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ML LAB : A - 7

CSE-A

A7:- Predicting Diabetes using decision tree

Aim:- Develop a python program to predict diabetics using Decision Tree Model. Visualize the features from the dataset and interpret the results obtained by the model using Matplotlib library.

The Diabetes prediction dataset is a collection of medical and demographic data from patients, along with their diabetes status (positive or negative). The data includes features such as age, gender, body mass index (BMI), hypertension, heart disease, smoking history, HbA1c level, and blood glucose level. This dataset can be used to build machine learning models to predict diabetes in patients based on their medical history and demographic information. This can be useful for healthcare professionals in identifying patients who may be at risk of developing diabetes and in developing personalized treatment plans. Additionally, the dataset can be used by researchers to explore the relationships between various medical and demographic factors and the likelihood of developing diabetes.

```
[1]: import pandas as pd
import numpy as np
import seaborn as sns
from scipy.stats import zscore
import matplotlib.pyplot as plt
from sklearn import tree
from sklearn.preprocessing import MinMaxScaler
from sklearn.metrics import classification_report, roc_auc_score, _
    confusion_matrix, ConfusionMatrixDisplay, RocCurveDisplay, roc_auc_score
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import MultinomialNB
from sklearn.tree import DecisionTreeClassifier
from sklearn import preprocessing
from sklearn.decomposition import PCA
```

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```
import scipy.stats
from sklearn.metrics import PrecisionRecallDisplay
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay
from sklearn.neighbors import KNeighborsClassifier
```

```
pd.set_option('display.float_format', lambda x: '%.2f' % x)
%matplotlib inline
```

C:\Users\Nithi\AppData\Local\Temp\ipykernel_13632\1512000984.py:1: DeprecationWarning: Pyarrow will become a required dependency of pandas in the next major release of pandas (pandas 3.0), (to allow more performant data types, such as the Arrow string type, and better interoperability with other libraries) but was not found to be installed on your system. If this would cause problems for you,

```
import pandas as pd
```

3 Loading dataset

```
[2]: data = pd.read_csv('C:/Users/ashwi/Downloads/ML Lab/A7/
↳diabetes_prediction_dataset.csv')
```

```
[3]: data.head()
```

```
[3]:
```

	gender	age	hypertension	heart_disease	smoking_history	bmi	\
0	Female	80.00	0	1	never	25.19	
1	Female	54.00	0	0	No Info	27.32	
2	Male	28.00	0	0	never	27.32	
3	Female	36.00	0	0	current	23.45	
4	Male	76.00	1	1	current	20.14	

	HbA1c_level	blood_glucose_level	diabetes
0	6.60	140	0
1	6.60	80	0
2	5.70	158	0
3	5.00	155	0
4	4.80	155	0

```
[4]: data.describe()
```

```
[4]:
```

	age	hypertension	heart_disease	bmi	HbA1c_level	\
count	100000.00	100000.00	100000.00	100000.00	100000.00	

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mean	41.89	0.07	0.04	27.32	5.53
std	22.52	0.26	0.19	6.64	1.07
min	0.08	0.00	0.00	10.01	3.50
25%	24.00	0.00	0.00	23.63	4.80
50%	43.00	0.00	0.00	27.32	5.80
75%	60.00	0.00	0.00	29.58	6.20
max	80.00	1.00	1.00	95.69	9.00

	blood_glucose_level	diabetes
count	100000.00	100000.00
mean	138.06	0.09
std	40.71	0.28
min	80.00	0.00
25%	100.00	0.00
50%	140.00	0.00
75%	159.00	0.00
max	300.00	1.00

```
[5] : #Find number of rows and columns

num_rows, num_columns = data.shape

print("Number of rows:", num_rows)
print("Number of columns:", num_columns)
```

Number of rows: 100000

Number of columns: 9

4 Pre-Processing the data

```
[6] : #Distribution
data['diabetes'].value_counts()
```

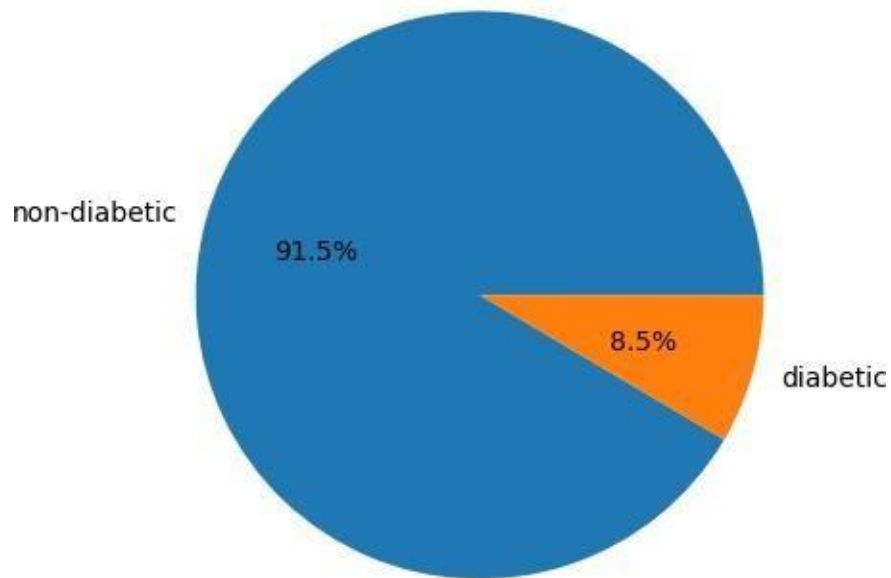
```
[6] : diabetes
0    91500
1     8500
Name: count, dtype: int64
```

```
[7] : plt.pie(data['diabetes'].value_counts(), labels = ['non-diabetic', 'diabetic'],
            autopct = '%1.1f%%')
plt.title("Distribution of diabetics in dataset")
plt.show()
```

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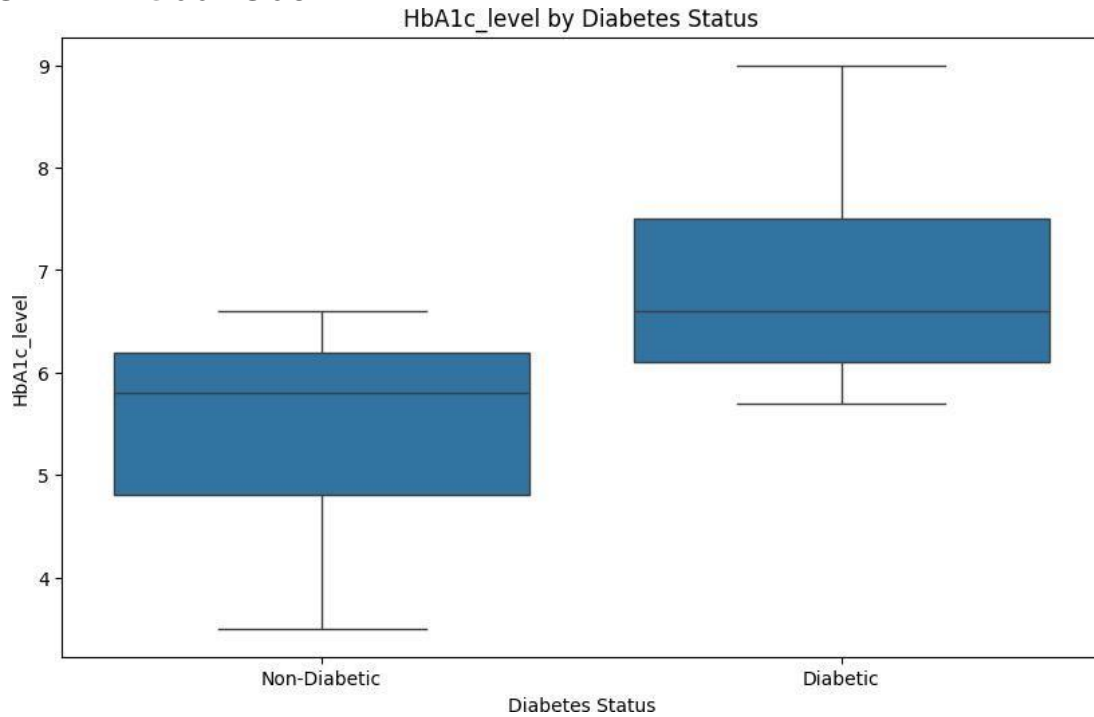
Distribution of diabetics in dataset



```
[8] : plt.figure(figsize=(10, 6))
sns.boxplot(x='diabetes', y='HbA1c_level', data=data)
plt.title('HbA1c_level by Diabetes Status')
plt.xlabel('Diabetes Status')
plt.ylabel('HbA1c_level')
plt.xticks([0, 1], ['Non-Diabetic', 'Diabetic']) # Adjust based on your
↳ 'diabetes' column encoding
plt.show()
```

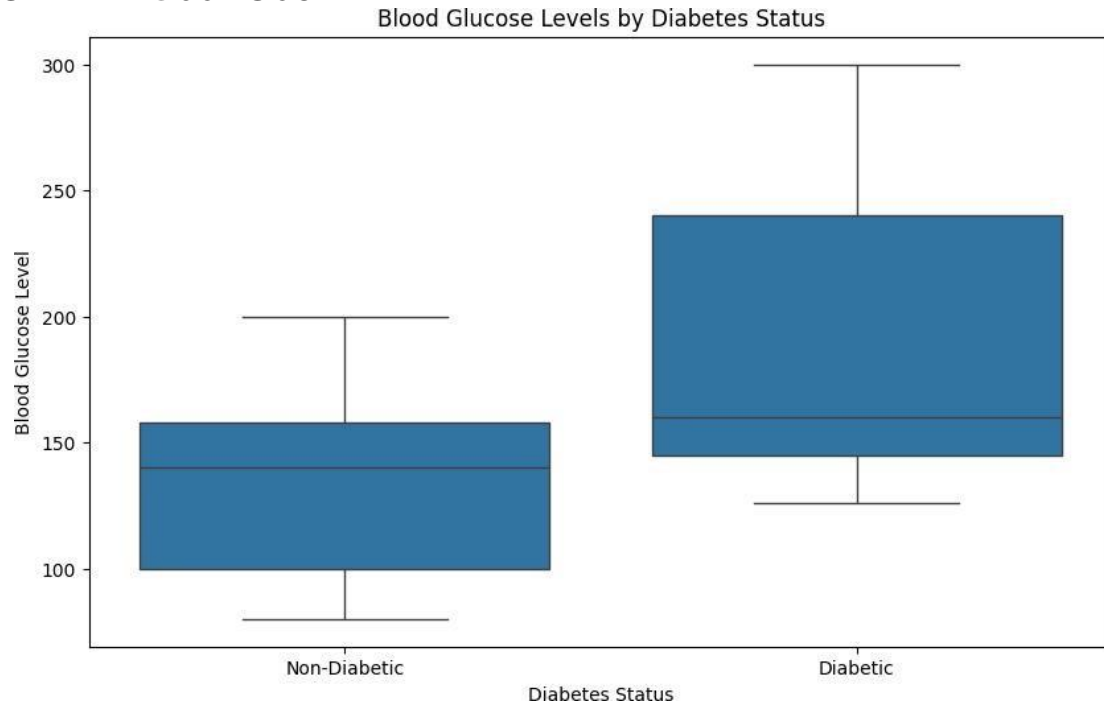
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```
[9] : plt.figure(figsize=(10, 6))
sns.boxplot(x='diabetes', y='blood_glucose_level', data=data)
plt.title('Blood Glucose Levels by Diabetes Status')
plt.xlabel('Diabetes Status')
plt.ylabel('Blood Glucose Level')
plt.xticks([0, 1], ['Non-Diabetic', 'Diabetic']) # Adjust based on your
↳ 'diabetes' column encoding
plt.show()
```

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[10] : *#Find Missing Values*

```
missing_values = data.isnull().sum().sum()
percentage_missing = (missing_values / data.shape[0]) * 100
print("Percentage of missing values:", percentage_missing)
```

Percentage of missing values: 0.0

[11] : *#Convert Categorical variables into binary and numeric*

```
label_encoder = preprocessing.LabelEncoder()
data['smoking_history'] = label_encoder.fit_transform(data['smoking_history'])
data['gender'] = label_encoder.fit_transform(data['gender'])
data.head()
```

```
[11]:  gender  age  hypertension  heart_disease  smoking_history  bmi \
0      0  80.00              0              1              4  25.19
1      0  54.00              0              0              0  27.32
2      1  28.00              0              0              4  27.32
3      0  36.00              0              0              1  23.45
4      1  76.00              1              1              1  20.14

      HbA1c_level  blood_glucose_level  diabetes
0              6.60              140          0
1              6.60              80          0
```

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2	5.70	158	0
3	5.00	155	0
4	4.80	155	0

```
[12] : numeric_data = data.select_dtypes(include='number')
print(numeric_data)
```

	gender	age	hypertension	heart_disease	smoking_history	bmi	\
0	0	80.00	0	1	4	25.19	
1	0	54.00	0	0	0	27.32	
2	1	28.00	0	0	4	27.32	
3	0	36.00	0	0	1	23.45	
4	1	76.00	1	1	1	20.14	
...
99995	0	80.00	0	0	0	27.32	
99996	0	2.00	0	0	0	17.37	
99997	1	66.00	0	0	3	27.83	
99998	0	24.00	0	0	4	35.42	
99999	0	57.00	0	0	1	22.43	

	HbA1c_level	blood_glucose_level	diabetes
0	6.60	140	0
1	6.60	80	0
2	5.70	158	0
3	5.00	155	0
4	4.80	155	0
...
99995	6.20	90	0
99996	6.50	100	0
99997	5.70	155	0
99998	4.00	100	0
99999	6.60	90	0

[100000 rows x 9 columns]

```
[13] : # Selecting the numerical columns (excluding binary columns for hypertension,
      *heart_disease, diabetes)
      numerical_columns = ['age', 'bmi', 'HbA1c_level', 'smoking_history',
      ↪ 'blood_glucose_level']
```

```
[14] : # Calculate Z-scores for numeric columns
      z_scores = data[numerical_columns].apply(zscore)
      print(z_scores)
```

	age	bmi	HbA1c_level	smoking_history	blood_glucose_level
0	1.69	-0.32	1.00	0.96	0.05

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1	0.54	-0.00	1.00	-1.15	-1.43
2	-0.62	-0.00	0.16	0.96	0.49
3	-0.26	-0.58	-0.49	-0.62	0.42
4	1.52	-1.08	-0.68	-0.62	0.42
...
99995	1.69	-0.00	0.63	-1.15	-1.18
99996	-1.77	-1.50	0.91	-1.15	-0.93
99997	1.07	0.08	0.16	0.43	0.42
99998	-0.79	1.22	-1.43	0.96	-0.93
99999	0.67	-0.74	1.00	-0.62	-1.18

[100000 rows x 5 columns]

[15] : *# Define threshold for outlier detection (e.g., Z-Score > 3)*

```
threshold = 3
# Find outliers
outliers = data[z_scores > threshold]
print(outliers)
```

	gender	age	hypertension	heart_disease	smoking_history	bmi	\
0	NaN	NaN	NaN	NaN	NaN	NaN	
1	NaN	NaN	NaN	NaN	NaN	NaN	
2	NaN	NaN	NaN	NaN	NaN	NaN	
3	NaN	NaN	NaN	NaN	NaN	NaN	
4	NaN	NaN	NaN	NaN	NaN	NaN	
...	
99995	NaN	NaN	NaN	NaN	NaN	NaN	
99996	NaN	NaN	NaN	NaN	NaN	NaN	
99997	NaN	NaN	NaN	NaN	NaN	NaN	
99998	NaN	NaN	NaN	NaN	NaN	NaN	
99999	NaN	NaN	NaN	NaN	NaN	NaN	

	HbA1c_level	blood_glucose_level	diabetes
0	NaN	NaN	NaN
1	NaN	NaN	NaN
2	NaN	NaN	NaN
3	NaN	NaN	NaN
4	NaN	NaN	NaN
...
99995	NaN	NaN	NaN
99996	NaN	NaN	NaN
99997	NaN	NaN	NaN
99998	NaN	NaN	NaN
99999	NaN	NaN	NaN

[100000 rows x 9 columns]

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```
[16] : # Count outliers
outliers_count = (z_scores.abs() > threshold).sum().sum()

print("Number of outliers:", outliers_count)
```

Number of outliers: 4012

```
[17] : # normalization

# Initialize the MinMaxScaler
scaler = MinMaxScaler()

# Fit the scaler to the data and transform it
data[numerical_columns] = scaler.fit_transform(data[numerical_columns])

# Display the first few rows to verify the normalization
print(data.head())
```

	gender	age	hypertension	heart_disease	smoking_history	bmi \
0	0	1.00	0	1	0.80	0.18
1	0	0.67	0	0	0.00	0.20
2	1	0.35	0	0	0.80	0.20
3	0	0.45	0	0	0.20	0.16
4	1	0.95	1	1	0.20	0.12

	HbA1c_level	blood_glucose_level	diabetes
0	0.56	0.27	0
1	0.56	0.00	0
2	0.40	0.35	0
3	0.27	0.34	0
4	0.24	0.34	0

```
[18] : data.head()
```

```
[18]:
```

	gender	age	hypertension	heart_disease	smoking_history	bmi \
0	0	1.00	0	1	0.80	0.18
1	0	0.67	0	0	0.00	0.20
2	1	0.35	0	0	0.80	0.20
3	0	0.45	0	0	0.20	0.16
4	1	0.95	1	1	0.20	0.12

	HbA1c_level	blood_glucose_level	diabetes
0	0.56	0.27	0
1	0.56	0.00	0
2	0.40	0.35	0
3	0.27	0.34	0

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4

0.24

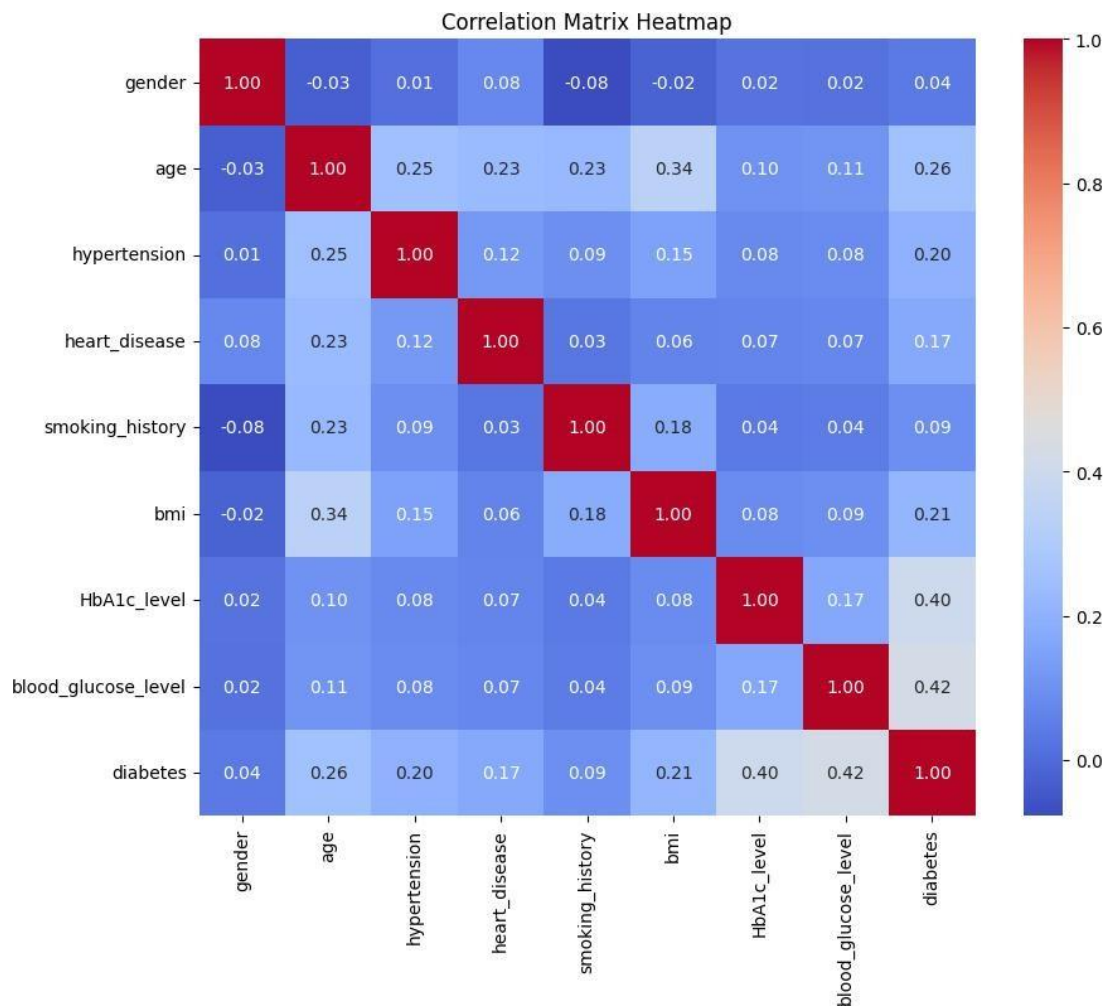
0.34

0

5 Exploratory Data Analysis

```
[19] : # Calculate the correlation matrix
corr_matrix = data.corr()

# Plot the heatmap
plt.figure(figsize=(10, 8)) # Set the figure size as desired
sns.heatmap(corr_matrix, annot=True, fmt=".2f", cmap='coolwarm', cbar=True, square=True)
plt.title('Correlation Matrix Heatmap')
plt.show()
```



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6 Split the data into training, testing and validation sets

```
[20] : X = data.drop(columns=['diabetes'], axis=1)
      y = data['diabetes']
```

```
[21] : X_train_raw, X_test_raw, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)
```

```
[22] : X_train = pd.DataFrame(X_train_raw, columns=X_train_raw.columns)
      X_test = pd.DataFrame(X_test_raw, columns=X_test_raw.columns)
      X_test.head()
```

```
[22]:
```

	gender	age	hypertension	heart_disease	smoking_history	bmi	\
75721	0	0.16	0	0	0.00	0.13	
80184	0	0.04	0	0	0.00	0.13	
19864	1	0.79	0	0	0.60	0.18	
76699	0	0.02	0	0	0.80	0.09	
92991	0	0.41	0	0	1.00	0.35	

	HbA1c_level	blood_glucose_level
75721	0.42	0.21
80184	0.27	0.30
19864	0.00	0.55
76699	0.47	0.21
92991	0.49	0.55

7 Train the model

```
[23] : pca = PCA(random_state=42)
      pca.fit(X_train)
```

```
[23] : PCA(random_state=42)
```

```
[24] : # Calculate the cumulative explained variance ratio
      cumulative_variance = pca.explained_variance_ratio_.cumsum()

      # Find the number of components needed for 90% variance
      n_components_90 = (cumulative_variance <= 0.90).sum()

      print("Number of components to explain 90% variance:", n_components_90)
```

Number of components to explain 90% variance: 5

```
[25] : pca = PCA(n_components=5, random_state=42)
      pca.fit(X_train)
```

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```
X_train_PCA = pd.DataFrame(pca.transform(X_train))  
X_test_PCA = pd.DataFrame(pca.transform(X_test))
```

```
[26] : X_train_PCA.columns = [str(column_name) for column_name in X_train_PCA.columns]  
X_test_PCA.columns = [str(column_name) for column_name in X_test_PCA.columns]
```

```
[27] : X_train_PCA.head()
```

```
[27]:
```

	0	1	2	3	4
0	0.58	0.06	-0.01	-0.11	-0.06
1	0.51	0.47	-0.09	-0.19	-0.33
2	-0.37	-0.39	-0.13	0.07	-0.26
3	-0.38	-0.22	0.20	-0.17	0.17
4	0.66	-0.46	-0.13	0.12	0.02

8 Test the model

```
[28] : model = tree.DecisionTreeClassifier()
```

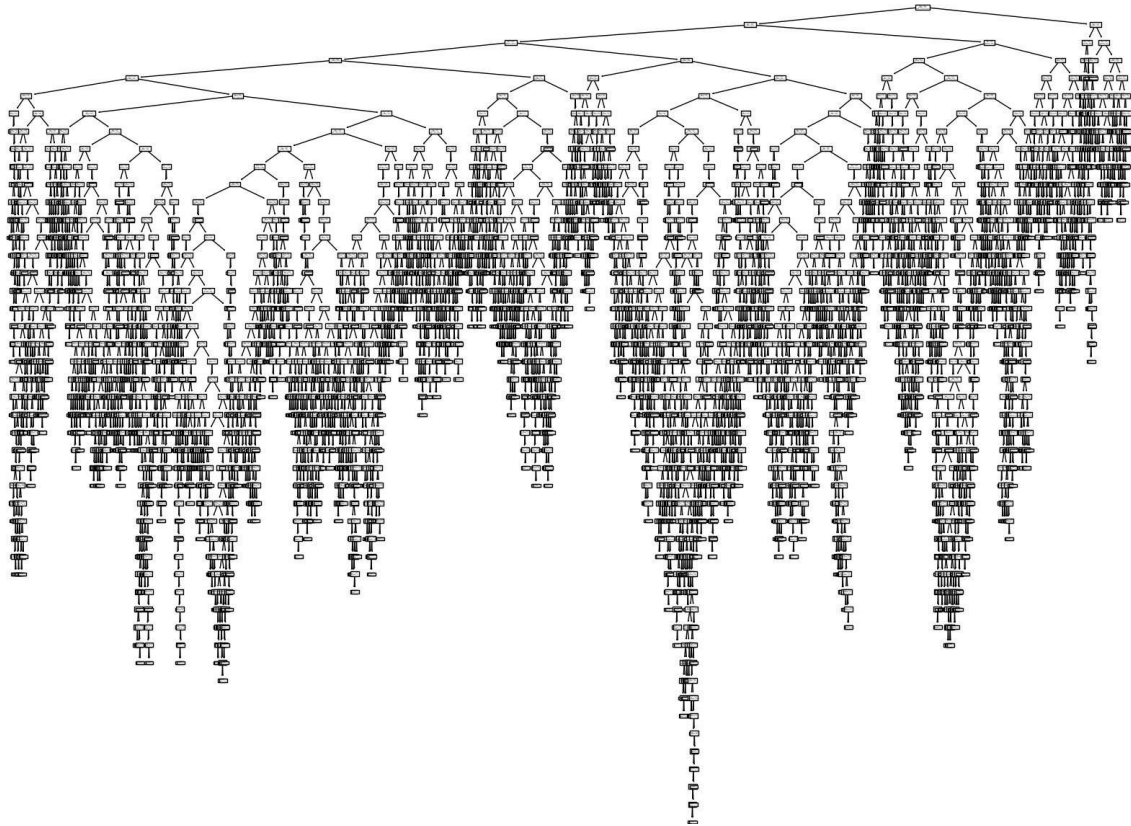
```
[29] : model.fit(X_train_PCA, y_train)
```

```
[29] : DecisionTreeClassifier()
```

```
[30] : fig = plt.figure(figsize=(20,15))  
tree.plot_tree(model);
```

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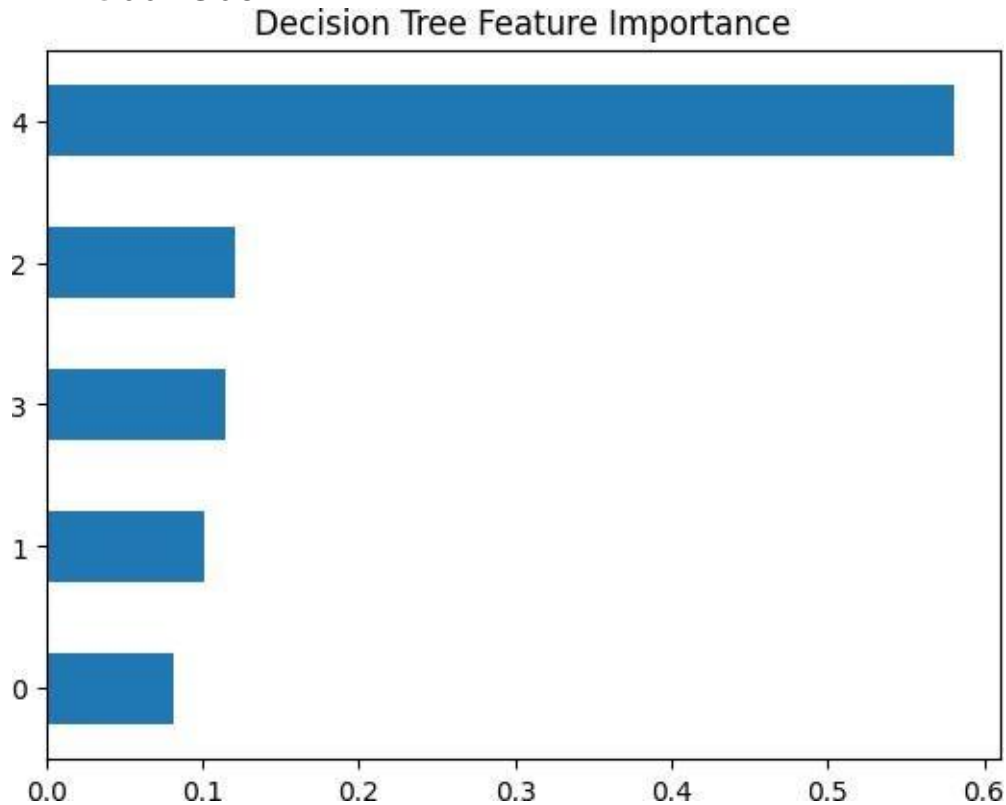
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```
[31] : feature_importances = pd.Series(model.feature_importances_, model.  
    ↳ feature_names_in_).sort_values()  
feature_importances.plot.barh();  
plt.title('Decision Tree Feature Importance');
```

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```
[32] : y_pred_test = model.predict(X_test_PCA)
      y_pred_train= model.predict(X_train_PCA)
```

9 Measure the performance of the trained model

```
[33] : train_decision_tree_report = classification_report(y_train, y_pred_train)
      print(train_decision_tree_report)
```

	precision	recall	f1-score	support
0	1.00	1.00	1.00	64047
1	1.00	0.99	1.00	5953
accuracy			1.00	70000
macro avg	1.00	1.00	1.00	70000
weighted avg	1.00	1.00	1.00	70000

```
[34] : test_decision_tree_report = classification_report(y_test, y_pred_test)
      print(test_decision_tree_report)
```

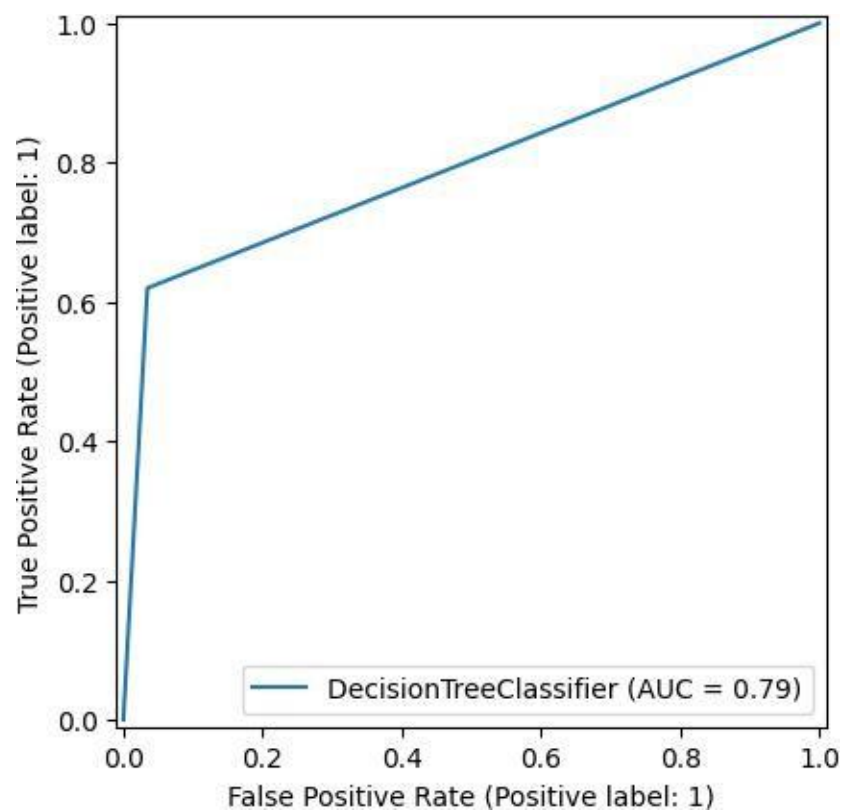
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	precision	recall	f1-score	support
0	0.96	0.97	0.97	27453
1	0.62	0.62	0.62	2547
accuracy			0.94	30000
macro avg	0.79	0.79	0.79	30000
weighted avg	0.94	0.94	0.94	30000

10 Represent the results using graphs

```
[35] : RocCurveDisplay.from_estimator(model, X_test_PCA, y_test)
plt.show()
```



```
[36] : from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score
from sklearn.decomposition import PCA
from sklearn.model_selection import train_test_split
import numpy as np
```

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```
X_train, X_test, y_train, y_test = train_test_split(X_train_PCA, y_train,
                                                    test_size=0.2, random_state=42)

dt_entropy = DecisionTreeClassifier(criterion='entropy', random_state=42)
dt_entropy.fit(X_train, y_train)

y_pred_entropy = dt_entropy.predict(X_test)

accuracy_entropy = accuracy_score(y_test, y_pred_entropy)
print("Accuracy using Entropy impurity measure with PCA:", accuracy_entropy)

dt_gini = DecisionTreeClassifier(criterion='gini', random_state=42)
dt_gini.fit(X_train, y_train)

y_pred_gini = dt_gini.predict(X_test)

accuracy_gini = accuracy_score(y_test, y_pred_gini)
print("Accuracy using Gini-index impurity measure with PCA:", accuracy_gini)
```

Accuracy using Entropy impurity measure with PCA: 0.9377857142857143
Accuracy using Gini-index impurity measure with PCA: 0.9399285714285714

```
[37] : from sklearn.tree import DecisionTreeClassifier
      from sklearn.metrics import accuracy_score

dt_classifier = DecisionTreeClassifier(random_state=42)
dt_classifier.fit(X_train, y_train)

y_pred = dt_classifier.predict(X_test)

accuracy_without_pca = accuracy_score(y_test, y_pred)
print("Accuracy without PCA:", accuracy_without_pca)
```

Accuracy without PCA: 0.9399285714285714

```
[44]: from sklearn.tree import DecisionTreeClassifier
      from sklearn.metrics import accuracy_score
      from sklearn.model_selection import train_test_split
      import pandas as pd

dt_entropy = DecisionTreeClassifier(criterion='entropy', random_state=42)
dt_entropy.fit(X_train_raw, y_train)
```


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```
y_pred_entropy = dt_entropy.predict(X_test_raw)
accuracy_entropy = accuracy_score(y_test, y_pred_entropy)
print("Accuracy using Entropy impurity measure without PCA:", accuracy_entropy)

dt_gini = DecisionTreeClassifier(criterion='gini', random_state=42)
dt_gini.fit(X_train_raw, y_train)

y_pred_gini = dt_gini.predict(X_test_raw)

accuracy_gini = accuracy_score(y_test, y_pred_gini)
print("Accuracy using Gini-index impurity measure without PCA:", accuracy_gini)
```

Accuracy using Entropy impurity measure without PCA: 0.9542666666666667
Accuracy using Gini-index impurity measure without PCA: 0.9530333333333333

```
[43]: X = data.drop(columns=['diabetes'], axis=1)
      y = data['diabetes']

X_train_raw, X_test_raw, y_train, y_test = train_test_split(X, y, test_size=0.
↳ 3, random_state=42)

print("X_train_raw shape:", X_train_raw.shape)
print("y_train shape:", y_train.shape)
print("X_test_raw shape:", X_test_raw.shape)
print("y_test shape:", y_test.shape)

dt_entropy = DecisionTreeClassifier(criterion='entropy', random_state=42)
dt_entropy.fit(X_train_raw, y_train)

y_pred_entropy = dt_entropy.predict(X_test_raw)

accuracy_entropy = accuracy_score(y_test, y_pred_entropy)
print("Accuracy using Entropy impurity measure without PCA:", accuracy_entropy)

dt_gini = DecisionTreeClassifier(criterion='gini', random_state=42)
dt_gini.fit(X_train_raw, y_train)

y_pred_gini = dt_gini.predict(X_test_raw)

accuracy_gini = accuracy_score(y_test, y_pred_gini)
print("Accuracy using Gini-index impurity measure without PCA:", accuracy_gini)

X_train_raw shape: (70000, 8)
y_train shape: (70000,)
X_test_raw shape: (30000, 8)
```

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y_test shape: (30000,)

Accuracy using Entropy impurity measure without PCA: 0.9542666666666667

Accuracy using Gini-index impurity measure without PCA: 0.9530333333333333

```
[45]: from sklearn.metrics import roc_curve, auc
import matplotlib.pyplot as plt
```

```
y_pred_entropy_no_pca = dt_entropy.predict(X_test_raw)
```

```
y_pred_gini_no_pca = dt_gini.predict(X_test_raw)
```

```
fpr_entropy_pca, tpr_entropy_pca, _ = roc_curve(y_test, y_pred_entropy)
roc_auc_entropy_pca = auc(fpr_entropy_pca, tpr_entropy_pca)
```

```
fpr_gini_pca, tpr_gini_pca, _ = roc_curve(y_test, y_pred_gini)
roc_auc_gini_pca = auc(fpr_gini_pca, tpr_gini_pca)
```

```
fpr_entropy_no_pca, tpr_entropy_no_pca, _ = roc_curve(y_test,
↳ y_pred_entropy_no_pca)
roc_auc_entropy_no_pca = auc(fpr_entropy_no_pca, tpr_entropy_no_pca)
```

```
fpr_gini_no_pca, tpr_gini_no_pca, _ = roc_curve(y_test, y_pred_gini_no_pca)
roc_auc_gini_no_pca = auc(fpr_gini_no_pca, tpr_gini_no_pca)
```

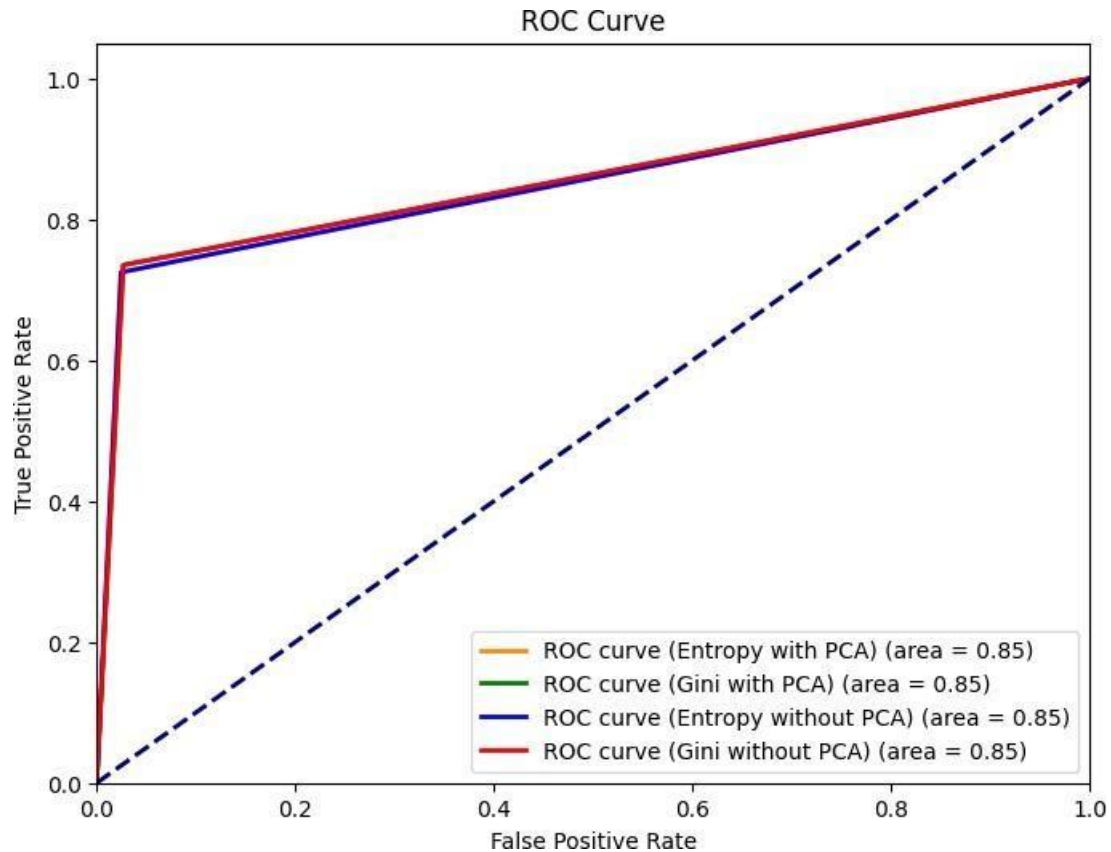
```
# Plot ROC curve
```

```
plt.figure(figsize=(8, 6))
plt.plot(fpr_entropy_pca, tpr_entropy_pca, color='darkorange', lw=2, label='ROC_
↳ curve (Entropy with PCA) (area = %0.2f)' % roc_auc_entropy_pca)
plt.plot(fpr_gini_pca, tpr_gini_pca, color='green', lw=2, label='ROC curve_
↳ (Gini with PCA) (area = %0.2f)' % roc_auc_gini_pca)
plt.plot(fpr_entropy_no_pca, tpr_entropy_no_pca, color='blue', lw=2, label='ROC_
↳ curve (Entropy without PCA) (area = %0.2f)' % roc_auc_entropy_no_pca)
plt.plot(fpr_gini_no_pca, tpr_gini_no_pca, color='red', lw=2, label='ROC curve_
↳ (Gini without PCA) (area = %0.2f)' % roc_auc_gini_no_pca)
plt.plot([0, 1], [0, 1], color='navy', 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('ROC Curve')
plt.legend(loc="lower right")
```

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```
plt.show()
```



```
[46]: print("X_train_raw shape:", X_train_raw.shape)
      print("y_train shape:", y_train.shape)
      print("X_test_raw shape:", X_test_raw.shape)
      print("y_test shape:", y_test.shape)
```

X_train_raw shape: (70000, 8)

y_train shape: (70000,)

X_test_raw shape: (30000, 8)

y_test shape: (30000,)

11 Inference

1.

Accuracy using Entropy impurity measure without PCA: 0.9542666666666667

Accuracy using Gini-index impurity measure without PCA: 0.9530333333333333

2.

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Accuracy using Entropy impurity measure with PCA: 0.9377857142857143

Accuracy using Gini-index impurity measure with PCA: 0.9399285714285714

As we can clearly see that the accuracy of the decision tree classifier using Gini-index and Entropy using PCA gives less accuracy than without using PCA.

12 Learning Outcomes

1. Applying standardisation and other pre-processing techniques.
2. Splitting the data according to PCA.
3. Understanding Decision Tree classifier Algorithm.
4. Implementing decision tree classifier model.
5. Implementing the decision tree model with using PCA and without using PCA.

GITHUB LINK :

<https://github.com/KavinSiva13/ML-A4/tree/main/ML%20-%20A7>