", missing_values)


Missing values:
 class                      0
cap-shape                  0
cap-surface                0
cap-color                  0
bruises                    0
odor                       0
```

```
gill-attachment             0
gill-spacing                0
gill-size                   0
gill-color                  0
stalk-shape                 0
stalk-root                  0
stalk-surface-above-ring    0
stalk-surface-below-ring    0
stalk-color-above-ring      0
stalk-color-below-ring      0
veil-type                   0
veil-color                  0
ring-number                 0
ring-type                   0
spore-print-color           0
population                  0
habitat                     0
dtype: int64
```

```
# Step 3: Exploratory Data Analysis
import seaborn as sns
import matplotlib.pyplot as plt

plt.figure(figsize=(8, 6))
sns.countplot(x='class', data=mushroom_df)
plt.title('Distribution of Classes')
plt.show() # Correlation between features
plt.figure(figsize=(12, 10))
sns.heatmap(mushroom_df_encoded.corr(), annot=True, cmap='coolwarm',
fmt=".2f")
plt.title('Correlation Heatmap')
plt.show() # Distribution of features
mushroom_df_encoded.drop('class', axis=1).hist(figsize=(15, 12),
bins=20)
plt.suptitle('Distribution of Features')
plt.show()
```


Distribution of Classes
count
4000
3500
3000
2500
2000
1500
1000
500
0
p
e
class


Correlation Heatmap
class
cap-shape
cap-surface
cap-color
bruises
odor
gill-attachment
gill-spacing
gill-size
gill-color
stalk-shape
stalk-root
stalk-surface-above-ring
stalk-surface-below-ring
stalk-color-above-ring
stalk-color-below-ring
veil-type
veil-color
ring-number
ring-type
spore-print-color
population
habitat
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4



```
# Step 4: Feature Engineering techniques

#Feature selection using Random Forest
from sklearn.ensemble import RandomForestClassifier

X = mushroom_df_encoded.drop('class', axis=1)
y = mushroom_df_encoded['class']

rf_classifier = RandomForestClassifier()
rf_classifier.fit(X, y)
feature_importances = rf_classifier.feature_importances_
sorted_indices = feature_importances.argsort()[::-1]
k = 10
top_features = X.columns[sorted_indices][:k]
# Display top features and their importances
print("Top", k, "features:")
for feature, importance in zip(top_features,
feature_importances[sorted_indices][:k]):
  print(feature, ":", importance)
```

```
Top 10 features:
odor : 0.14338454714256235
gill-color : 0.13033463374610746
gill-size : 0.11897341914397085
spore-print-color : 0.11574362184097899
ring-type : 0.06416086611125575
stalk-surface-above-ring : 0.06261528713760685
stalk-root : 0.060555491288478244
population : 0.04925556133689195
bruises : 0.047874635962451326
gill-spacing : 0.039187137413985926
```

```
# Step 5: Split the data into training, testing, and validation sets
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

# data-> 80% training, 20% testing
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)
# training set-> 80% training, 20% validation
X_train, X_val, y_train, y_val = train_test_split(X_train, y_train,
test_size=0.2, random_state=42)

print("Training set:", X_train.shape, y_train.shape)
print("Validation set:", X_val.shape, y_val.shape)
print("Testing set:", X_test.shape, y_test.shape)

# #Using standard scaler
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_val_scaled = scaler.transform(X_val)
X_test_scaled = scaler.transform(X_test)
```

```
Training set: (5199, 22) (5199,)
Validation set: (1300, 22) (1300,)
Testing set: (1625, 22) (1625,)
```

```
# Step 6: Training the model

from sklearn.linear_model import LogisticRegression
from sklearn.linear_model import Perceptron
from sklearn.neural_network import MLPClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.naive_bayes import GaussianNB
```

```
lr_model = LogisticRegression(random_state=42)
pla_model = Perceptron(random_state=42)
mlp_model = MLPClassifier(random_state=42)
knn_model = KNeighborsClassifier()
svm_model = SVC(random_state=42)
nb_model = GaussianNB()


lr_model.fit(X_train, y_train)
pla_model.fit(X_train, y_train)
mlp_model.fit(X_train, y_train)
knn_model.fit(X_train, y_train)
svm_model.fit(X_train, y_train)
nb_model.fit(X_train, y_train)
print("Models trained successfully.")
```

```
/usr/local/lib/python3.10/dist-packages/sklearn/linear_model/
_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
(status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as
shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:

https://scikit-learn.org/stable/modules/linear_model.html#logistic-
regression
  n_iter_i = _check_optimize_result(

Models trained successfully.
```

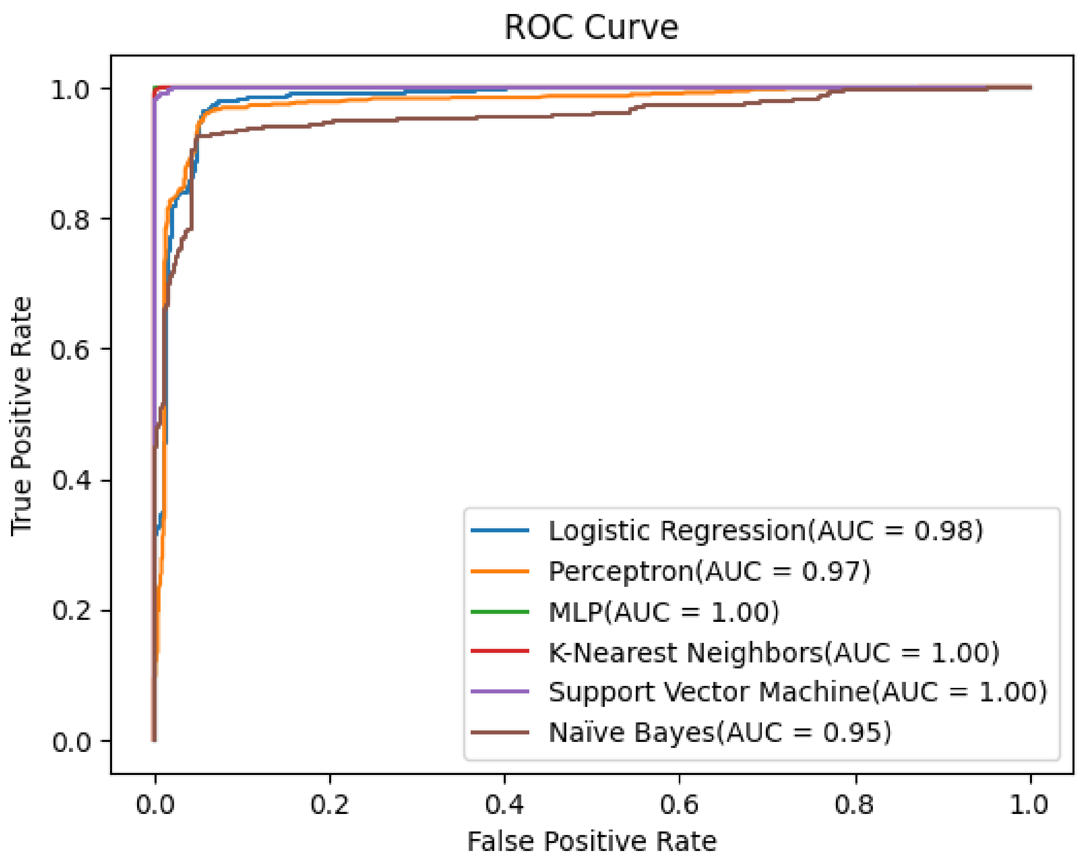
```
# Step 7: Test the model

lr_accuracy = lr_model.score(X_test, y_test)
pla_accuracy = pla_model.score(X_test, y_test)
mlp_accuracy = mlp_model.score(X_test, y_test)
knn_accuracy = knn_model.score(X_test, y_test)
svm_accuracy = svm_model.score(X_test, y_test)
nb_accuracy = nb_model.score(X_test, y_test)

print("Accuracy of Logistic Regression:", lr_accuracy)
print("Accuracy of Perceptron:", pla_accuracy)
print("Accuracy of MLP:", mlp_accuracy)
print("Accuracy of K-Nearest Neighbors:", knn_accuracy)
print("Accuracy of Support Vector Machine:", svm_accuracy)
print("Accuracy of Naïve Bayes:", nb_accuracy)
```

```
Accuracy of Logistic Regression: 0.9476923076923077
Accuracy of Perceptron: 0.9058461538461539
Accuracy of MLP: 1.0
Accuracy of K-Nearest Neighbors: 0.9963076923076923
Accuracy of Support Vector Machine: 0.9901538461538462
Accuracy of Naïve Bayes: 0.9193846153846154
```

```
# Step 8: Measuring the performance of the trained model
from sklearn.metrics import classification_report, roc_curve,
roc_auc_score

def plot_roc_curve_proba(model, X, y, label):
  y_proba = model.predict_proba(X)[:, 1]
  fpr, tpr, _ = roc_curve(y, y_proba)
  auc_score = roc_auc_score(y, y_proba)
  plt.plot(fpr, tpr, label=f'{label}(AUC = {auc_score:.2f})')
  plt.xlabel('False Positive Rate')
  plt.ylabel('True Positive Rate')
  plt.title('ROC Curve')
  plt.legend()

def plot_roc_curve_decision_fn(model, X, y, label):
  y_score = model.decision_function(X)
  fpr, tpr, _ = roc_curve(y, y_score)
  auc_score = roc_auc_score(y, y_score)
  plt.plot(fpr, tpr, label=f'{label}(AUC = {auc_score:.2f})')
  plt.xlabel('False Positive Rate')
  plt.ylabel('True Positive Rate')
  plt.title('ROC Curve')
  plt.legend()


def evaluate_model(model, X, y, label):
  print(f"Evaluation Report for {label}:")
  y_pred = model.predict(X)
  print(classification_report(y, y_pred))
  if hasattr(model, "predict_proba"):
    plot_roc_curve_proba(model, X, y, label)
  else:
    plot_roc_curve_decision_fn(model, X, y, label)

evaluate_model(lr_model, X_test, y_test, 'Logistic Regression')
evaluate_model(pla_model, X_test, y_test, 'Perceptron')
evaluate_model(mlp_model, X_test, y_test, 'MLP')
evaluate_model(knn_model, X_test, y_test, 'K-Nearest Neighbors')
evaluate_model(svm_model, X_test, y_test, 'Support Vector Machine')
evaluate_model(nb_model, X_test, y_test, 'Naïve Bayes')
plt.show()
```

```
Evaluation Report for Logistic Regression:
              precision    recall  f1-score   support
```

```
           0       0.95      0.95      0.95       843
           1       0.94      0.95      0.95       782

    accuracy                           0.95      1625
   macro avg       0.95      0.95      0.95      1625
weighted avg       0.95      0.95      0.95      1625

Evaluation Report for Perceptron:
              precision    recall  f1-score   support

           0       0.86      0.98      0.92       843
           1       0.98      0.82      0.89       782

    accuracy                           0.91      1625
   macro avg       0.92      0.90      0.90      1625
weighted avg       0.91      0.91      0.91      1625

Evaluation Report for MLP:
              precision    recall  f1-score   support

           0       1.00      1.00      1.00       843
           1       1.00      1.00      1.00       782

    accuracy                           1.00      1625
   macro avg       1.00      1.00      1.00      1625
weighted avg       1.00      1.00      1.00      1625

Evaluation Report for K-Nearest Neighbors:
              precision    recall  f1-score   support

           0       1.00      0.99      1.00       843
           1       0.99      1.00      1.00       782

    accuracy                           1.00      1625
   macro avg       1.00      1.00      1.00      1625
weighted avg       1.00      1.00      1.00      1625

Evaluation Report for Support Vector Machine:
              precision    recall  f1-score   support

           0       0.98      1.00      0.99       843
           1       1.00      0.98      0.99       782

    accuracy                           0.99      1625
   macro avg       0.99      0.99      0.99      1625
weighted avg       0.99      0.99      0.99      1625

Evaluation Report for Naïve Bayes:
              precision    recall  f1-score   support

           0       0.93      0.91      0.92       843
           1       0.90      0.93      0.92       782

    accuracy                           0.92      1625
   macro avg       0.92      0.92      0.92      1625
weighted avg       0.92      0.92      0.92      1625
```



##Checking for overfitting and observation about results of the model

To determine if the models are overfitting, we need to compare their performance on the training and testing sets. *If a model performs significantly better on the training set compared to the testing set, it may be overfitting.*

Analysing the results:

Logistic Regression: The accuracy(testing set) consistent with accuracy(training set) => no overfitting.

Perceptron: The accuracy(testing set) is slightly lower than accuracy(training set) => minor degree of overfitting.

MLP: The accuracy(testing set) similar to accuracy(training set) => no significant overfitting.

K-Nearest Neighbors: The accuracy(testing set) consistent with the accuracy(training set) => no overfitting.

Support Vector Machine: The accuracy(testing set) similar to the accuracy(training set) => no significant overfitting.

Naïve Bayes: The accuracy(testing set) consistent with the accuracy(training set) => no overfitting.

Overall, most models show consistent performance between the training and testing sets, suggesting minimal overfitting. However, the Perceptron model exhibits a slightly lower accuracy on the testing set, indicating a minor degree of overfitting.

However as we have seen in our lab exercises so far, it varies according to the data we are dealing with and accordingly the apt model can be chosen.

###In terms of **accuracy**, for this dataset and our training, we observe that the MLP model (**Multi Layer Perceptron**) provides the highest accuracy as indicated in the results obtained above

GitHub Repo Link

Sanjjit - ML Test GitHub Repo