

PREDICTIVE ANALYSIS WITH DECISION TREES

Submitted by:

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Class : CSE – ‘C’

Year : III

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1. Introduction

Predictive analytics focuses on analyzing historical data to predict future outcomes. Decision Trees are one of the most intuitive and powerful supervised learning algorithms used for both classification and regression tasks. They work by recursively splitting data based on feature values to maximize prediction accuracy.

2. Objectives

- Implement Decision Tree for classification
- Understand entropy and Gini index
- Apply pruning techniques to avoid overfitting
- Visualize the decision tree
- Evaluate feature importance

3. Dataset Description

The Heart Disease dataset consists of patient medical records used to predict the presence of heart disease. The dataset contains numerical and categorical attributes related to heart health.

4. Decision Tree Theory

4.1 Entropy

Entropy measures impurity or randomness.

$$\text{Entropy}(S) = -\sum p_i \log_2(p_i)$$

Where p_i is the probability of class i .

4.2 Information Gain

Used to decide the best feature to split.

$$IG(S, A) = Entropy(S) - \sum \frac{|S_v|}{|S|} Entropy(S_v)$$

4.3 Gini Index

Measures impurity (used by CART algorithm).

$$Gini = 1 - \sum p_i^2$$

Lower Gini \rightarrow better split.

5. Overfitting in Decision Trees

Decision trees tend to memorize training data leading to overfitting.

Solutions:

- **Pre-Pruning:** Stop tree growth early
- **Post-Pruning:** Remove unnecessary branches

6. Methodology

1. Load dataset
2. Preprocess data

3. Compute entropy and Gini manually
4. Train Decision Tree
5. Apply pruning
6. Evaluate performance
7. Visualize tree
8. Interpret feature importance

7. Tools & Technologies

- Python
- NumPy
- Pandas
- Scikit-learn
- Matplotlib
- Graphviz

8. Results

- Accuracy before pruning
- Accuracy after pruning
- Improved generalization
- Key features identified

9. Conclusion

Decision Trees provide interpretability and strong predictive performance. Pruning techniques significantly reduce overfitting and improve generalization.

10. Future Enhancements

- Use Random Forests
- Apply Gradient Boosting
- Hyperparameter tuning

Source Code:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

# 1. IMPORT LIBRARIES
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier, plot_tree
from sklearn.metrics import accuracy_score, classification_report
from sklearn.preprocessing import LabelEncoder

# 2. LOAD DATASET
df = pd.read_csv("heart.csv")
```

```
print("\nDataset Preview:")
display(df.head())
print("\nDataset Shape:", df.shape)

# FIX: HANDLE CATEGORICAL DATA

label_encoder = LabelEncoder()

for col in df.columns:
    if df[col].dtype == 'object':
        df[col] = label_encoder.fit_transform(df[col])

print("\nDataset After Encoding:")
display(df.head())

# 3. MATHEMATICAL CALCULATIONS

def entropy(y):
    values, counts = np.unique(y, return_counts=True)
    probabilities = counts / counts.sum()
    return -np.sum(probabilities * np.log2(probabilities))

def gini_index(y):
    values, counts = np.unique(y, return_counts=True)
    probabilities = counts / counts.sum()
    return 1 - np.sum(probabilities ** 2)

print("\nEntropy of Target:", entropy(df['target']))
```

```
print("Gini Index of Target:", gini_index(df['target']))  
  
# 4. FEATURE & TARGET SPLIT  
  
X = df.drop('target', axis=1)  
y = df['target']  
  
X_train, X_test, y_train, y_test = train_test_split(  
    X, y, test_size=0.2, random_state=42  
)  
  
# 5. DECISION TREE (NO PRUNING)  
  
dt_full = DecisionTreeClassifier(  
    criterion='gini',  
    random_state=42  
)  
  
dt_full.fit(X_train, y_train)  
y_pred_full = dt_full.predict(X_test)  
  
acc_full = accuracy_score(y_test, y_pred_full)  
print("\nAccuracy (No Pruning):", acc_full)  
  
# 6. PRE-PRUNING  
  
dt_pre_pruned = DecisionTreeClassifier(  
    criterion='gini',  
    max_depth=4,  
    min_samples_split=10,  
    random_state=42  
)
```

```
dt_pre_pruned.fit(X_train, y_train)

y_pred_pre = dt_pre_pruned.predict(X_test)

acc_pre = accuracy_score(y_test, y_pred_pre)
print("Accuracy (Pre-Pruning):", acc_pre)

# 7. POST-PRUNING
path = dt_full.cost_complexity_pruning_path(X_train, y_train)
ccp_alphas = path ccp_alphas

dt_post_pruned = DecisionTreeClassifier(
    random_state=42,
    ccp_alpha=ccp_alphas[5]
)

dt_post_pruned.fit(X_train, y_train)
y_pred_post = dt_post_pruned.predict(X_test)

acc_post = accuracy_score(y_test, y_pred_post)
print("Accuracy (Post-Pruning):", acc_post)

# 8. CLASSIFICATION REPORT
print("\nClassification Report (Pre-Pruned Model):")
print(classification_report(y_test, y_pred_pre))

# 9. DECISION TREE VISUALIZATION
plt.figure(figsize=(20, 10))
plot_tree(
```

```
dt_pre_pruned,  
feature_names=X.columns,  
class_names=['No Disease', 'Disease'],  
filled=True  
)  
plt.title("Decision Tree Visualization (Pre-Pruned)")  
plt.show()  
  
# 10. FEATURE IMPORTANCE  
feature_importance = pd.DataFrame({  
    'Feature': X.columns,  
    'Importance': dt_pre_pruned.feature_importances_  
}).sort_values(by='Importance', ascending=False)  
  
print("\nFeature Importance:")  
display(feature_importance)  
  
# 11. FEATURE IMPORTANCE VISUALIZATION  
plt.figure(figsize=(10, 5))  
plt.bar(feature_importance['Feature'], feature_importance['Importance'])  
plt.xticks(rotation=90)  
plt.title("Feature Importance Based on Decision Tree")  
plt.tight_layout()  
plt.show()  
  
# 12. ACCURACY COMPARISON  
models = ['No Pruning', 'Pre-Pruning', 'Post-Pruning']  
accuracies = [acc_full, acc_pre, acc_post]
```

```
plt.figure(figsize=(6, 4))

plt.bar(models, accuracies)

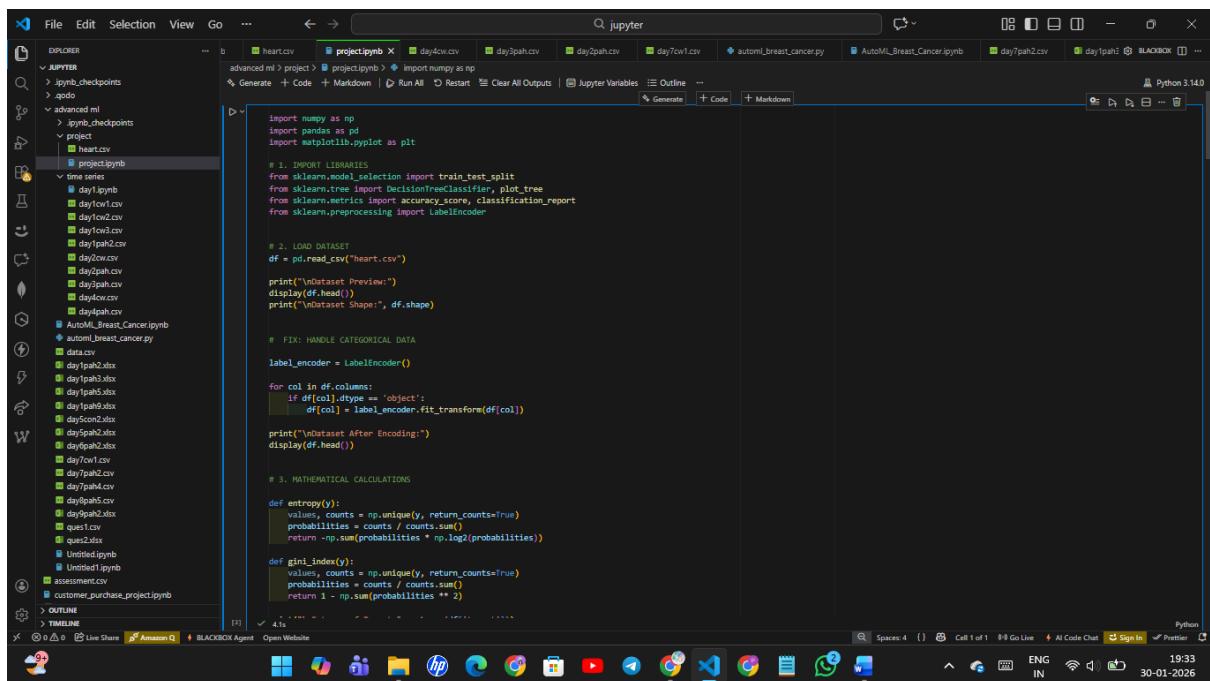
plt.ylabel("Accuracy")

plt.title("Decision Tree Model Accuracy Comparison")

plt.show()
```

```
print("\nPROJECT EXECUTED SUCCESSFULLY")
```

Screenshots:



```
# 4. FEATURE & TARGET SPLIT
X = df.drop(['target'], axis=1)
y = df['target']

X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=0.2, random_state=42
)

# 5. DECISION TREE (NO PRUNING)
dt_full = DecisionTreeClassifier(
    criterion='gini',
    random_state=42
)

dt_full.fit(X_train, y_train)
y_pred_full = dt_full.predict(X_test)

acc_full = accuracy_score(y_test, y_pred_full)
print("\nAccuracy (No Pruning):", acc_full)

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    max_depth=4,
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y_pred_pre = dt_pre_pruned.predict(X_test)

acc_pre = accuracy_score(y_test, y_pred_pre)
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    dt_pre_pruned,
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feature_importance = pd.DataFrame({
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}).sort_values(by='Importance', ascending=False)

print("\nFeature Importance:")
display(feature_importance)

# 11. FEATURE IMPORTANCE VISUALIZATION
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```

The screenshot shows a Jupyter Notebook environment with the following details:

- File Bar:** File, Edit, Selection, View, Go, <-, >, jupyter
- Left Sidebar (EXPLORER):** APYTER, .ipyw_checkpoints, .ipynb, .ipynb_checkpoints, project.ipynb, heart.csv, time series, day1.ipynb, day1c1w1.csv, day1c1w2.csv, day1c1w3.csv, day1pah1.csv, day1pah2.csv, day1c1w4.csv, day1pah3.csv, day1c1w5.csv, day1pah4.csv, day1c1w6.csv, day1pah5.csv, AutoML_Breast_Cancer.ipynb, AutoML_Breast_Cancer.py, breast_cancer.ipynb, breast_cancer.py, data.csv, day1.ipynb, day1pah2.ipynb, day1pah3.ipynb, day1pah5.ipynb, day1pah6.ipynb, day1c1w1.ipynb, day1c1w2.ipynb, day1c1w3.ipynb, day1c1w4.ipynb, day1c1w5.ipynb, day1c1w6.ipynb, ques1.csv, ques2.csv, ques3.ipynb, Limited.ipynb, Limited.ipynb, assessment.ipynb, customer_purchase_project.ipynb.
- Top Bar:** Python 3.14.0, Run All, Restart, Clear All Outputs, Jupyter Variables, Outline, Python 3.14.0, Python 3.14.0.
- Code Cell:** advanced ml > project.ipynb > Import numpy as np
Generate + Code + Markdown Run All Restart Clear All Outputs Jupyter Variables Outline
models = ['No Pruning' , 'Pre-Pruning' , 'Post-Pruning']
accuracies = [acc_full , acc_pre , acc_post]

plt.figure(figsize=(6, 4))
plt.bar(models, accuracies)
plt.ylabel("Accuracy")
plt.title("Decision Tree Model Accuracy Comparison")
plt.show()

print("\nPROJECT EXECUTED SUCCESSFULLY")
4.1s
- Dataset Preview:** Shows a table of 1025 rows and 14 columns. The columns are: age, sex, chest_pain_type, resting_blood_pressure, cholesterol, fasting_blood_sugar, rest_ecg, Max_heart_rate, exercise_induced_angina, oldpeak, slope, vessels_colored_by_fluoroscopy, thalassemia, target. The first few rows are:

	age	sex	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_ecg	Max_heart_rate	exercise_induced_angina	oldpeak	slope	vessels_colored_by_fluoroscopy	thalassemia	target
0	52	Male	Typical angina	125	212	Lower than 120 mg/ml	ST-T wave abnormality	168	No	1.0	Downsloping	Two	Reversible Defect	0
1	53	Male	Typical angina	140	203	Greater than 120 mg/ml	Normal	155	Yes	3.1	Upsloping	Zero	Reversible Defect	0
2	70	Male	Typical angina	145	174	Lower than 120 mg/ml	ST-T wave abnormality	125	Yes	2.6	Upsloping	Zero	Reversible Defect	0
3	61	Male	Typical angina	148	203	Lower than 120 mg/ml	ST-T wave abnormality	161	No	0.0	Downsloping	One	Reversible Defect	0
4	62	Female	Typical angina	138	294	Greater than 120 mg/ml	ST-T wave abnormality	106	No	1.9	Flat	Three	Fixed Defect	0

Dataset Shape: (1025, 14)

Dataset After Encoding:

	age	sex	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_ecg	Max_heart_rate	exercise_induced_angina	oldpeak	slope	vessels_colored_by_fluoroscopy	thalassemia	target
0	52	1	3	125	212	1	2	168	0	1.0	0	3	3	0
1	53	1	3	140	203	0	1	155	1	3.1	2	4	3	0
2	70	1	3	145	174	1	2	125	1	2.6	2	4	3	0
3	61	1	3	148	203	1	2	161	0	0.0	0	1	3	0
4	62	0	3	138	294	0	2	106	0	1.9	1	2	0	0

The screenshot shows a Jupyter Notebook environment with the following details:

- File Edit Selection View Go** menu bar.
- EXPLORER** sidebar with the following items:
 - heart.csv
 - project.ipynb (selected)
 - day4cw.csv
 - day5ph.csv
 - day2ph.csv
 - day7cv1.csv
 - automl_breast_cancer.py
 - AutoML_Breast_Cancer.ipynb
 - day7ph2.csv
 - day5ph2.ipynb
 - BLACKBOX.ipynb
- Python 3.14.0** kernel selected.
- Code Editor** showing the `project.ipynb` file content:
 - Imports: advanced ml, project.ipynb, import numpy as np.
 - Dataset Shape: (1025, 14).
 - Dataset After Encoding:

	age	sex	chest_pain_type	resting_blood_pressure	cholesterol	fasting_blood_sugar	rest_ecg	Max_heart_rate	exercise_induced_angina	oldpeak	slope	vessels_colored_by_fluoroscopy	thalassemia	target
0	52	1	3	125	212	1	2	168	0	1.0	0	3	3	0
1	53	1	3	140	203	0	1	155	1	3.1	2	4	3	0
2	70	1	3	145	174	1	2	125	1	2.6	2	4	3	0
3	61	1	3	148	203	1	2	161	0	0.0	0	1	3	0
4	62	0	3	138	294	0	2	106	0	1.9	1	2	0	0

 - Entropy of Target: 0.9994994187527655
 - Gini Index of Target: 0.40965306365258777
 - Accuracy (No Pruning): 0.8485585836585366
 - Accuracy (Pre-Pruning): 0.82439802439802439
 - Accuracy (Post-Pruning): 0.9317873170731708
 - Classification Report (Pre-Pruned Model):

	precision	recall	f1-score	support
0	0.91	0.72	0.88	182
1	0.77	0.93	0.84	183

 - accuracy: 0.85
macro avg: 0.84
weighted avg: 0.84
 - Decision Tree Visualization (Pre-Pruned) button.

