Sri Sivasubramaniya Nadar College of Engineering, Kalavakkam – 603 110

(An Autonomous Institution, Affiliated to Anna University, Chennai)

UCS2612 Machine Learning Laboratory

Academic Year: 2023-2024 Even Batch: 2021-2025 Faculty In-charges: Y.V. Lokeswari VI Semester A

Assignment 7: Predicting Diabetes using decision tree

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• Aim:-

To 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.

Code:-

from sklearn.preprocessing import LabelEncoder from sklearn.preprocessing import MinMaxScaler import pandas as pd from sklearn.metrics import accuracy_score import seaborn as sns import matplotlib.pyplot as plt from sklearn.tree import DecisionTreeClassifier from sklearn.model_selection import train_test_split

• Loading dataset

df = pd.read_csv('diabetes_prediction_dataset.csv') df.head(10)

[3]:	gender	age	hypertension	heart_disease	smoking_history	bmi	HbA1c_level	blood_glucose_level	diabetes
0	Female	80.0	0	1	never	25.19	6.6	140	0
1	Female	54.0	0	0	No Info	27.32	6.6	80	0
2	Male	28.0	0	0	never	27.32	5.7	158	0
3	Female	36.0	0	0	current	23.45	5.0	155	0
4	Male	76.0	1	1	current	20.14	4.8	155	0
5	Female	20.0	0	0	never	27.32	6.6	85	0
6	Female	44.0	0	0	never	19.31	6.5	200	1
7	Female	79.0	0	0	No Info	23.86	5.7	85	0
8	Male	42.0	0	0	never	33.64	4.8	145	0
9	Female	32.0	0	0	never	27.32	5.0	100	0

Preprocessing

#Checking Null
any_null = df.isnull().any()
print(any_null)

```
gender
                     False
                     False
hypertension
                     False
heart_disease
                     False
smoking history
                    False
                     False
HbA1c_level
                    False
blood_glucose_level False
diabetes
                    False
dtype: bool
```

```
#Encoding
label_encoder = LabelEncoder()
df['smoking_history'] = label_encoder.fit_transform(df['smoking_history'])
df['gender'] = label_encoder.fit_transform(df['gender'])
df.head(10)
```

	gender	age	hypertension	heart_disease	smoking_history	bmi	HbA1c_level	blood_glucose_level	diabetes
0	0	80.0	0	1	4	0.177171	0.563636	0.272727	0
1	0	54.0	0	0	0	0.202031	0.563636	0.000000	0
2	1	28.0	0	0	4	0.202031	0.400000	0.354545	0
3	0	36.0	0	0	1	0.156863	0.272727	0.340909	0
4	1	76.0	1	1	1	0.118231	0.236364	0.340909	0
5	0	20.0	0	0	4	0.202031	0.563636	0.022727	0
6	0	44.0	0	0	4	0.108543	0.545455	0.545455	1
7	0	79.0	0	0	0	0.161648	0.400000	0.022727	0
8	1	42.0	0	0	4	0.275794	0.236364	0.295455	0
9	0	32.0	0	0	4	0.202031	0.272727	0.090909	0

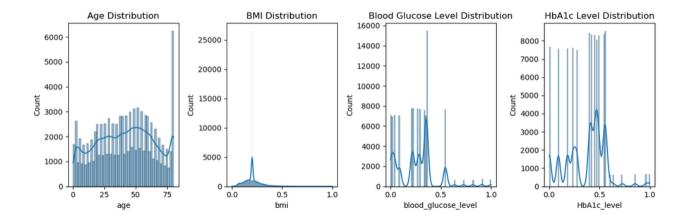
```
#Scaling
scaler = MinMaxScaler()
# Specify columns to scale
columns_to_scale = ['bmi','HbA1c_level', 'blood_glucose_level']
```

[100000 rows x 9 columns]

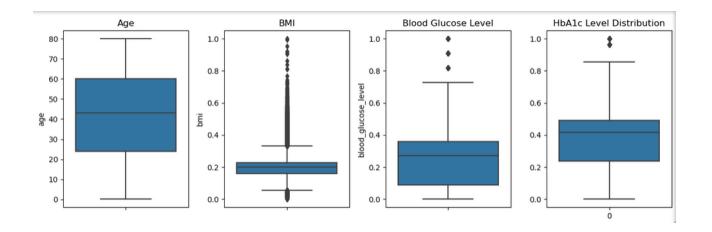
iic —	LOIII	.,		, blood		CVCI		
	gender	age	hypertension he	art_disease	smoking_history	bmi	\	df[columns_to_scale
0	0	80.0	0	1	4	0.177171		
1	0	54.0	0	0	0	0.202031		=
2	1	28.0	Θ	Θ	4	0.202031		1 6 (
3	0	36.0	0	0	1	0.156863		scaler.fit_transform(
4	1	76.0	1	1	1	0.118231		· ·
								df[columns to scale
99995	0	80.0	0	0	0	0.202031		_ = =
99996	0	2.0	Θ	Θ	0	0.085901		1)
99997	1	66.0	0	0	3	0.207983		"D' 1 1 1 1 1
99998	0	24.0	0	0	4	0.296569		# Display the scaled
99999	0	57.0	0	0	1	0.144958		* *
								DataFrame
	HbA1c_l	evel	blood_glucose_lev	el diabetes				/(10)
Θ	0.56	3636	0.2727	27 Θ				print(df)
1	0.56	3636	0.0000	00 0				1 , ,
2	0.40	0000	0.3545	45 0				
3	0.27	2727	0.3409	09 0				
4	0.23	6364	0.3409	09 0				
99995	0.49	0909	0.0454	55 0				
99996	0.54	5455	0.0909	09 0				
99997	0.40	0000	0.3409	09 0				
99998	0.09	0909	0.0909	09 0				
99999	0.56	3636	0.0454	55 0				

• Exploratory Data Analysis

```
# Distribution plots
plt.figure(figsize=(12, 4))
plt.subplot(1, 4, 1)
sns.histplot(df['age'], kde=True)
plt.title('Age Distribution')
plt.subplot(1, 4, 2)
sns.histplot(df['bmi'], kde=True)
plt.title('BMI Distribution')
plt.subplot(1, 4, 3)
sns.histplot(df['blood_glucose_level'], kde=True)
plt.title('Blood Glucose Level Distribution')
plt.subplot(1, 4, 4)
sns.histplot(df['HbA1c_level'], kde=True)
plt.title('HbA1c Level Distribution')
plt.tight_layout()
plt.show()
```



```
# Box plots
plt.figure(figsize=(12, 4))
plt.subplot(1, 4, 1)
sns.boxplot(y=df['age'])
plt.title('Age')
plt.subplot(1, 4, 2)
sns.boxplot(y=df['bmi'])
plt.title('BMI')
plt.subplot(1, 4, 3)
sns.boxplot(y=df['blood_glucose_level'])
plt.title('Blood Glucose Level')
plt.subplot(1, 4, 4)
sns.boxplot(df['HbA1c_level'])
plt.title('HbA1c Level Distribution')
plt.tight_layout()
plt.show()
```



Decision Tree Algorithm before feature selection

```
X = df.drop(columns=['diabetes'])
y = df['diabetes']
X train, X test, y train, y test = train test split(X, y, test size=0.3, random state=42)
dt_model_entropy = DecisionTreeClassifier(criterion='entropy', random_state=42)
dt_model_entropy.fit(X_train, y_train)
# Evaluate Decision Tree model using Entropy
y_pred_entropy = dt_model_entropy.predict(X_test)
accuracy entropy = accuracy score(y test, y pred entropy)
print("Accuracy using Entropy:", accuracy_entropy)
# Train Decision Tree model using Gini-index
dt_model_gini = DecisionTreeClassifier(criterion='gini', random_state=42)
dt_model_gini.fit(X_train, y_train)
# Evaluate Decision Tree model using Gini-index
y pred gini = dt model gini.predict(X test)
accuracy_gini = accuracy_score(y_test, y_pred_gini)
print("Accuracy using Gini-index:", accuracy gini)
            Accuracy using Entropy: 0.9542333333333334
```

Accuracy using Gini-index: 0.9530666666666666

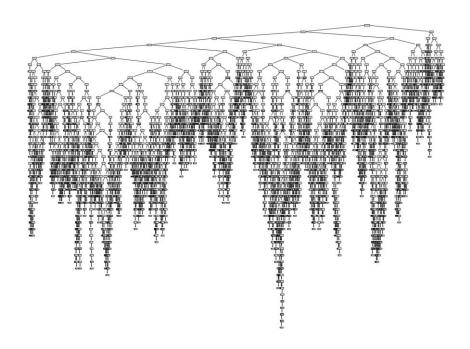
Feature selection

```
top_k = 3
top_features_indices = feature_importances.argsort()[-top_k:][::-1]
```

```
# Get names of top features
top_features_names = X.columns[top_features_indices]
print("Top", top_k, "features:", top_features_names)
# Rebuild model with selected features
X train selected = X train.iloc[:, top features indices]
X_test_selected = X_test.iloc[:, top_features_indices]
# Retrain the model using selected features
dt model selected = DecisionTreeClassifier(random_state=42)
dt_model_selected.fit(X_train_selected, y_train)
          Top 3 features: Index(['HbA1c_level', 'blood_glucose_level', 'bmi'], dtype='object')
dt_model_entropy_sel = DecisionTreeClassifier(criterion='entropy', random_state=42)
dt model entropy sel.fit(X train selected, y train)
# Evaluate Decision Tree model using Entropy
y_pred_entropy = dt_model_entropy_sel.predict(X_test_selected)
accuracy_entropy = accuracy_score(y_test, y_pred_entropy)
print("Accuracy using Entropy:", accuracy_entropy)
   • Decision Tree Algorithm after feature selection
# Train Decision Tree model using Gini-index
dt model gini sel = DecisionTreeClassifier(criterion='gini', random state=42)
dt_model_gini_sel.fit(X_train_selected, y_train)
  Accuracy using Entropy: 0.9555666666666667
Evaluate Decision Tree model using Gini-index
y_pred_gini = dt_model_gini_sel.predict(X_test_selected)
accuracy gini = accuracy score(y test, y pred gini)
print("Accuracy using Gini-index:", accuracy_gini)
Accuracy using Gini-index: 0.955166666666667
```

• Decision Tree

```
fig = plt.figure(figsize=(20,15))
tree.plot_tree(dt_model_entropy);
```



• Inference:

1. Accuracy using Entropy impurity measure without Feature Selction: 0.95423333333333334

Accuracy using Gini-index impurity measure without Feature Selection: 0.95306666666666666

2. Accuracy using Entropy impurity measure with Feature Selction(n=3): 0.9555666666666667

3. Accuracy using Entropy and gini-index impurity measure with Feature (n>3) goes below 0.93 as n increases

Therefore, we can obseve that the accuracy of the decision tree classifier using Gini-index and Entropy using feature selection gives higher accuracy if we choose the number of features correctly. But, we can also see that without applying feature selection, itself we can obtain better entropy and gini-index measures.

• Github Link:

https://github.com/gk3204/ML-Assignment7

• Learning Outcomes:

- 1. Applying standardization, normalization and other pre-processing techniques.
- 2. Understanding Decision Tree classifier Algorithm.
- 3. Implementing decision tree classifier model.
- 4. Implementing the decision tree model with & without using feature selection.