```
import pandas as pd
import numpy as np
from sklearn.model_selection import train_test_split, cross_val_score
                                                                                Enable
from sklearn.tree import DecisionTreeClassifier, plot tree
                                                                                Settina
                                                                                executi
from sklearn.metrics import accuracy_score, confusion_matrix, classification_
import matplotlib.pyplot as plt
                                                                                   OŁ
data = pd.read csv('/content/diabetes prediction dataset.csv')
print(data.head())
       gender
                                    heart_disease smoking_history
                      hypertension
                                                                      bmi
                 age
                                                             never 25.19
      Female 80.0
                                 0
                                                 1
       Female 54.0
                                                           No Info
                                                                    27.32
    1
                                 0
                                                 0
    2
         Male 28.0
                                 0
                                                 0
                                                             never
                                                                    27.32
    3
       Female 36.0
                                 0
                                                 0
                                                           current 23.45
                                 1
         Male 76.0
                                                 1
                                                           current 20.14
       HbA1c level
                     blood_glucose_level
                                          diabetes
    0
                6.6
                                     140
    1
                6.6
                                                  0
                                      80
    2
                5.7
                                     158
                                                  0
    3
                5.0
                                     155
                                                  0
    4
                4.8
                                     155
                                                  0
data = data[['bmi', 'diabetes']]
X = data[['bmi']]
v = data['diabetes']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_sta
model = DecisionTreeClassifier(random state=42)
model.fit(X_train, y_train)
y pred = model.predict(X test)
accuracy = accuracy_score(y_test, y_pred)
conf_matrix = confusion_matrix(y_test, y_pred)
class_report = classification_report(y_test, y_pred)
print("Accuracy:", accuracy)
print("Confusion Matrix:\n", conf_matrix)
print("Classification Report:\n", class_report)
cross_val_scores = cross_val_score(model, X, y, cv=5)
print("Cross-validation scores:". cross val scores)
```

print("Mean cross-validation score:", np.mean(cross_val_scores))

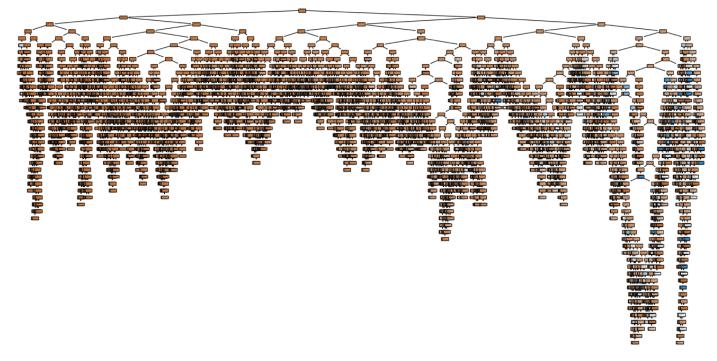
plt.figure(figsize=(20,10))
plot_tree(model, feature_names=['bmi'], class_names=['No Diabetes', 'Diabetes'], fiplt.show()

 $\overline{\mathbf{x}}$

Accuracy: 0.912 Confusion Matrix: [[27300 153] [2487 60]]

Classification Report:

| | precision | recall | f1-score | support |
|--------------|-----------|--------|----------|---------|
| 0 | 0.92 | 0.99 | 0.95 | 27453 |
| 1 | 0.28 | 0.02 | 0.04 | 2547 |
| accuracy | | | 0.91 | 30000 |
| macro avg | 0.60 | 0.51 | 0.50 | 30000 |
| weighted avg | 0.86 | 0.91 | 0.88 | 30000 |



```
y_pred_prob = model.predict_proba(X_test)[:, 1]
fpr, tpr, thresholds = roc_curve(y_test, y_pred_prob)
roc_auc = auc(fpr, tpr)
```

plt.figure()

14 mlat/fmm tmm salam lbl.sel lv. 2 labal IDOC sumus /sman 000 2f\l 0 mas sus\

```
ptt.ptot(ipi, tpi, cotor= blue , tw=z, tabet= koc curve (area = %0.21) % roc_auc)
plt.plot([0, 1], [0, 1], color='gray', lw=2, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic (ROC) Curve')
plt.legend(loc="lower right")
plt.show()

optimal_idx = np.argmax(tpr - fpr)
optimal_threshold = thresholds[optimal_idx]
print("Optimal BMI threshold:", optimal_threshold)
```

$\overline{\Sigma}$

Receiver Operating Characteristic (ROC) Curve 1.0 0.8 True Positive Rate 0.6 0.4 0.2 ROC curve (area = 0.62) 0.0 0.2 0.4 0.6 0.8 0.0 1.0 False Positive Rate

Optimal BMI threshold: 0.08333333333333333