AI BASED DIABETES PREDICTION

TEAM MEMBER

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PHASE 3 PROJECT SUBMISSION

INTRODUCTION



In AI-based diabetes prediction, data loading and preprocessing are crucial steps to ensure the accuracy and reliability of your predictive model. Here's a step-by-step guide on how to load and preprocess data for diabetes prediction:

1. Data Collection

- First, you need to obtain a dataset that contains relevant information about individuals, such as age, gender, body mass index (BMI), blood pressure, glucose levels, and whether they have diabetes or not. You can find such datasets from sources like the UCI Machine Learning Repository or government health agencies.

2. Data Loading

- Import necessary libraries such as pandas and numpy in Python. ```python import pandas as pd import numpy as np
- Load your dataset into a pandas DataFrame. Here's an example of loading a CSV file:

```
'``python

data = pd.read csv('diabetes dataset.csv')
```

PROGRAM

1. Import the important

Libraries In [1]:

import pandas as pd import numpy as np import matplotlib.pyplot as plt import seaborn as sns from statistics import mean, stdev from sklearn.model selection import StratifiedKFold from sklearn.preprocessing import StandardScaler from sklearn.model selection import GridSearchCV, cross val score from sklearn.metrics import confusion matrix, accuracy score, mean squared error from sklearn.linear model import LogisticRegression from sklearn.metrics import accuracy score from sklearn.neighbors import KNeighborsClassifier from sklearn.svm import SVC from sklearn.tree import **DecisionTreeClassifier** from sklearn.ensemble import RandomForestClassifier from sklearn.ensemble import GradientBoostingClassifier from lightgbm import LGBMClassifier import warnings warnings.filterwarnings("ignore", category=DeprecationWarning) warnings.filterwarnings("ignore", category=FutureWarning) warnings.filterwarnings("ignore", category=UserWarning)

2. Loading the Dataset

In [2]:

diabetes = pd.read_csv("/kaggle/input/diabetesdataset/diabetes.csv")

3. Inspecting the

Dataset In [3]:

diabetes.head()

Out[3]:

	Pregnancie s	Glucos e	BloodPressur e	SkinThicknes s	Insuli n	BMI	DiabetesPedigreeFunctio n	Ag e	Outcom e
0	6	148	72	35	0	33. 6	0.627	50	1
	Pregnancie s	Glucos e	BloodPressur e	SkinThicknes s	Insuli n	BMI	DiabetesPedigreeFunctio n	Ag e	Outcom e
1	1	85	66	29	0	26. 6	0.351	31	0
2	8	183	64	0	0	23.	0.672	32	1

3	1	89	66	23	94	28.	0.167	21	0
4	0	137	40	35	168	43.	2.288	33	1

In [4]:

diabetes.info()

<class 'pandas.core.frame.DataFrame'>

RangeIndex: 768 entries, 0 to 767 Data

columns (total 9 columns):

#	Column	Non-Null Count Dtype					
0	Pregnancies	768 non-null	int64				
1	Glucose	768 non-null	int64				
2	BloodPressure	768 non-null	int64				

3 SkinThickness 768 non-null int64

4 Insulin 768 non-null int64

5 BMI 768 non-null float64

6 DiabetesPedigreeFunction 768 non-null float64

7 Age 768 non-null int64 8

Outcome 768 non-null int64

dtypes: float64(2), int64(7) memory

usage: 54.1 KB

In [5]:

diabetes.describe() Out[5]:

	Pregnan cies	Glucose	BloodPres sure	SkinThick ness	Insulin	ВМІ	DiabetesPedigreeF unction	Age	Outcom e
cou nt	768.000 000	768.000 000	768.00000 0	768.0000 00	768.000 000	768.000 000	768.000000	768.000 000	768.000 000
me an	3.84505 2	120.894 531	69.105469	20.53645	79.7994 79	31.9925 78	0.471876	33.2408 85	0.34895 8
std	3.36957 8	31.9726 18	19.355807	15.95221 8	115.244 002	7.88416 0	0.331329	11.7602 32	0.47695 1
min	0.00000	0.00000	0.000000	0.000000	0.00000	0.00000	0.078000	21.0000 00	0.00000
25%	1.00000	99.0000 00	62.000000	0.000000	0.00000	27.3000 00	0.243750	24.0000 00	0.00000
50%	3.00000	117.000 000	72.000000	23.00000	30.5000 00	32.0000 00	0.372500	29.0000 00	0.00000
75%	6.00000	140.250	80.000000	32.00000	127.250	36.6000	0.626250	41.0000	1.00000

	Pregnan cies	Glucose	BloodPres sure	SkinThick ness	Insulin	ВМІ	DiabetesPedigreeF unction	Age	Outcom e
	0	000		0	000	00		00	0
max	17.0000 00	199.000 000	122.00000 0	99.00000	846.000 000	67.1000 00	2.420000	81.0000 00	1.00000

3. Data Exploration

- Explore your dataset to understand its structure and characteristics. This can include checking for missing values, understanding the distribution of features, and performing descriptive statistics.

```python

# Check for missing values

print(data.isnull().sum

# 4. Data Preprocessing:

- Data preprocessing is essential to clean and transform the data for machine learning. Common preprocessing steps include:

- Handling Missing Values: You can either remove rows with missing data or impute missing values using techniques like mean, median, or machine learning-based imputation.

  Python data = data.dropna()
- Encoding Categorical Variables: If your dataset contains categorical variables (e.g., gender), you may need to encode them into numerical values using one-hot encoding or label encoding. ```python

data = pd.get\_dummies(data, columns=['gender'],
drop first=True) # One-hot encoding

## **INPUT**:

diabetes.drop\_duplicates()

# Out[6]:

| Pregnancie<br>s | Glucos<br>e | BloodPressur<br>e | SkinThicknes<br>s | Insuli<br>n | BMI | DiabetesPedigreeFunctio<br>n | Ag<br>e | Outcom<br>e |
|-----------------|-------------|-------------------|-------------------|-------------|-----|------------------------------|---------|-------------|
|                 |             |                   |                   |             |     |                              |         |             |

|         | Pregnancie<br>s | Glucos<br>e | BloodPressur<br>e | SkinThicknes<br>s | Insuli<br>n | BMI      | DiabetesPedigreeFunctio<br>n | Ag<br>e | Outcom<br>e |
|---------|-----------------|-------------|-------------------|-------------------|-------------|----------|------------------------------|---------|-------------|
| 0       | 6               | 148         | 72                | 35                | 0           | 33.<br>6 | 0.627                        | 50      | 1           |
| 1       | 1               | 85          | 66                | 29                | 0           | 26.<br>6 | 0.351                        | 31      | 0           |
| 2       | 8               | 183         | 64                | 0                 | 0           | 23.      | 0.672                        | 32      | 1           |
| 3       | 1               | 89          | 66                | 23                | 94          | 28.      | 0.167                        | 21      | 0           |
| 4       | 0               | 137         | 40                | 35                | 168         | 43.      | 2.288                        | 33      | 1           |
|         |                 |             |                   |                   |             |          |                              |         |             |
| 76<br>3 | 10              | 101         | 76                | 48                | 180         | 32.<br>9 | 0.171                        | 63      | 0           |
| 76<br>4 | 2               | 122         | 70                | 27                | 0           | 36.<br>8 | 0.340                        | 27      | 0           |

| 76<br>5 | 5               | 121         | 72                | 23                | 112         | 26.<br>2 | 0.245                        | 30      | 0           |
|---------|-----------------|-------------|-------------------|-------------------|-------------|----------|------------------------------|---------|-------------|
|         | Pregnancie<br>s | Glucos<br>e | BloodPressur<br>e | SkinThicknes<br>s | Insuli<br>n | BMI      | DiabetesPedigreeFunctio<br>n | Ag<br>e | Outcom<br>e |
| 76<br>6 | 1               | 126         | 60                | 0                 | 0           | 30.<br>1 | 0.349                        | 47      | 1           |
| 76<br>7 | 1               | 93          | 70                | 31                | 0           | 30.<br>4 | 0.315                        | 23      | 0           |

 $768 \text{ rows} \times 9 \text{ columns}$ 

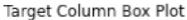
#### 4.1 Outliers

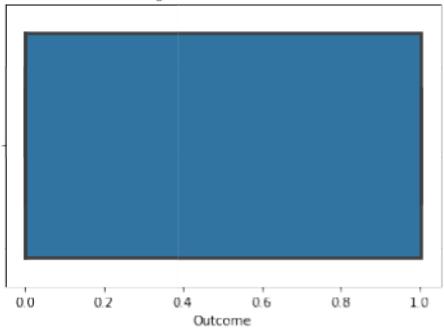
Checking for outliers using the box plot.

In [7]:

linkcode

```
#first store the features in a seperate dataframe. features = diabetes.drop("Outcome",axis = 1).copy() #Now plot a boxplot to identify the outliers in our features. sns.boxplot(data = features, orient = 'h', palette = 'Set3', linewidth = 2.5) plt.title("Features Box Plot") Out[7]: Text(0.5, 1.0, 'Features Box Plot')
```





from scipy import stats def

removeoutliers(df=None, columns=None):

for column in columns:

Q1 = df[column].quantile(0.25)

Q3 = df[column].quantile(0.75)

IQR = Q3 - Q1

floor, ceil = Q1 - 1.5 \* IQR, Q3 + 1.5 \* IQR

df[column] = df[column].clip(floor, ceil)

print(f"The columnn: {column}, has been treated for outliers.\n")

### return df

diabetes = removeoutliers(diabetes,[col for col in features.columns])

The column: Pregnancies, has been treated for outliers.

The columnn: Glucose, has been treated for outliers.

The column: BloodPressure, has been treated for outliers.

The columnn: SkinThickness, has been treated for outliers.

The column: Insulin, has been treated for outliers.

The column: BMI, has been treated for outliers.

The column: DiabetesPedigreeFunction, has been treated for outliers.

The column: Age, has been treated for outliers.

In [10]:

sns.boxplot(data = diabetes, orient = 'h', palette = 'Set3', linewidth = 2.5)

plt.title("Box Plot after treating outliers")

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