AI-BASED DIABETES PREDICTION SYSTEM

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Phase 3 Submission Document:

PROJECT TITLE:Diabetes Prediction System

PHASE 3: Development Part 1

TOPIC: *Start building the AI-Based Diabetes Prediction System by loading and preprocessing the dataset*

Diabetes Prediction System:

Introduction:

- ❖ The development of a diabetes prediction system is a crucial step in leveraging technology to improve healthcare outcomes. With the increasing prevalence of diabetes worldwide, such a system holds immense promise in early detection and prevention.

- ❖ In this endeavor, we aim to harness the power of data analytics, machine learning, and medical expertise to create a robust predictive tool. This system will not only aid individuals in assessing their risk of diabetes but also assist healthcare providers in delivering personalized care and interventions.

- ❖ In this introduction, we will explore the significance of such a system, the underlying technology, and the potential benefits it can bring to individuals and the healthcare ecosystem.

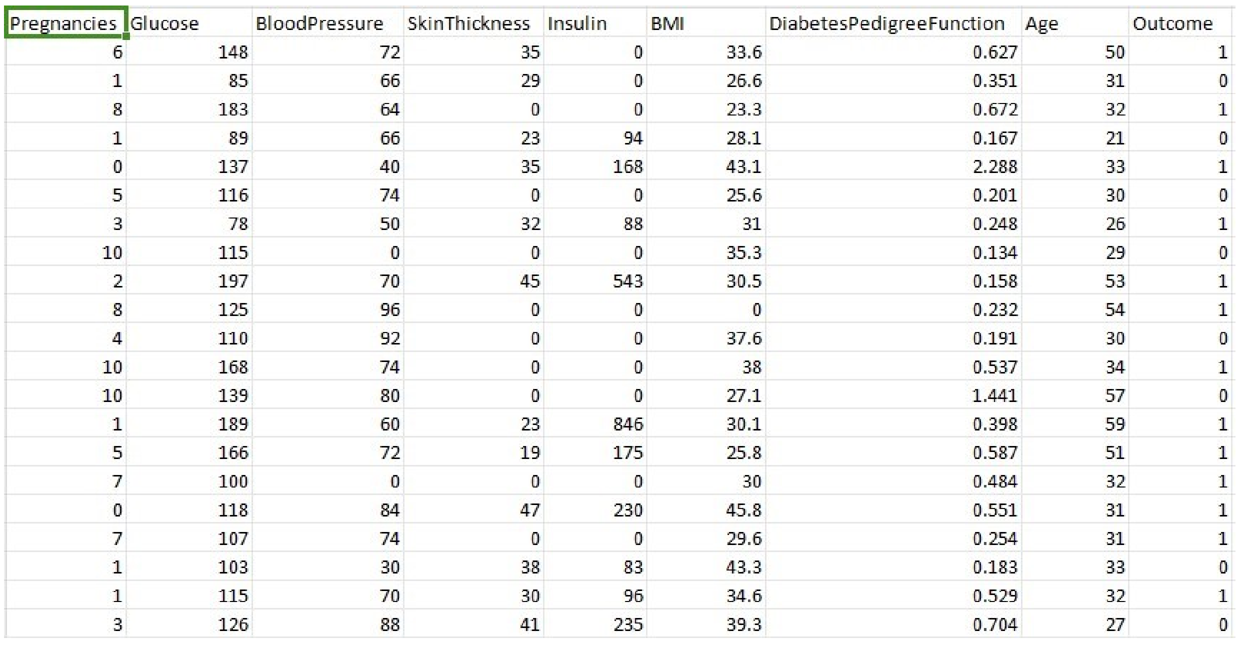
Dataset:

Necessary Steps to follow:

1.Import Libraries

Start by importing the necessary libraries

```
Import pandas as pd

import seaborn as sns

import matplotlib.pyplot as plt

from matplotlib import rcParams


from sklearn import model_selection

from sklearn.model_selection import train_test_split

from sklearn.metrics import accuracy_score, precision_score, recall_score,
roc_auc_score from sklearn.metrics import f1_score, confusion_matrix,
precision_recall_curve, roc_curve from sklearn.metrics import
ConfusionMatrixDisplay
from sklearn.preprocessing import StandardScaler

import plotly.express as px

from plotly.subplots import make_subplots import plotly.graph_objects as
go

import warnings warnings.filterwarnings(action=‘ignore’)
```



Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
6	148	72	35	0	33.6	0.627	50	1
1	85	66	29	0	26.6	0.351	31	0
8	183	64	0	0	23.3	0.672	32	1
1	89	66	23	94	28.1	0.167	21	0
0	137	40	35	168	43.1	2.288	33	1
5	116	74	0	0	25.6	0.201	30	0
3	78	50	32	88	31	0.248	26	1
10	115	0	0	0	35.3	0.134	29	0
2	197	70	45	543	30.5	0.158	53	1
8	125	96	0	0	0	0.232	54	1
4	110	92	0	0	37.6	0.191	30	0
10	168	74	0	0	38	0.537	34	1
10	139	80	0	0	27.1	1.441	57	0
1	189	60	23	846	30.1	0.398	59	1
5	166	72	19	175	25.8	0.587	51	1
7	100	0	0	0	30	0.484	32	1
0	118	84	47	230	45.8	0.551	31	1
7	107	74	0	0	29.6	0.254	31	1
1	103	30	38	83	43.3	0.183	33	0
1	115	70	30	96	34.6	0.529	32	1
3	126	88	41	235	39.3	0.704	27	0

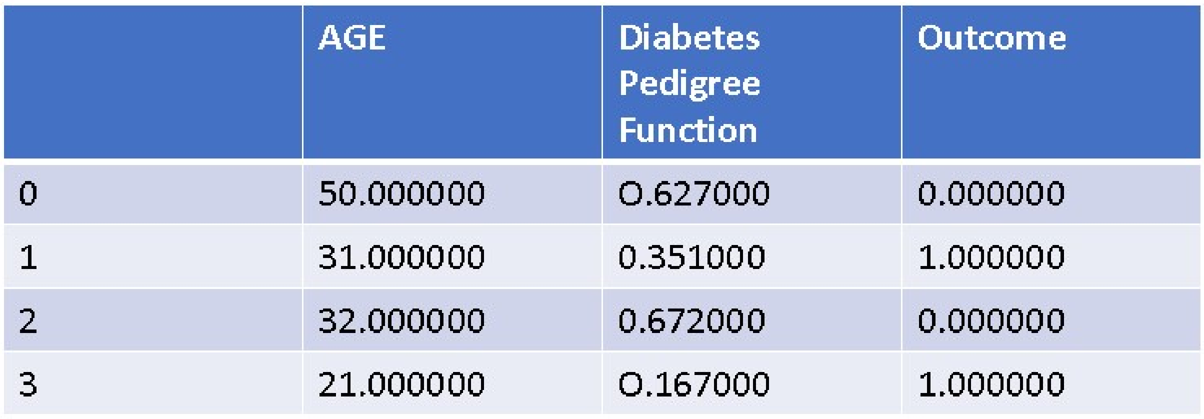
2.Designing Utility Functions:

```
Def get_clf_eval(y_test, pred=None, pred_proba=None): confusion =
confusion_matrix( y_test, pred)

accuracy = accuracy_score(y_test , pred)

precision = precision_score(y_test , pred) recall = recall_score(y_test , pred)

f1 = f1_score(y_test,pred)

roc_auc = roc_auc_score(y_test, pred_proba) # ROC-AUC print

print('accuracy: {0:.4f}, precision: {1:.4f}, recall: {2:.4f},\
F1: {3:.4f}, AUC:{4:.4f}'.format(accuracy, precision, recall, f1, roc_auc))

return confusion
```

3.Reading and checking data:

```
Diabetes_df = pd.read_csv(“D:/diabetes.csv”)

diabetes_df.head().T.style.set_properties(**{‘background-color’: ‘grey’,
‘color’: ‘white’,
‘border-color’: ‘white’})
```

Given Dataset:



	AGE	Diabetes Pedigree Function	Outcome
0	50.000000	0.627000	0.000000
1	31.000000	0.351000	1.000000
2	32.000000	0.672000	0.000000
3	21.000000	0.167000	1.000000

DiabetesPedigreeFunction has a long name.

Change to DPF

```
diabetes_df.rename(columns
={“DiabetesPedigreeFunction”:”DPF”},inplace=True)
```

4.Exploratory Data analysis (EDA):

Perform EDA to understand your data better. This include checking for missing values, exploring the data’s statistics, and visualizing it to identify patterns.

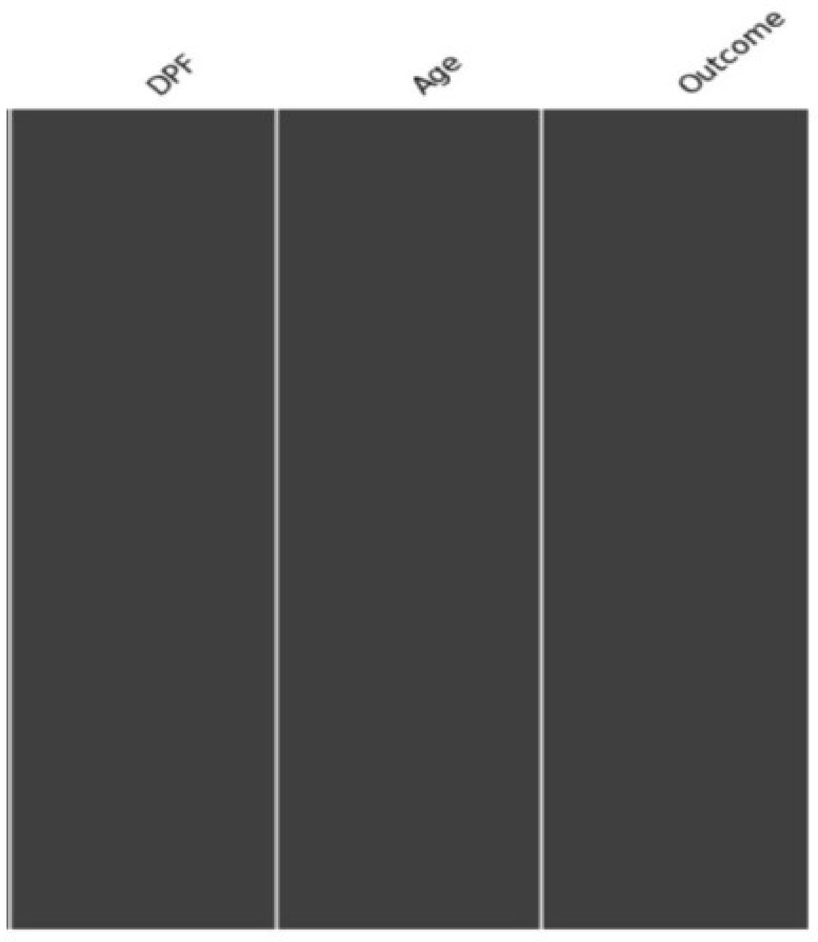
PROGRAM:

INPUT:

```
import missingno as msno msno.matrix(diabetes_df)
```

OUTPUT:

```
<AxesSubplot:>
```

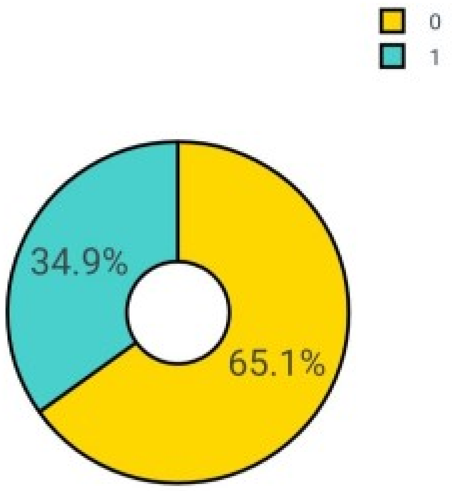


5.Checking Target Imbalance:

```
Colors = [‘gold’, ‘mediumturquoise’] labels = [‘0’,’1’]
```

```
values=diabetes_df['Outcome'].value_counts()/diabetes_df['Outcome'].sha
pe[0]

# Use `hole` to create a donut-like pie chart
fig = go.Figure(data=[go.Pie(labels=labels, values=values, hole=.3)])
fig.update_traces(hoverinfo='label+percent', textinfo='percent',
textfont_size=20,
marker=dict(colors=colors, line=dict(color='#000000', width=2)))
fig.update_layout( title_text="Outcome")
```

OUTCOME:



6. Checking statistics:

```
    Def highlight_min(s, props=''):
    return np.where(s == np.nanmin(s.values), props, '')

    diabetes_df.describe().style.apply(highlight_min,
    props='color:Black;background-color:Grey', axis=0)
```

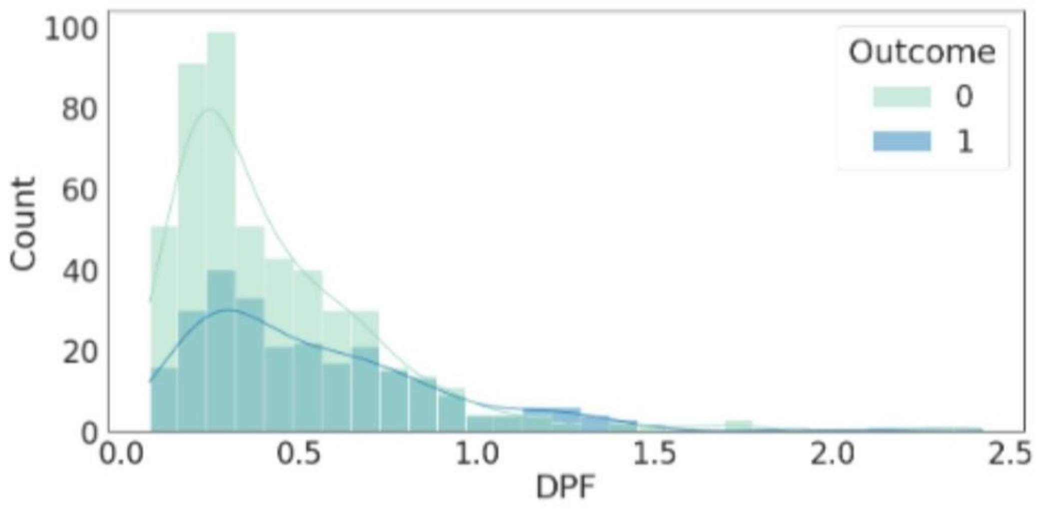
OUTPUT:

Count	768.000000
Mean	0.348958
Std	0.476951
Min	0.000000
25%	0.000000
50%	0.000000
75%	1.000000
Max	1.000000

7.Checking and removing outliers:

Input:

```
feature_names = [cname for cname in diabetes_df.loc[:,:’Age’].columns]

rcParams[‘figure.figsize’] = 40,60 sns.set(font_scale = 3)
sns.set_style(“white”) sns.set_palette(“bright”)

plt.subplots_adjust(hspace=0.5) i = 1;
```



```
for name in feature_names: plt.subplot(5,2,i)
sns.histplot(data=diabetes_df, x=name,
hue="Outcome",kde=True,palette="YlGnBu")
i = i + 1
```

PREPROCESSING:

Input:

```
    #Tra nsform the data to integer
    Data["Diabetes_binary"] = data["Diabetes_binary"].astype(int)
    data["HighBP"] = data["HighBP"].astype(int)
    data["HighChol"] = data["HighChol"].astype(int)
    data["CholCheck"] = data["CholCheck"].astype(int)
    data["BMI"] = data["BMI"].astype(int)
    data["Smoker"] = data["Smoker"].astype(int) data["Stroke"] =
    data["Stroke"].astype(int)
    data["HeartDiseaseorAttack"] =
    data["HeartDiseaseorAttack"].astype(int)
    data["PhysActivity"] = data["Phys Activity"].astype(int)
    data["Fruits"] = data["Fruits"].astype(int)
    data["Veggies"] = data["Veggies"].astype(int)
    data["HvyAlcoholConsump"] =
    data["HvyAlcoholConsump"].astype(int)
    data["AnyHealthcare"] = data["AnyHealthcare "].astype(int)
    data["NoDocbcCost"] = data["NoDocbcCost"].astype(int)
```

```
data[“GenHlth”] = data[“GenHlth”].astype(int)
data[“MentHlth”] = data[“MentHlth”].astype(int) data[“PhysHlth”] =
data[“Phys Hlth”].astype(int) data[“DiffWalk”] =
data[“DiffWalk”].astype(int)
data[“Sex”] = data[“Sex”].astype(int)
data[“Age”] = data[“Age”].astype(int)
data[“Education”] = data[“Education”].astype(int)
 Data.info()
```

OUTPUT:

```
<class ‘pandas.core.frame.DataFrame’>
RangeIndex: 253680 entries, 0 to 253679
Data columns (total 22 columns):
#       Column     Non-Null Count Dtype

0       Diabetes_binary 253680 non-null int64
1       HighBP     253680 non-null int64
2       HighChol   253680 non-null int64
3       CholCheck253680 non-null int64
4       BMI  253680 non-null int64
5       Smoker     253680 non-null int64
6       Stroke     253680 non-null int64
7       HeartDiseaseorAttack 253680 non-null int64
8       PhysActivity     253680 non-null int64
9       Fruits     253680 non-null int64
10 Veggies         253680 non-null int64
11 HvyAlcoholConsump     253680 non-null int64
12 AnyHealthcare       253680 non-null int64
13 NoDocbcCost         253680 non-null int64
14 GenHlth         253680 non-null int64
15 MentHlth        253680 non-null int64
```

```
    16 PhysHlth       253680 non-null int64
    17 DiffWalk       253680 non-null int64
```

Check null values:

Input:

```
data.isnull().sum() Output:
```

```
    Diabetes_binary 0
    HighBP     0
    HighChol   0
    CholCheck0
    BMI  0
    Smoker     0
    Stroke     0
    HeartDiseaseorAttack 0
    PhysActivity     0
    Fruits     0
    Veggies    0
    HvyAlcoholConsump 0
    AnyHealthcare    0
    NoDocbcCost      0
    GenHlth    0
    MentHlth   0
    PhysHlth   0
    DiffWalk   0
    Sex   0
    Age   0
    Education  0
    Income     0
```

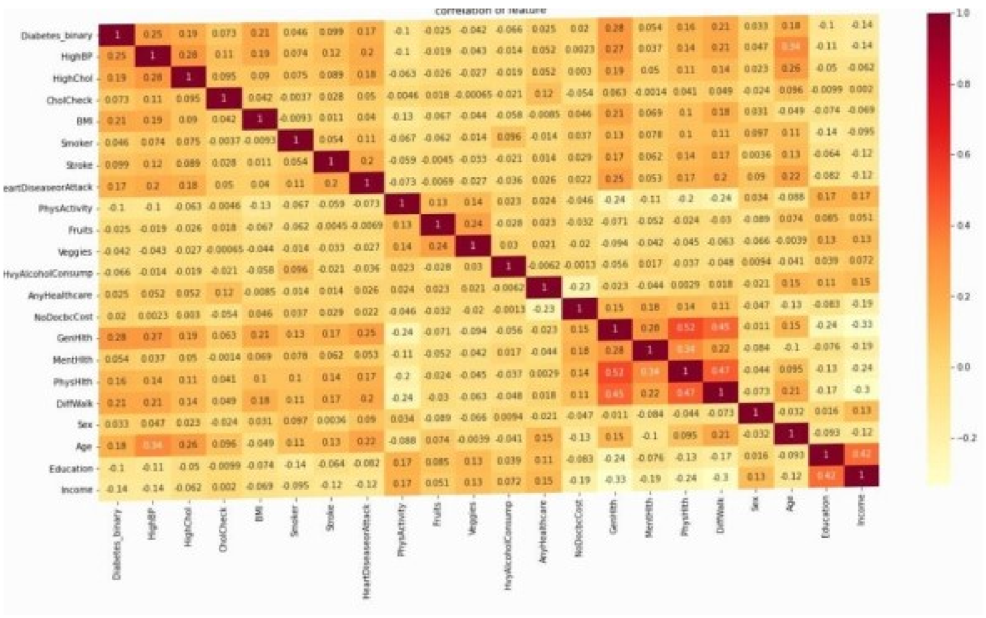
dtype: int64

EDA:
Input:

```
#using heatmap to understand correlation better in dataset data
#Heatmap of correlation
plt.figure(figsize = (20,10))
sns.heatmap(data.corr(),annot=True , cmap ='YlOrRd' )
plt.title("correlation of feature")
```

Output:

```
text(0.5, 1.0, 'correlation of feature')
```



Correlation heatmap show relation between columns:

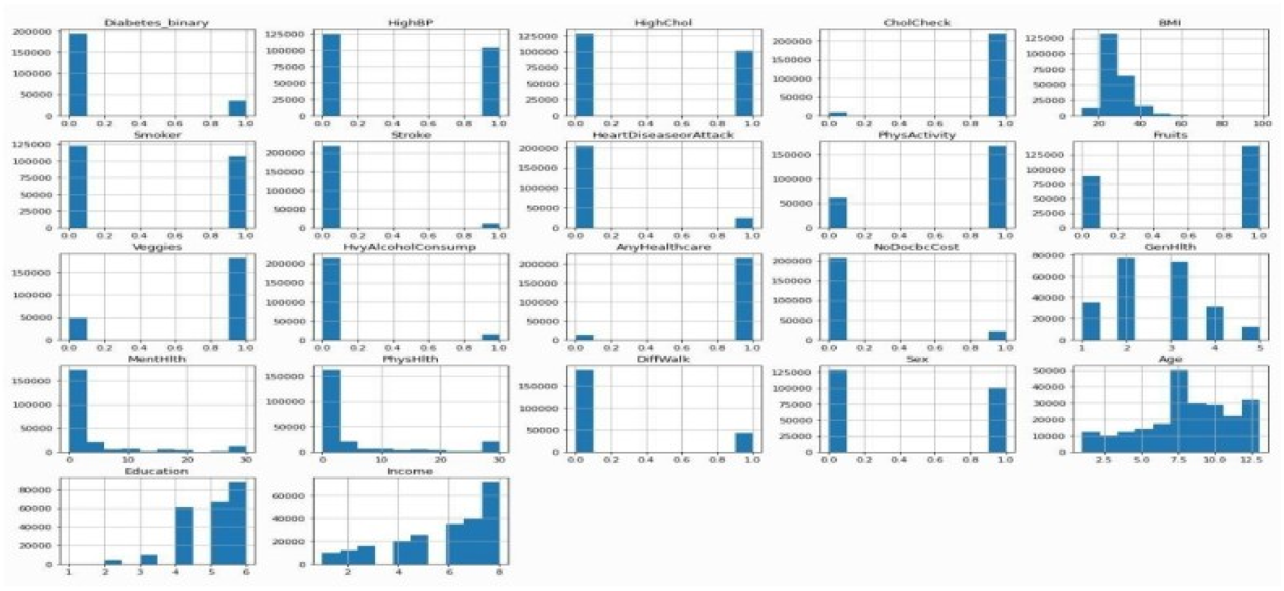
(GenHlth ,PhysHlth),(PhysHlth , DiffWalk),(GenHlth ,DiffWalk)are highly correleted with each other => positive relation

(GenHlth ,Income) , (DiffWalk , Income) are highly correleted with each other => Nagative relation Input:

#using histogram to understand dataset data better

data.hist(figsize=(20,15));

Output:



Visualization Of [Yes – NO] Columns and their relation with the target:

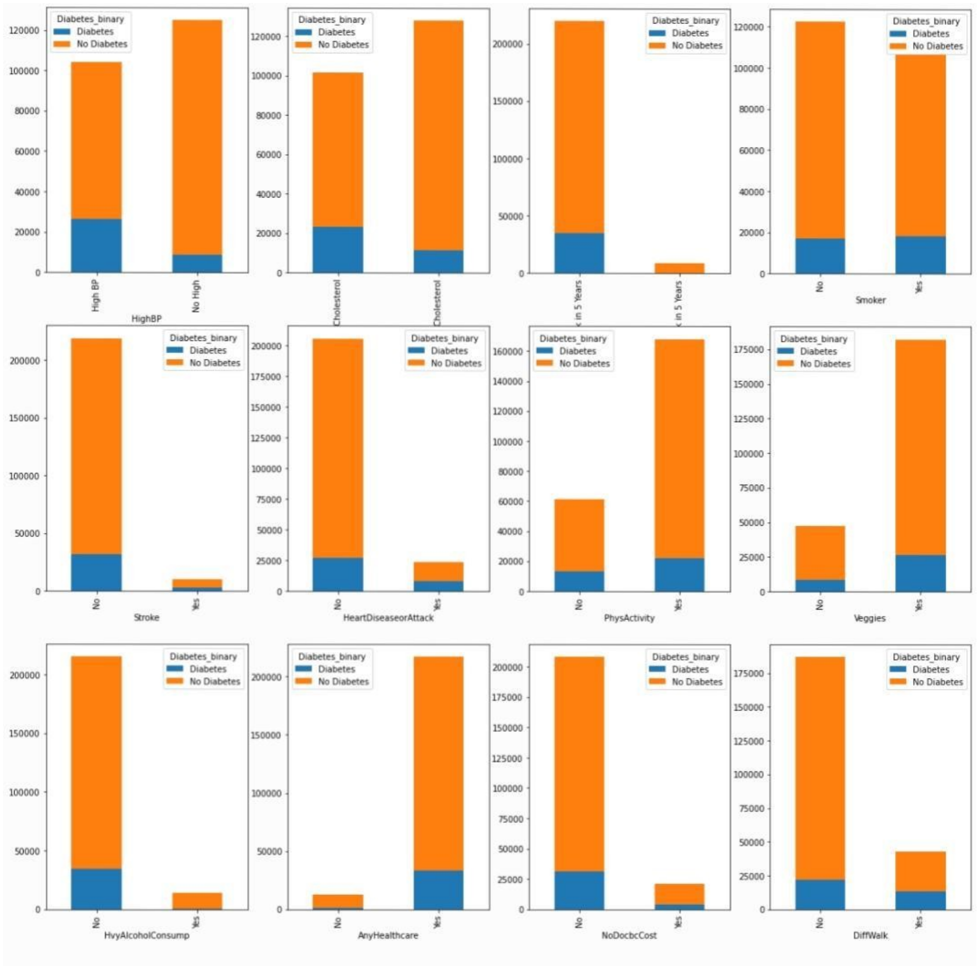
Input:

Cols = [‘HighBP’, ‘HighChol’, ‘CholCheck’,’Smoker’, ‘Stroke’, ‘HeartDiseaseorAttack’, ‘PhysActivity’, ‘Veggies’, ‘HvyAlcoholConsump’, ‘AnyHealthcare’, ‘NoDocbcCost’, ‘DiffWalk’]

def create_plot_pivot(data2, x_column):

```
“”” Create a pivot table for satisfaction versus another rating for easy
plotting. “””
_df_plot = data2.groupby([x_column, ‘Diabetes_binary’]).size() \
.reset_index().pivot(columns=‘Diabetes_binary’, index=x_column,
values=0) return _df_plot
fig, ax = plt.subplots(3, 4, figsize=(20,20))
axe = ax.ravel() c = len(cols)
for i in range(c):
create_plot_pivot(data2, cols[i]).plot(kind=‘bar’,stacked=True,
ax=axe[i])
axe[i].set_xlabel(cols[i])
```

Output:



Let's view our target values ***"Diabetes_binary"***

Input:

```
#average of column Daibetes_binary
# 0 for non-Diabetic person and 1 for Diabetic person
data2["Diabetes_binary"].value_counts()
```

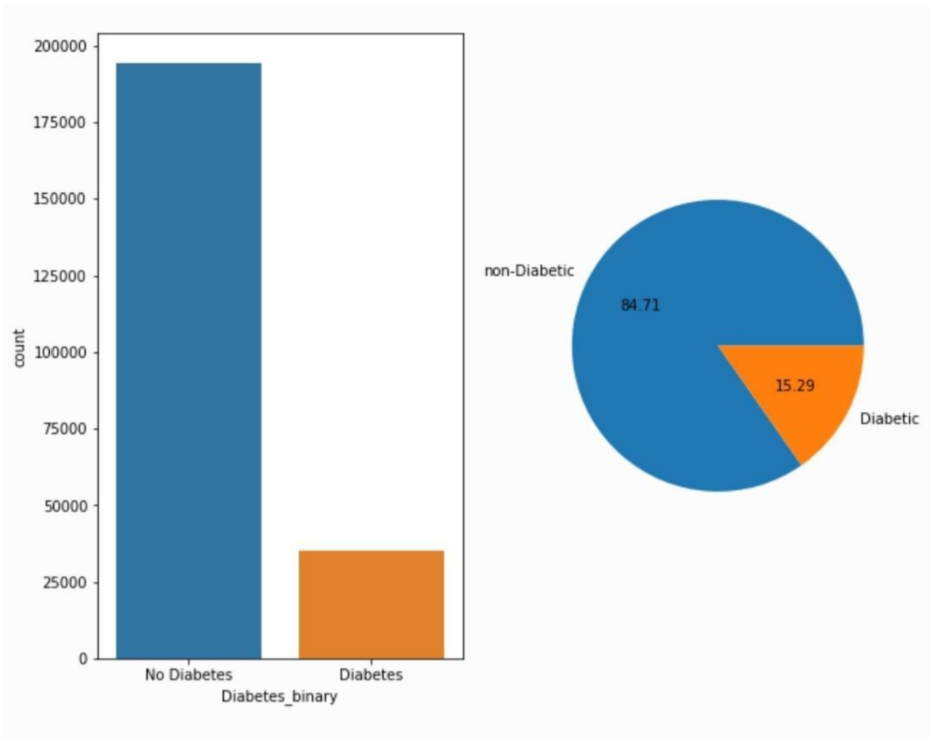
Output:

```
No Diabetes      194377
Diabetes    35097
Name: Diabetes_binary, dtype: int64
```

Input:

```
#checking the value count of Diabetes_binary_str by using countplot
figure1, plot1 = plt.subplots(1,2,figsize=(10,8))
sns.countplot(data2['Diabetes_binary'],ax=plot1[0]) #checking
diabetic and non diabetic pepoles average by pie labels=["non-
Diabetic","Diabetic"]
plt.pie(data2["Diabetes_binary"].value_counts() , labels
=labels ,autopct='%.02f' );
```

Output:



Conclusion:

The loading and preprocessing phase plays a critical role in the development of an AI-based diabetes prediction system. It serves as the foundation for accurate and reliable model training and evaluation. Proper data loading ensures that relevant datasets are acquired, while effective preprocessing techniques, such as data cleaning, normalization, and feature engineering, help in enhancing the quality and relevance of the data. The success of the entire system depends on the careful execution of these steps, ultimately leading to a more robust and effective diabetes prediction model. It is essential to continuously refine and optimize the loading and preprocessing processes to keep the AI system up-to-date with the latest data and scientific advancements in the field of diabetes prediction.