

ML_Assignment

November 8, 2024

ML_Assignment: Model For Classification of Drug Type

Done By : Gopika and Prateek Kumar

```
[ ]: import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.preprocessing import LabelEncoder

# Load the dataset
df = pd.read_csv('drug_type_classification.csv')

# Encode the target variable 'Drug' (if it's categorical)
label_encoder = LabelEncoder()
df['Drug'] = label_encoder.fit_transform(df['Drug'])

# Separate features and target variable
X = df.drop('Drug', axis=1)
y = df['Drug']

# Convert categorical features to numerical using one-hot encoding
X = pd.get_dummies(X, drop_first=True)

# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
                                                    random_state=42)

# Train a Random Forest Classifier
model = RandomForestClassifier(n_estimators=100, random_state=42)
model.fit(X_train, y_train)

# Evaluate the model
y_pred = model.predict(X_test)
print("Classification Report:")
print(classification_report(y_test, y_pred))

print("Confusion Matrix:")
```

```
print(confusion_matrix(y_test, y_pred))
```

```
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from sklearn.model_selection import train_test_split
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print("Confusion Matrix:")
print(confusion_matrix(y_test, y_pred))

# Calculate accuracy
accuracy = accuracy_score(y_test, y_pred)
print("Model Accuracy:", accuracy)
```

Classification Report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	15
1	1.00	1.00	1.00	6

2	1.00	1.00	1.00	3
3	1.00	1.00	1.00	5
4	1.00	1.00	1.00	11
accuracy			1.00	40
macro avg	1.00	1.00	1.00	40
weighted avg	1.00	1.00	1.00	40

Confusion Matrix:

```
[[15  0  0  0  0]
 [ 0  6  0  0  0]
 [ 0  0  3  0  0]
 [ 0  0  0  5  0]
 [ 0  0  0  0 11]]
```

Model Accuracy: 1.0

```
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from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.preprocessing import LabelEncoder

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model = RandomForestClassifier(n_estimators=100, random_state=42)
model.fit(X_train, y_train)

# Evaluate the model
y_pred = model.predict(X_test)
print("Classification Report:")
```

```

print(classification_report(y_test, y_pred))

print("Confusion Matrix:")
print(confusion_matrix(y_test, y_pred))

# Print feature names to identify exact column names
print("Feature names used during training:", X.columns)

# Define a function to make manual predictions with correct feature names
def manual_test(model, label_encoder):
    # Define input data with exact feature names
    input_data = {
        'Age': [43],                # Example age
        'Sex_M': [1],               # 1 for male, 0 for female (encoded as 1)
        'BP_LOW': [0],              # 1 if BP is Low, else 0
        'BP_NORMAL': [0],           # 1 if BP is Normal, else 0
        'Cholesterol_NORMAL': [0],  # 1 if Cholesterol is Normal, else 0
        'Na_to_K': [13.927]         # Example Sodium-to-Potassium ratio
    }

    # Convert to DataFrame to match input format
    input_df = pd.DataFrame(input_data)

    # Ensure the input has all required columns in the same order as training data
    input_df = input_df.reindex(columns=X.columns, fill_value=0)

    # Predict using the model
    prediction = model.predict(input_df)

    # Decode the prediction back to the original class name
    predicted_drug = label_encoder.inverse_transform(prediction)

    print("Predicted Drug Type:", predicted_drug[0])

# Run the function to test manually
manual_test(model, label_encoder)

```

Classification Report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	15
1	1.00	1.00	1.00	6
2	1.00	1.00	1.00	3
3	1.00	1.00	1.00	5
4	1.00	1.00	1.00	11

accuracy			1.00	40
macro avg	1.00	1.00	1.00	40
weighted avg	1.00	1.00	1.00	40

Confusion Matrix:

```
[[15  0  0  0  0]
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 [ 0  0  0  5  0]
 [ 0  0  0  0 11]]
```

Feature names used during training: Index(['Age', 'Na_to_K', 'Sex_M', 'BP_LOW', 'BP_NORMAL', 'Cholesterol_NORMAL'], dtype='object')

Predicted Drug Type: drugA

```
[18]: import matplotlib.pyplot as plt
import numpy as np
from sklearn.metrics import accuracy_score

# 1. Plot Training and Testing Accuracy at Different Numbers of Estimators
train_accuracies = []
test_accuracies = []
n_estimators_range = range(10, 210, 10)

for n in n_estimators_range:
    temp_model = RandomForestClassifier(n_estimators=n, random_state=42)
    temp_model.fit(X_train, y_train)
    train_accuracies.append(accuracy_score(y_train, temp_model.
    ↪predict(X_train)))
    test_accuracies.append(accuracy_score(y_test, temp_model.predict(X_test)))

plt.figure(figsize=(10, 6))
plt.plot(n_estimators_range, train_accuracies, label="Training Accuracy",
    ↪marker='o')
plt.plot(n_estimators_range, test_accuracies, label="Testing Accuracy",
    ↪marker='o')
plt.xlabel("Number of Estimators")
plt.ylabel("Accuracy")
plt.title("Training vs Testing Accuracy for Different Estimator Counts")
plt.legend()
plt.show()

# 2. Evaluation Metrics Plot (Precision, Recall, F1-score for each class)
from sklearn.metrics import precision_recall_fscore_support

# Get precision, recall, f1-score for each class
precision, recall, f1_score, _ = precision_recall_fscore_support(y_test, y_pred)
```

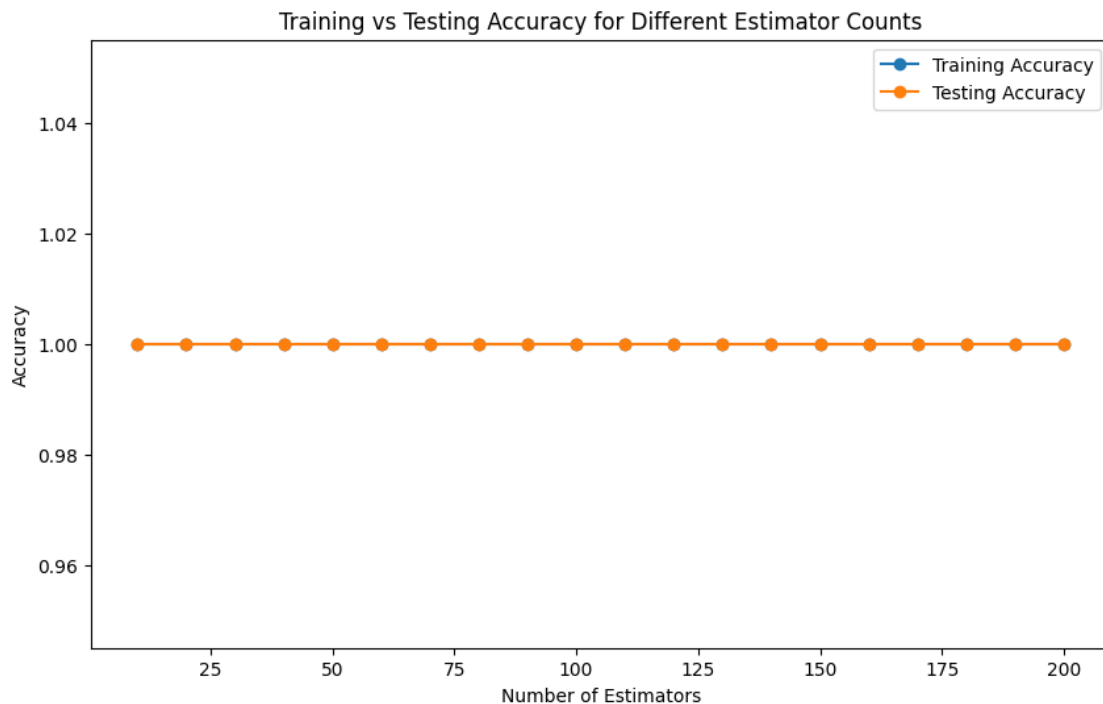
```

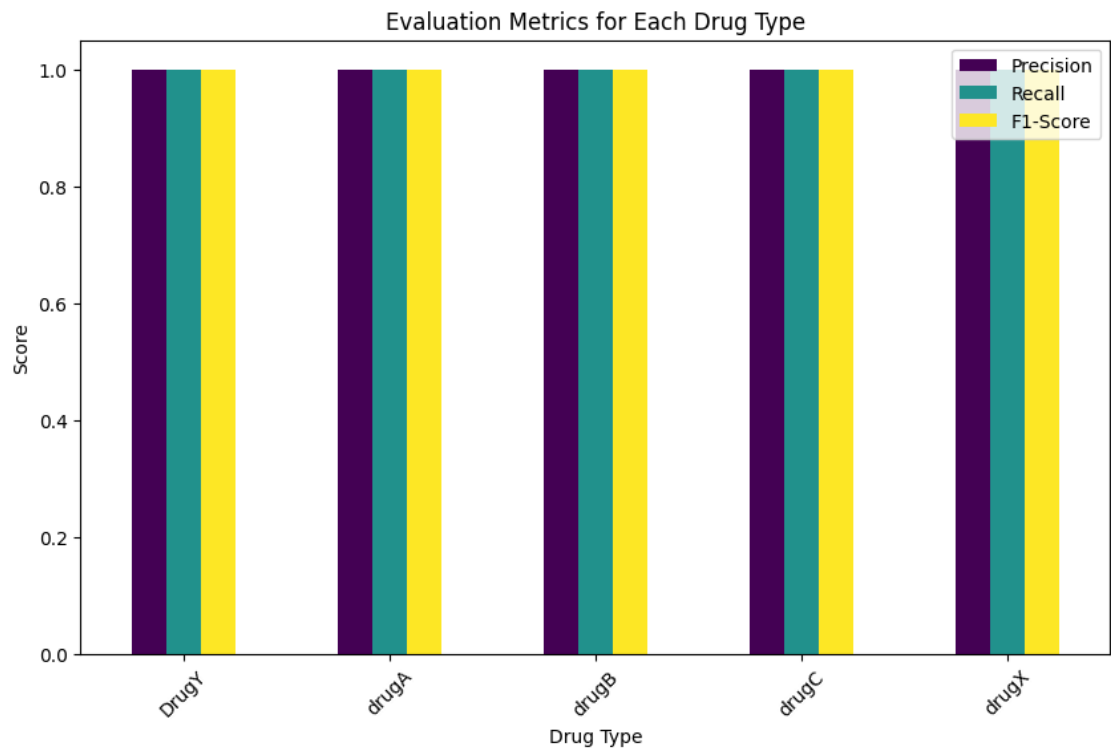
metrics_df = pd.DataFrame({'Precision': precision, 'Recall': recall, 'F1-Score':
    ↪ f1_score},
                           index=label_encoder.inverse_transform(np.unique(y)))

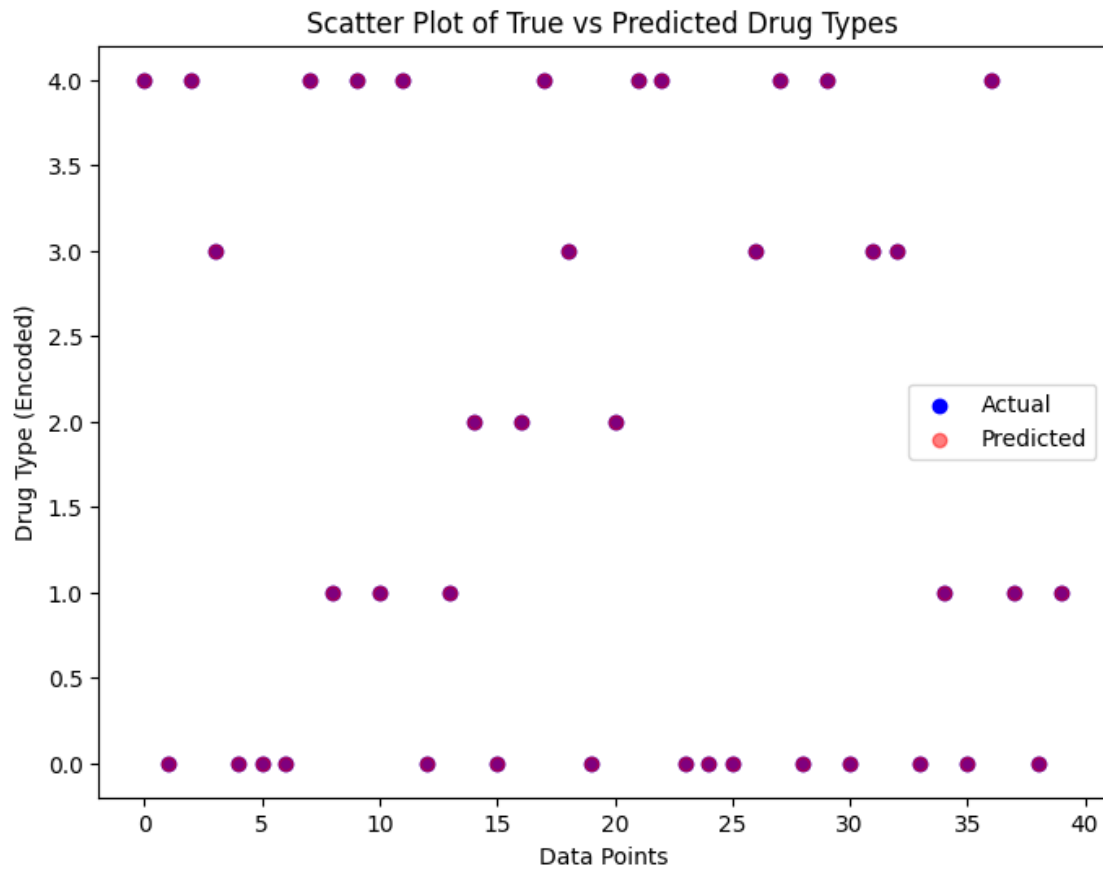
metrics_df.plot(kind='bar', figsize=(10, 6), colormap='viridis')
plt.title("Evaluation Metrics for Each Drug Type")
plt.xlabel("Drug Type")
plt.ylabel("Score")
plt.xticks(rotation=45)
plt.show()

# 3. Scatter Plot of True vs Predicted Data Points
plt.figure(figsize=(8, 6))
plt.scatter(range(len(y_test)), y_test, color="blue", label="Actual")
plt.scatter(range(len(y_pred)), y_pred, color="red", alpha=0.5,
    ↪ label="Predicted")
plt.xlabel("Data Points")
plt.ylabel("Drug Type (Encoded)")
plt.title("Scatter Plot of True vs Predicted Drug Types")
plt.legend()
plt.show()

```







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