# Applications of ML HW 2

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Part 2:
Code:
from sklearn import tree
from sklearn.metrics import accuracy score, precision score, recall score, f1 score,
confusion matrix
import pandas as pd
import pydotplus
def writegraphtofile(clf, featurelabels, filename):
  dot data = tree.export graphviz(clf, feature names=featurelabels, out file=None)
  graph = pydotplus.graph from dot data(dot data)
  graph.write png(filename)
data = pd.read excel("AlienMushrooms.xlsx")
clf = tree.DecisionTreeClassifier(criterion="entropy")
feature labels = data.columns[:-1]
features = data[feature_labels]
target label = data.columns[-1]
target = data[target label]
clf.fit(features, target)
writegraphtofile(clf, feature labels, "Assignment 2" + "tree pic.png")
predictions = clf.predict(features)
# Calculate metrics
accuracy = accuracy_score(target, predictions)
precision = precision score(target, predictions, average='macro') # Use 'macro' for multi-class
classification
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recall = recall score(target, predictions, average='macro')

f1 = f1\_score(target, predictions, average='macro')
conf matrix = confusion matrix(target, predictions)

# Print the metrics

print(f"Accuracy: {accuracy:.4f}")
print(f"Precision: {precision:.4f}")

print(f"Recall: {recall:.4f}")
print(f"F1 Score: {f1:.4f}")
print("Confusion Matrix:")

print(conf matrix)

## Console Output:

/usr/local/bin/python3.11

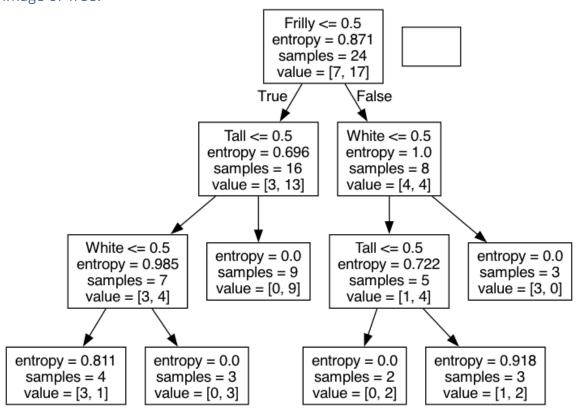
/Users/srilalithnampally/Classes/AppML\_Assignments/Assignment\_2/Q2.py

Accuracy: 0.9167 Precision: 0.8992 Recall: 0.8992 F1 Score: 0.8992 Confusion Matrix:

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Process finished with exit code 0

## Image of Tree:



### Discussion on Part 1 Tree vs Part 2 Tree:

The tree structure produced from manual calculations is identical to that generated by the software. However, there appears to be a labeling reversal in the code-generated tree, where 'Frilly=0' is labeled as True and 'Frilly=1' as False, which might make the manually calculated tree seem like a mirror image of the software-generated one. Upon examining the tree's leaves, it's evident that nodes with zero entropy are reached at the same decision level in both trees. Additionally, the manual calculations accurately reflect the count of samples filtered at each decision point.

## Part 3:

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Code:
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```
import numpy as np
from sklearn import tree
from sklearn.preprocessing import OneHotEncoder
from sklearn.preprocessing import OrdinalEncoder
from sklearn.impute import SimpleImputer
from sklearn.pipeline import Pipeline
from sklearn.compose import ColumnTransformer
from sklearn.model selection import train test split
from sklearn.metrics import accuracy score
import pandas as pd
import pydotplus
def loadData(filename):
  # Load data
  data = pd.read excel(filename)
  return data
def writegraphtofile(clf, featurelabels, filename):
  dot data = tree.export graphviz(clf, feature names=featurelabels, out file=None)
  graph = pydotplus.graph from dot data(dot data)
  graph.write png(filename)
def preprocessData(data):
  mix col = []
  for col in data.columns:
    unique types = data[col].apply(type).unique()
    if len(unique types) > 1:
      mix col.append(col)
  data[mix col] = data[mix col].astype(str)
  data.replace("?", np.nan, inplace=True)
  # Separate features and target
  X = data.iloc[:, :-1] # All columns except the last one
  y = data.iloc[:, -1] # The last column
  X = X.drop(['encounter_id', 'patient_nbr'], axis=1)
  # Identify categorical columns (modify this list based on your dataset)
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categorical_features = ["race", "gender", "age", "weight", "admission_type_id",
"discharge disposition id",
               "admission_source_id", "payer_code", "medical_specialty", "diag_1", "diag_2",
"diag 3",
               'max glu serum', 'A1Cresult', 'change', 'diabetesMed'] # Example column
names
  # Identify Ordinal columns (for medications)
  ordinal features medications = ['metformin', 'repaglinide', 'nateglinide', 'chlorpropamide',
'glimepiride',
                    'acetohexamide', 'glipizide', 'glyburide', 'tolbutamide', 'pioglitazone',
                    'rosiglitazone', 'acarbose', 'miglitol', 'troglitazone', 'tolazamide', 'examide',
                    'citoglipton', 'insulin', 'glyburide-metformin', 'glipizide-metformin',
                    'glimepiride-pioglitazone', 'metformin-rosiglitazone', 'metformin-
pioglitazone', ]
  medication order = [['No', 'Steady', 'Up', 'Down']]
  medication order for all columns = medication order * len(ordinal features medications)
  # Imputers for categorical and ordinal features
  categorical imputer = SimpleImputer(strategy='constant', fill value='unknown')
  ordinal imputer = SimpleImputer(strategy='most frequent')
  # Identify numerical columns (assuming all other columns are numerical if not categorical or
ordinal)
  numerical features = [col for col in X.columns if col not in categorical features +
ordinal features medications]
  # Imputers
  numerical imputer = SimpleImputer(strategy='mean') # Impute numerical columns with their
mean
  # Encoder
  one hot encoder = OneHotEncoder()
  ordinal encoder = OrdinalEncoder(categories=medication order for all columns)
  # Update ColumnTransformer to include numerical imputation
  preprocessor = ColumnTransformer(
    transformers=[
      ('cat', Pipeline([('imputer', categorical imputer), ('encoder', one hot encoder)]),
categorical features),
      ('ord meds', Pipeline([('imputer', ordinal imputer),
                   ('encoder', ordinal encoder)]),
       ordinal features medications),
      ('num', numerical imputer, numerical features)
```

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1,
    remainder='passthrough' # Ensure no column is left unprocessed
  # Check for NaN values post-imputation
  print("Finished Pre-Processing, Starting Transformation")
  # Apply transformations
  X_encoded = preprocessor.fit_transform(X)
  # Extracting new feature names after preprocessing
  feature_names = []
  # Getting feature names for categorical features
  for cat_feature, one_hot in zip(categorical_features,
                    preprocessor.named transformers ['cat']['encoder'].categories ):
    feature names.extend([f"{cat feature} {category}" for category in one hot])
  # Adding ordinal feature names as is
  feature names.extend(ordinal features medications)
  # Adding numerical feature names as is
  feature names.extend(numerical features)
  print("Finished Transformation of dataset")
  return X encoded, y, feature names
def MultiClassPrediction(X encoded, y):
  # Split data for the multiclass classification model
  X_train_multi, X_test_multi, y_train_multi, y_test_multi = train_test_split(X_encoded, y,
test size=0.2,
                                            random state=42)
  # Initialize and train the multiclass classifier
  clf multiclass = tree.DecisionTreeClassifier(criterion="entropy", max depth=4)
  clf_multiclass.fit(X_train_multi, y_train_multi)
  # Predictions for multiclass classification
  predictions multi = clf multiclass.predict(X test multi)
  predictions multi train = clf multiclass.predict(X train multi)
  # Evaluate the multiclass model
  accuracy multi = accuracy score(y test multi, predictions multi)
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print(f"Multiclass Classification Accuracy with Test Set: {accuracy multi:.4f}")
  accuracy_multi_train = accuracy_score(y_train_multi, predictions_multi_train)
  print(f"Multiclass Classification Accuracy with Train Set: {accuracy multi train:.4f}")
  # Plotting the multiclass classification tree
  return clf multiclass
def BinaryClassification(X encoded, y):
  # Binary target preprocessing
  y binary = y.replace({'NO': 0, '<30': 1, '>30': 1})
  # Split data for the binary classification model
  X train bin, X test bin, y train bin, y test bin = train test split(X encoded, y binary,
test size=0.2,
                                        random state=42)
  # Initialize and train the binary classifier
  clf binary = tree.DecisionTreeClassifier(criterion="entropy", max depth=4)
  clf binary.fit(X train bin, y train bin)
  # Predictions for binary classification
  predictions bin test = clf binary.predict(X test bin)
  predictions_bin_train = clf_binary.predict(X_train_bin)
  # Evaluate the binary model
  accuracy bin test = accuracy score(y test bin, predictions bin test)
  print(f"Binary Classification Accuracy with Test Set: {accuracy bin test:.4f}")
  accuracy bin train = accuracy score(y train bin, predictions bin train)
  print(f"Binary Classification Accuracy with Train Set: {accuracy bin train:.4f}")
  # Plotting the binary classification tree
  return clf binary
if __name__ == "__main__":
  file location = "diabetic data.xlsx"
  dataframe = loadData(file location) # created a dataframe
  feature_labels = dataframe.columns[:-1].tolist()
  X, Y, feature names = preprocessData(dataframe) # Preprocessing the dataframe, and
obtaining (features, target)
  print("Dataset Is Ready \n")
```

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clf_binary = BinaryClassification(X, Y)
writegraphtofile(clf_binary, feature_names, "Assignment_2" + "tree_pic_binary.png")
clf_multiclass = MultiClassPrediction(X, Y)
writegraphtofile(clf_multiclass, feature_names, "Assignment_2" + "tree_pic_multiclass.png")
```

## Console Output:

/usr/local/bin/python3.11
/Users/srilalithnampally/Classes/AppML\_Assignments/Assignment\_2/Q3.py
Finished Pre-Processing, Starting Transformation
Finished Transformation of dataset
Dataset Is Ready

#### **Training Dataset**

 $/Users/srilal ithnampally/Classes/AppML\_Assignments/Assignment\_2/Q3.py:130:$ 

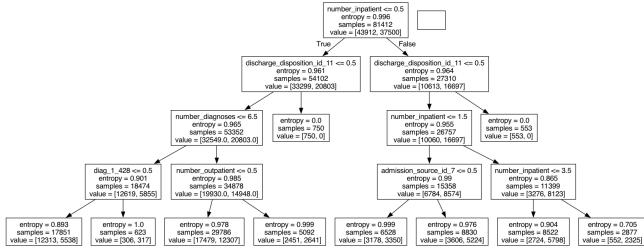
FutureWarning: Downcasting behavior in `replace` is deprecated and will be removed in a future version. To retain the old behavior, explicitly call `result.infer\_objects(copy=False)`. To opt-in to the future behavior, set `pd.set\_option('future.no\_silent\_downcasting', True)`

y\_binary = y.replace({'NO': 0, '<30': 1, '>30': 1})
Binary Classification Accuracy with Test Set: 0.6209
Binary Classification Accuracy with Train Set: 0.6234
Multiclass Classification Accuracy with Test Set: 0.5748
Multiclass Classification Accuracy with Train Set: 0.5735

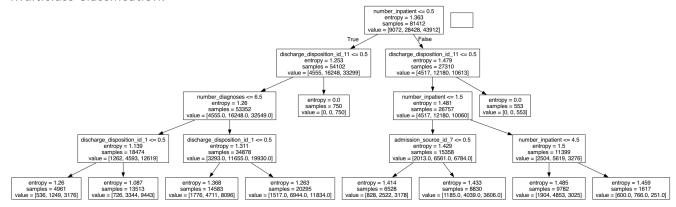
Process finished with exit code 0

#### Images Generated:

Binary Classification:



#### Multiclass Classification:



#### Discussion on the differences between the Trees:

- Entropy: The multi-class tree has higher entropy values, indicating more complexity and less purity at each node compared to the binary tree.
- Leaf Purity: The binary tree has leaves with zero entropy, showing perfect class separation, while the multi-class tree does not, suggesting some classes remain mixed at the leaves.
- Class Counts in Leaves: The binary tree's leaves show counts for two classes, whereas
  the multi-class tree's leaves have counts for multiple classes, reflecting the complexity of
  separating more classes.
- Tree Structure: The binary tree might be simpler with fewer splits to achieve class separation, while the multi-class tree may require more splits to handle additional classes.
- Decision Boundaries: The binary tree suggests clearer decision boundaries with leaves
  often fully belonging to one class, whereas the multi-class tree indicates less distinct
  boundaries due to the presence of multiple classes.