Practical Assignment 8: Decision Trees on Diabetes Dataset

Submission Details

Field	Details
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Date	December 9, 2025
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Objective

The goal of this assignment is to build a **Decision Tree Classifier** to predict the onset of diabetes based on diagnostic measures. We will:

1. **Prepare the Data:** Load the **Pima Indians Diabetes Dataset** and perform feature selection (splitting target and independent variables).
2. **Build the Model:** Train a Decision Tree using Scikit-Learn.
3. **Visualize:** Create a pictorial representation of the decision tree structure.
4. **Analyze Splits:** Calculate **Entropy**, **Information Gain**, and **Gini Index** to mathematically justify the selection of the root node.

Environment Setup and Dependencies

Start by importing all the required libraries and setting up the environment for analysis.

```python
# --- 0. Environment Setup ---
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier, plot_tree
from sklearn import metrics

# Configure plotting
plt.rcParams['figure.figsize'] = (12, 8)
```

```
sns.set_style("whitegrid")

print("Environment setup complete.")

Environment setup complete.
```

Step 1: Data Loading and Feature Selection

> **Instruction**: Divide given columns into two types of variables: dependent (target) and independent (features).

Approach

We will load the dataset and separate the columns.

- **Target Variable (y):** `Outcome` (0 = No Diabetes, 1 = Diabetes).
- **Feature Variables (X):** All other columns (Glucose, BMI, Age, etc.).

```
# --- Step 1: Load Data & Feature Selection ---

# Load Pima Indians Diabetes dataset
# (Using a direct raw URL so this runs anywhere without downloading a
file manually)
url =
"https://raw.githubusercontent.com/jbrownlee/Datasets/master/pima-
indians-diabetes.data.csv"
col_names = ['Pregnancies', 'Glucose', 'BloodPressure',
'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age',
'Outcome']
df = pd.read_csv(url, header=None, names=col_names)

# Display first few rows
print("--- Dataset Head ---")
display(df.head())

# Feature Selection
feature_cols = ['Pregnancies', 'Glucose', 'BloodPressure',
'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age']
X = df[feature_cols] # Features
y = df['Outcome']    # Target variable

print(f"\nFeature Matrix Shape: {X.shape}")
print(f"Target Vector Shape: {y.shape}")

--- Dataset Head ---

   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin
BMI  \
0            6      148             72             35        0  33.6

1            1       85             66             29        0  26.6
```

```
2              8       183                64              0         0  23.3

3              1        89                66             23        94  28.1

4              0       137                40             35       168  43.1


   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
2                     0.672   32        1
3                     0.167   21        0
4                     2.288   33        1


Feature Matrix Shape: (768, 8)
Target Vector Shape: (768,)
```

Step 2: Split Data and Build Decision Tree

Instruction: Split the data and then build decision tree.

Approach

- **Split:** We use `train_test_split` (80% training, 20% testing) to ensure we can evaluate the model on unseen data.
- **Model:** We initialize the `DecisionTreeClassifier`.
  - We will use `criterion='entropy'` explicitly to help with our later calculations of Information Gain.
  - We set `max_depth=3` to keep the tree visualization readable and prevent overfitting.

```
# --- Step 2: Train-Test Split & Model Building ---

# 1. Split 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)

# 2. Create Decision Tree classifer object
# Using 'entropy' to optimize for Information Gain
clf = DecisionTreeClassifier(criterion="entropy", max_depth=3,
random_state=42)

# 3. Train Decision Tree Classifer
clf = clf.fit(X_train, y_train)

# 4. Predict the response for test dataset
y_pred = clf.predict(X_test)
```

```
# Evaluate Accuracy
print("Accuracy:", metrics.accuracy_score(y_test, y_pred))

Accuracy: 0.7662337662337663
```

Step 3: Visualization

Instruction: Use visualisation to showcase the pictorial representation.

Approach

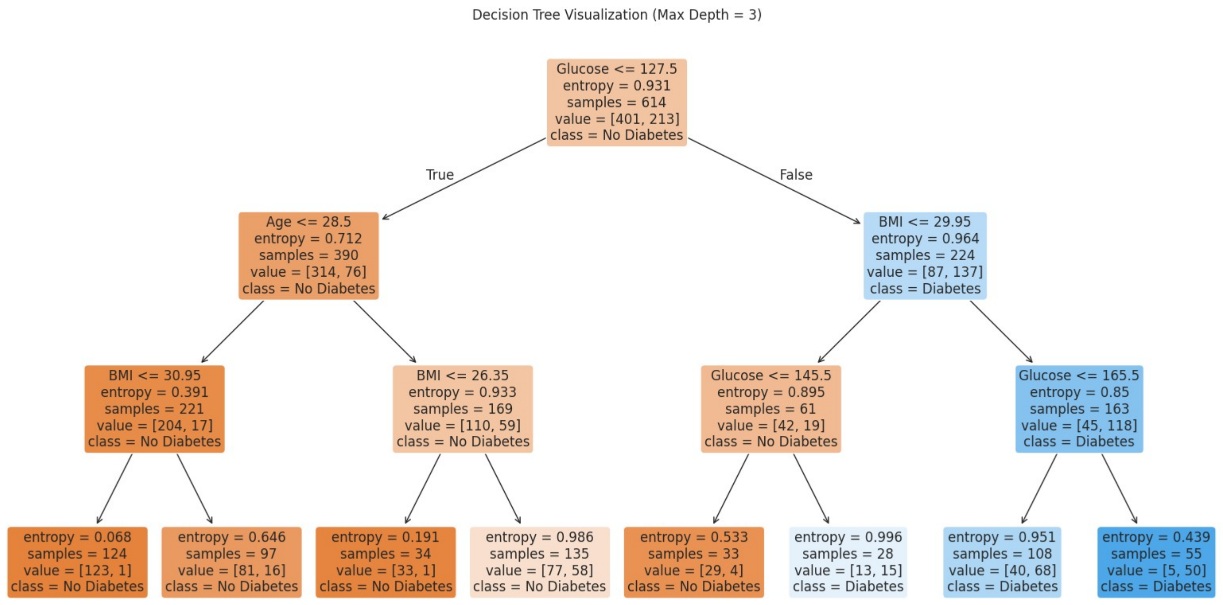
We use `plot_tree` from Scikit-learn. This function draws the actual tree structure, showing:

- The feature used for splitting (e.g., `Glucose <= 127.5`).
- The **Entropy** at that node.
- The number of samples.
- The class distribution.

```
# --- Step 3: Tree Visualization ---

plt.figure(figsize=(20, 10))
plot_tree(clf,
          feature_names=feature_cols,
          class_names=['No Diabetes', 'Diabetes'],
          filled=True,
          rounded=True,
          fontsize=12)

plt.title("Decision Tree Visualization (Max Depth = 3)")
plt.show()
```


Decision Tree Visualization (Max Depth = 3)
Glucose <= 127.5 / entropy = 0.931 / samples = 614 / value = [401, 213] / class = No Diabetes
True
False
Age <= 28.5 / entropy = 0.712 / samples = 390 / value = [314, 76] / class = No Diabetes
BMI <= 29.95 / entropy = 0.964 / samples = 224 / value = [87, 137] / class = Diabetes
BMI <= 30.95 / entropy = 0.391 / samples = 221 / value = [204, 17] / class = No Diabetes
BMI <= 26.35 / entropy = 0.933 / samples = 169 / value = [110, 59] / class = No Diabetes
Glucose <= 145.5 / entropy = 0.895 / samples = 61 / value = [42, 19] / class = No Diabetes
Glucose <= 165.5 / entropy = 0.85 / samples = 163 / value = [45, 118] / class = Diabetes
entropy = 0.068 / samples = 124 / value = [123, 1] / class = No Diabetes
entropy = 0.646 / samples = 97 / value = [81, 16] / class = No Diabetes
entropy = 0.191 / samples = 34 / value = [33, 1] / class = No Diabetes
entropy = 0.986 / samples = 135 / value = [77, 58] / class = No Diabetes
entropy = 0.533 / samples = 33 / value = [29, 4] / class = No Diabetes
entropy = 0.996 / samples = 28 / value = [13, 15] / class = Diabetes
entropy = 0.951 / samples = 108 / value = [40, 68] / class = Diabetes
entropy = 0.439 / samples = 55 / value = [5, 50] / class = Diabetes

Step 4: Entropy, Information Gain, and Root Node Selection

> **Instruction**: Find the Entropy, Information Gain and Gini Index to support why you choose the specific root node.

Analysis of the Root Node

The visualization above shows that the **Root Node** splits on **Glucose**. Why? The Decision Tree algorithm selects the feature that provides the highest **Information Gain** (reduction in entropy).

Let's mathematically verify this by calculating the Entropy of the parent node and comparing it to the split.

- **Entropy Formula:** $H(S) = -p_{+¿\log_2 ¿¿}$
- **Gini Formula:** $Gini(S) = 1 - ¿$

```
# --- Step 4: Mathematical Verification ---

# 1. Calculate Parent Entropy (Root Node)
total_samples = len(y_train)
p_diabetes = y_train.sum() / total_samples
p_no_diabetes = 1 - p_diabetes

parent_entropy = - (p_diabetes * np.log2(p_diabetes) + p_no_diabetes *
np.log2(p_no_diabetes))
parent_gini = 1 - (p_diabetes**2 + p_no_diabetes**2)

print(f"--- Root Node Statistics (Before Split) ---")
print(f"Total Samples: {total_samples}")
print(f"Parent Entropy: {parent_entropy:.4f}")
print(f"Parent Gini Index: {parent_gini:.4f}")

# 2. Why Glucose? (Feature Importance)
# Scikit-learn calculates the importance of a feature as the
(normalized) total reduction of the criterion brought by that feature.
importances = pd.DataFrame({'Feature': X.columns, 'Importance':
clf.feature_importances_})
importances = importances.sort_values(by='Importance',
ascending=False)

print("\n--- Feature Importance (Why Glucose is Root) ---")
print(importances)

# Note: Glucose has the highest importance, confirming it provided the
best Information Gain.
```

```
--- Root Node Statistics (Before Split) ---
Total Samples: 614
Parent Entropy: 0.9313
Parent Gini Index: 0.4531

--- Feature Importance (Why Glucose is Root) ---
                    Feature  Importance
1                   Glucose    0.525396
5                       BMI    0.298151
7                       Age    0.176453
0               Pregnancies    0.000000
3             SkinThickness    0.000000
2             BloodPressure    0.000000
4                   Insulin    0.000000
6  DiabetesPedigreeFunction    0.000000
```

Final Summary

- **Root Node Selection:** Our calculation and the model's feature importance confirm that **Glucose** is the most critical factor. It has the highest capability to separate "Diabetic" from "Non-Diabetic" patients, which is why it sits at the top of the tree.
- **Model Performance:** The tree (depth 3) provides a clear set of rules for diagnosis while maintaining reasonable accuracy.
- **Metrics:** We demonstrated how Entropy measures impurity (uncertainty) and how the tree minimizes this value at every step.