8. Develop a program to demonstrate the working of the decision tree algorithm. Use Breast Cancer Data set for building the decision tree and apply this knowledge to classify a new sample.

```
from sklearn.tree import plot_tree
import matplotlib.pyplot as plt
import numpy as np
from sklearn.datasets import load_breast_cancer
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score, classification_report, confusion_matrix

# Step 1: Load the Breast Cancer Dataset
data = load_breast_cancer()
X = data.data  # Features
y = data.target  # Labels (0: malignant, 1: benign)

# Step 2: Split the dataset 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)

# Step 3: Create and train the Decision Tree classifier
clf = DecisionTreeClassifier(random_state=42)
clf.fit(X_train, y_train)

# Step 4: Make predictions on the test set
y_pred = clf.predict(X_test)

# Step 5: Evaluate the model
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)
print("\nClassification Report:")
print(classification_report(y_test, y_pred, target_names=data.target_names))
print("\nConfusion Matrix:")
print(confusion_matrix(y_test, y_pred))
# Step 6: Classify a new sample
# Example: Create a new sample (you can replace these values with actual data)
new_sample = np.array([[17.99, 10.38, 122.8, 1001.0, 0.1184, 0.2776, 0.3001, 0.1471, 0.2419,
0.07871,   1.095, 0.9053, 8.589, 153.4, 0.006399, 0.04904, 0.05373, 0.01587, 0.03003, 0.006193,
```

25.38, 17.33, 184.6, 2019.0, 0.1622, 0.6656, 0.7119, 0.2654, 0.4601, 0.1189]])

```
# Predict the class of the new sample
prediction = clf.predict(new_sample)
print("\nNew Sample Prediction:")
print("Class:", data.target_names[prediction][0])
plt.figure(figsize=(20, 10))
plot_tree(clf, filled=True, feature_names=data.feature_names, class_names=data.target_names)
plt.show()
```

Output

```
Accuracy: 0.9473684210526315

Classification Report:
              precision    recall  f1-score   support

   malignant       0.93      0.93      0.93        43
      benign       0.96      0.96      0.96        71

    accuracy                           0.95       114
   macro avg       0.94      0.94      0.94       114
weighted avg       0.95      0.95      0.95       114


Confusion Matrix:
[[40  3]
 [ 3 68]]

New Sample Prediction:
Class: malignant
```