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import pandas as pd
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier, plot_tree
import matplotlib.pyplot as plt

# ---
# 1. Download and Load Data
# ---
# The Pima dataset is often stored without a header row.
# We'll load it from a reliable URL and provide the column names from
# your screenshot.
url =
"https://raw.githubusercontent.com/jbrownlee/Datasets/master/pima-
indians-diabetes.data.csv"
col_names = ['Pregnancies', 'Glucose', 'BloodPressure',
'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age',
'Outcome']
data = pd.read_csv(url, header=None, names=col_names)

print("--- Data Head ---")
print(data.head())
print("\n")

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--- Data Head ---

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	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

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# ---
# 2. Feature Selection (Independent vs. Dependent)
# ---
# 'Outcome' is the dependent (target) variable. All others are

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independent (features).
feature_cols = ['Pregnancies', 'Glucose', 'BloodPressure',
'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age']
X = data[feature_cols] # Independent variables
y = data.Outcome        # Dependent variable

# ---
# 3. Split Data and Build Decision Tree
# ---
# We'll split the data into 70% training and 30% testing
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.3, random_state=1)

# We will build two trees: one with Gini (the default) and one with
Entropy.
# We set max_depth=3 for a cleaner visualization.

# Building the tree using Gini Index
clf_gini = DecisionTreeClassifier(criterion="gini", max_depth=3,
random_state=1)
clf_gini.fit(X_train, y_train)

# Building the tree using Entropy (for Information Gain)
clf_entropy = DecisionTreeClassifier(criterion="entropy", max_depth=3,
random_state=1)
clf_entropy.fit(X_train, y_train)

DecisionTreeClassifier(criterion='entropy', max_depth=3,
random_state=1)

# ---
# 4. Visualization
# ---

# Visualize the Gini Tree
print("--- Displaying Gini Tree ---")
plt.figure(figsize=(15, 10))
plot_tree(clf_gini,
          filled=True,
          feature_names=feature_cols,
          class_names=['No Diabetes (0)', 'Diabetes (1)'],
          rounded=True)
plt.title("Decision Tree (Gini Index, max_depth=3)")
plt.show()

# Visualize the Entropy Tree
print("--- Displaying Entropy Tree ---")
plt.figure(figsize=(15, 10))
plot_tree(clf_entropy,
          filled=True,

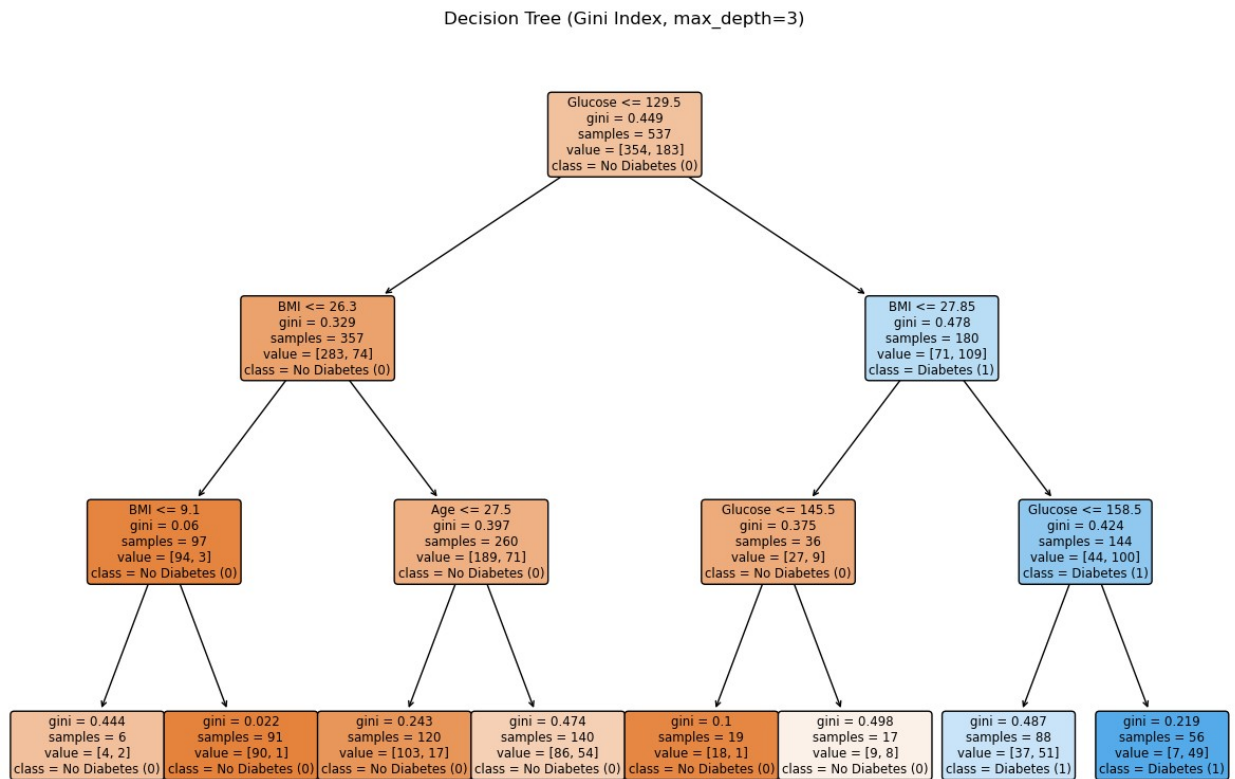
```

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feature_names=feature_cols,
class_names=['No Diabetes (0)', 'Diabetes (1)'],
rounded=True)
plt.title("Decision Tree (Entropy/Information Gain, max_depth=3)")
plt.show()

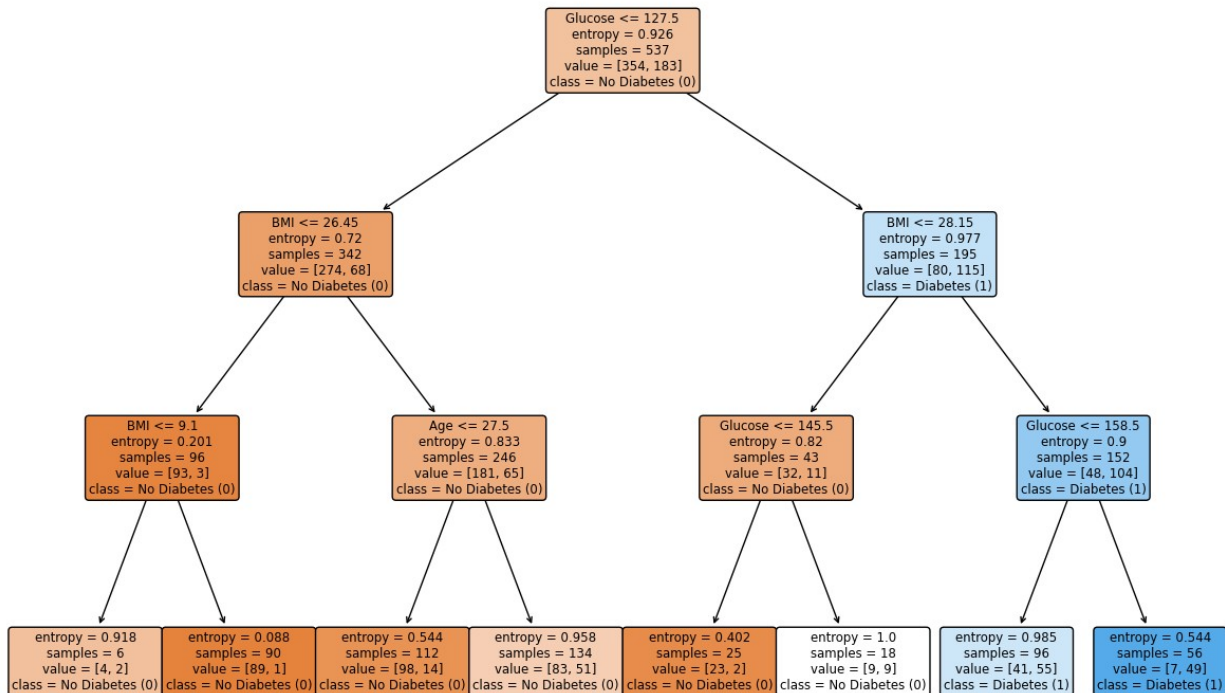
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--- Displaying Gini Tree ---



--- Displaying Entropy Tree ---

Decision Tree (Entropy/Information Gain, max\_depth=3)



## 5. Find Entropy, Information Gain, and Gini Index to support root node

Look at the root node (the very top box) of both trees you just plotted.

- Gini Tree Root Node:
- It will say something like "Glucose <= 127.5".
- It shows gini = 0.467 (or similar). This is the Gini impurity of all 537 samples in the training set.
- It shows samples = 537.
- Justification: "The algorithm chose 'Glucose' as the root node because splitting the dataset on the value '127.5' provided the greatest reduction in Gini Impurity compared to any other possible split on any other feature."
- Entropy Tree Root Node:
- It will also likely say "Glucose <= 127.5".
- It shows entropy = 0.952 (or similar). This is the Entropy of all 537 samples.
- Justification: "The algorithm chose 'Glucose' as the root node because splitting the dataset on the value '127.5' resulted in the highest Information Gain (the largest reduction in entropy) of all possible splits." The fact that Glucose is chosen by both

methods strongly supports that it is the single most informative feature to begin classifying the data

