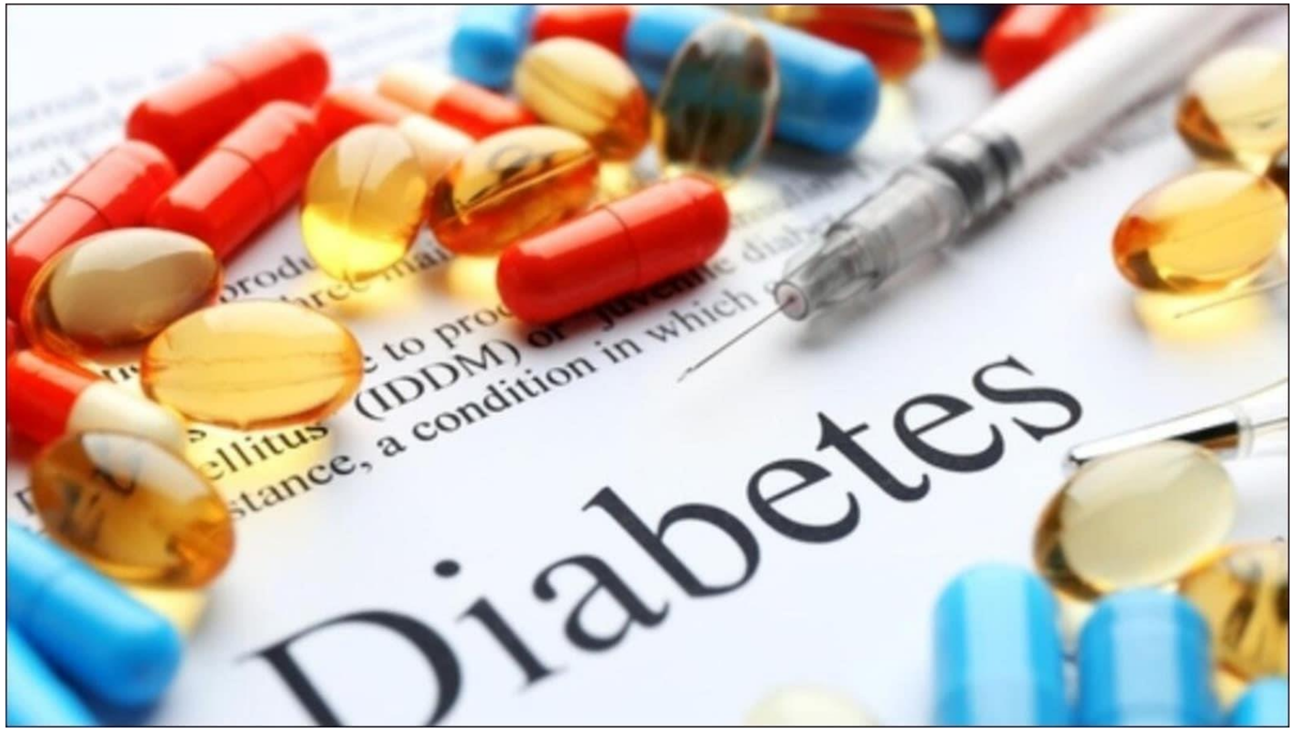
AI-Based Diabetes prediction system

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')
```

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(“../input/pima-indians-diabetes-database/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	O.627000	0.000000
1	31.000000	0.351000	1.000000
2	32.000000	0.672000	0.000000
3	21.000000	O.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.

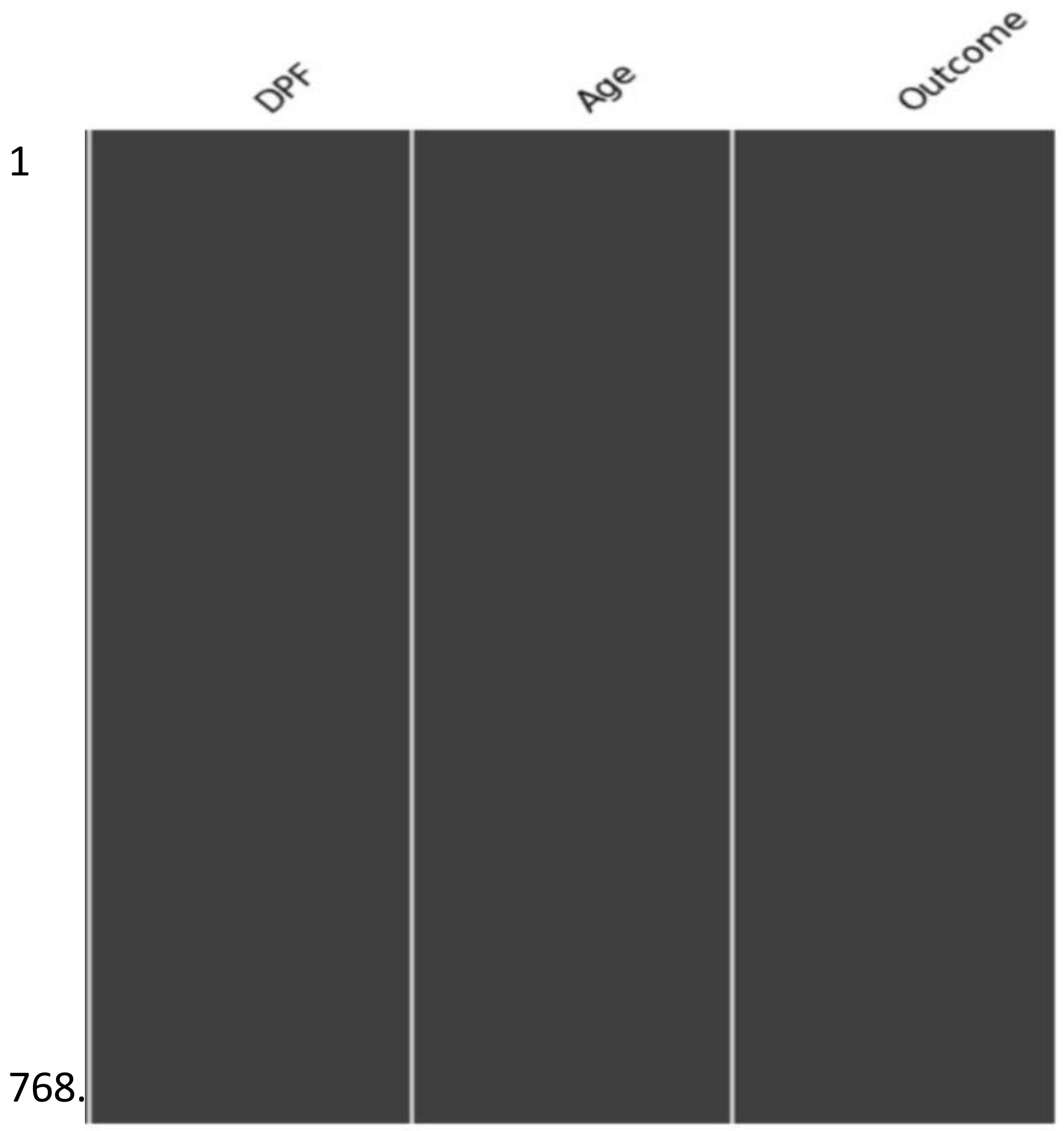
PROGRAM:

INPUT:

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

OUTPUT:

```
    <AxesSubplot:>
```

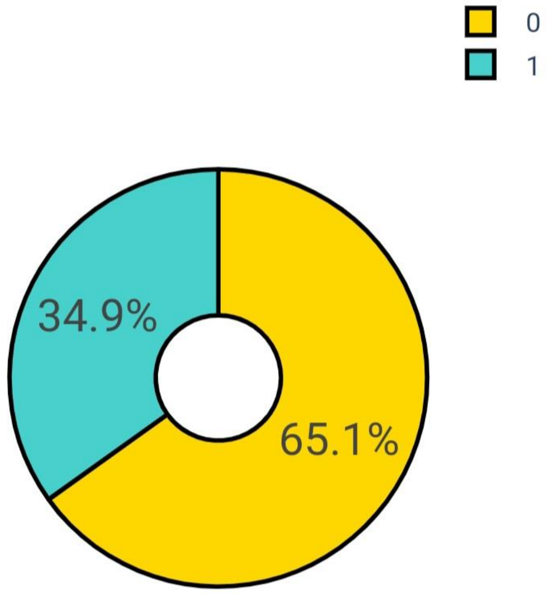

DPF
Age
Outcome
1
768.

5.Checking Target Imbalance:

```
Colors = [‘gold’, ‘mediumturquoise’]
labels = [‘0’,’1’]
values =
diabetes_df[‘Outcome’].value_counts()/diabetes_df[‘Outcome’].shape[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)
```

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

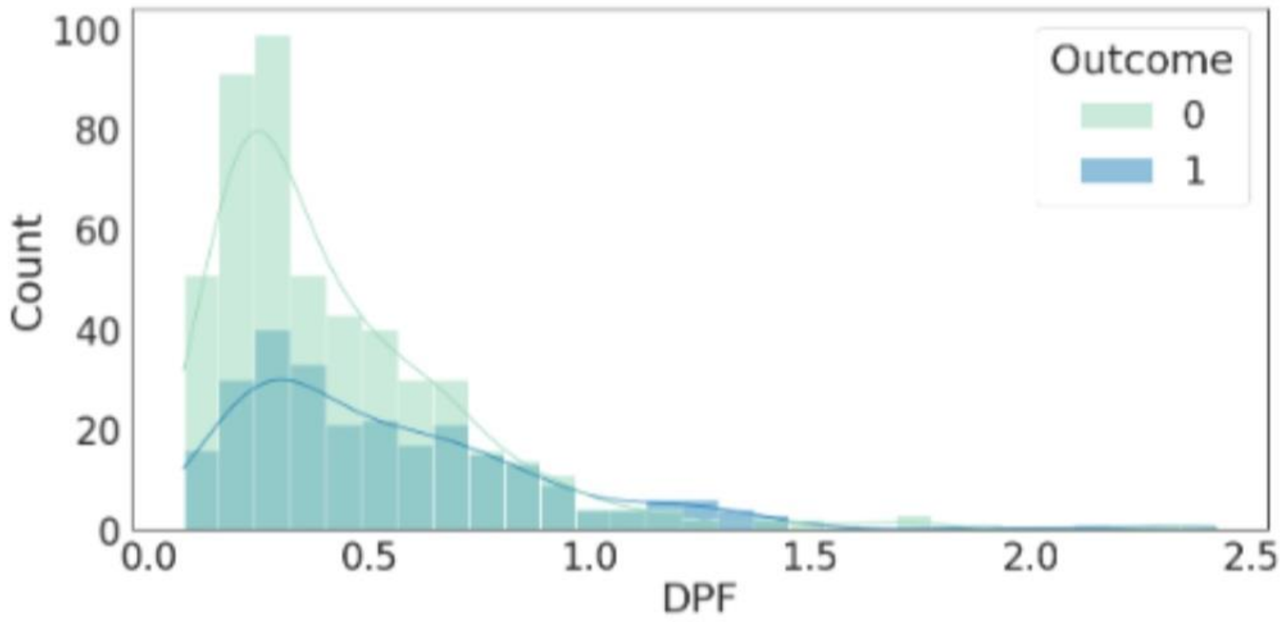
7.Checking and removing outliers:

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
```

Output:



PREPROCESSING:

Input:

```
#Transform 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[“PhysActivity”].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[“PhysHlth”].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()
• <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   CholCheck             253680 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
CholCheck                 0
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
```

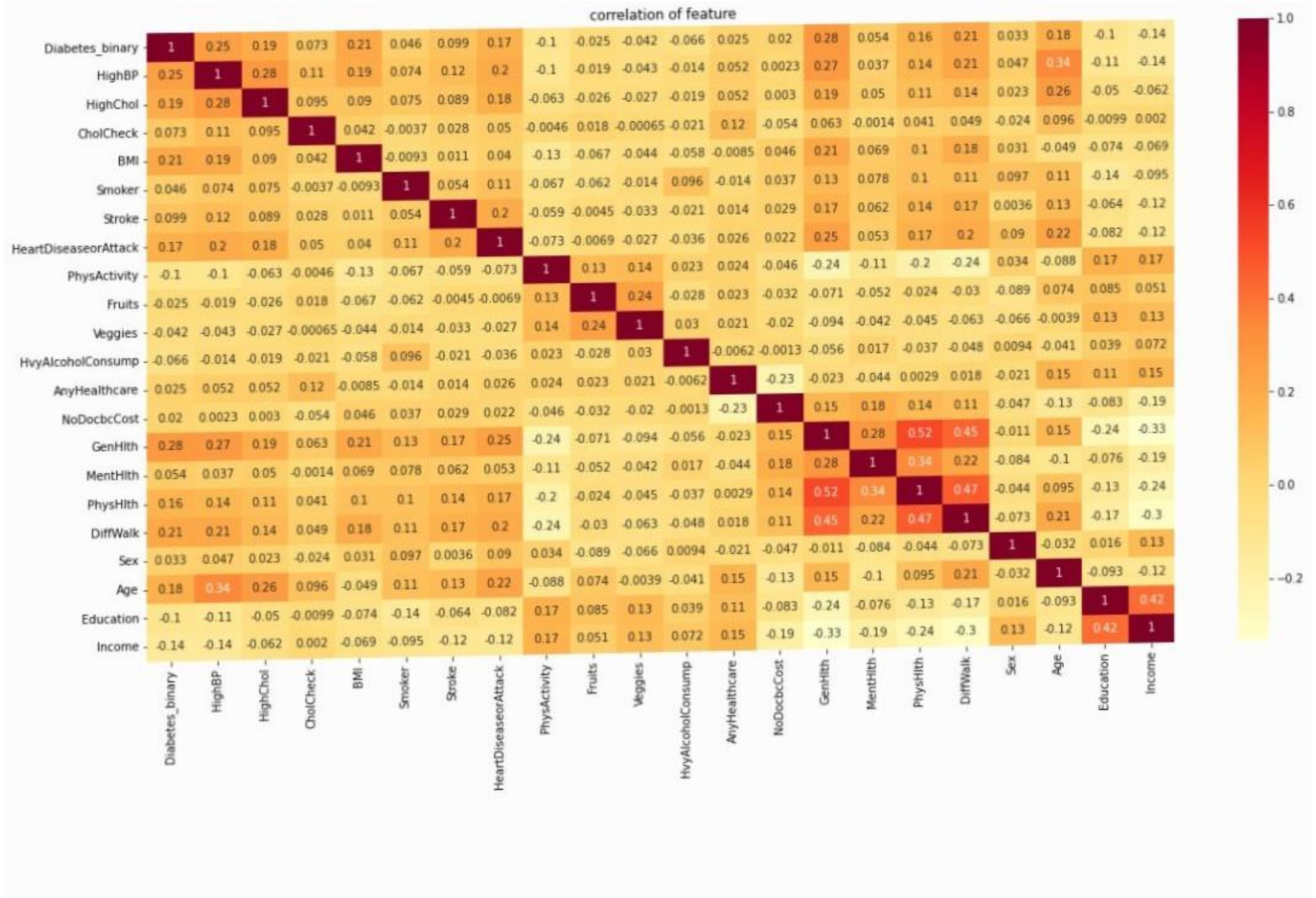
EDA:

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

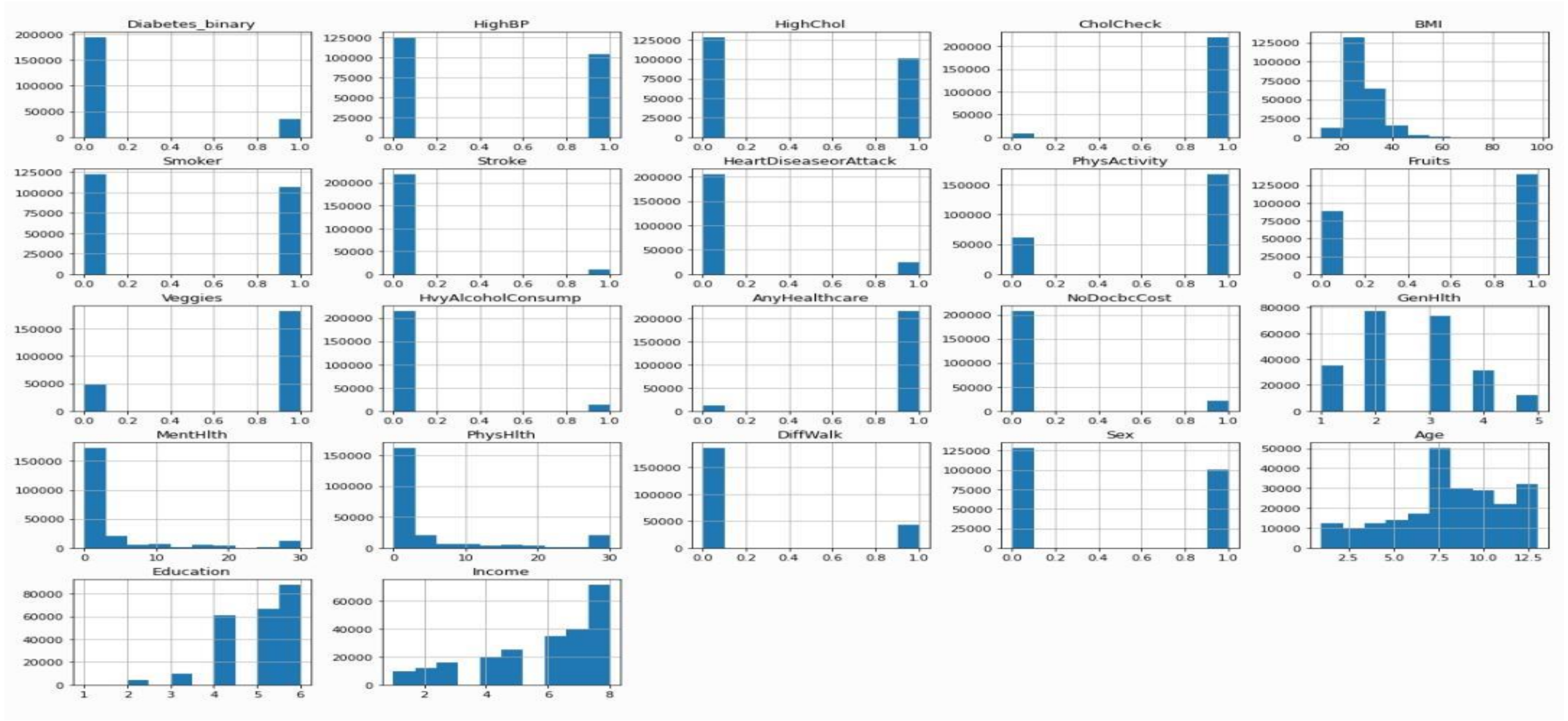
(GenHlth ,Income) , (DiffWalk , Income) are highly correleted with each other => Nagative relation

<u>Input:</u>

#using histogram to understand dataset data better

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

<u>Output:</u>

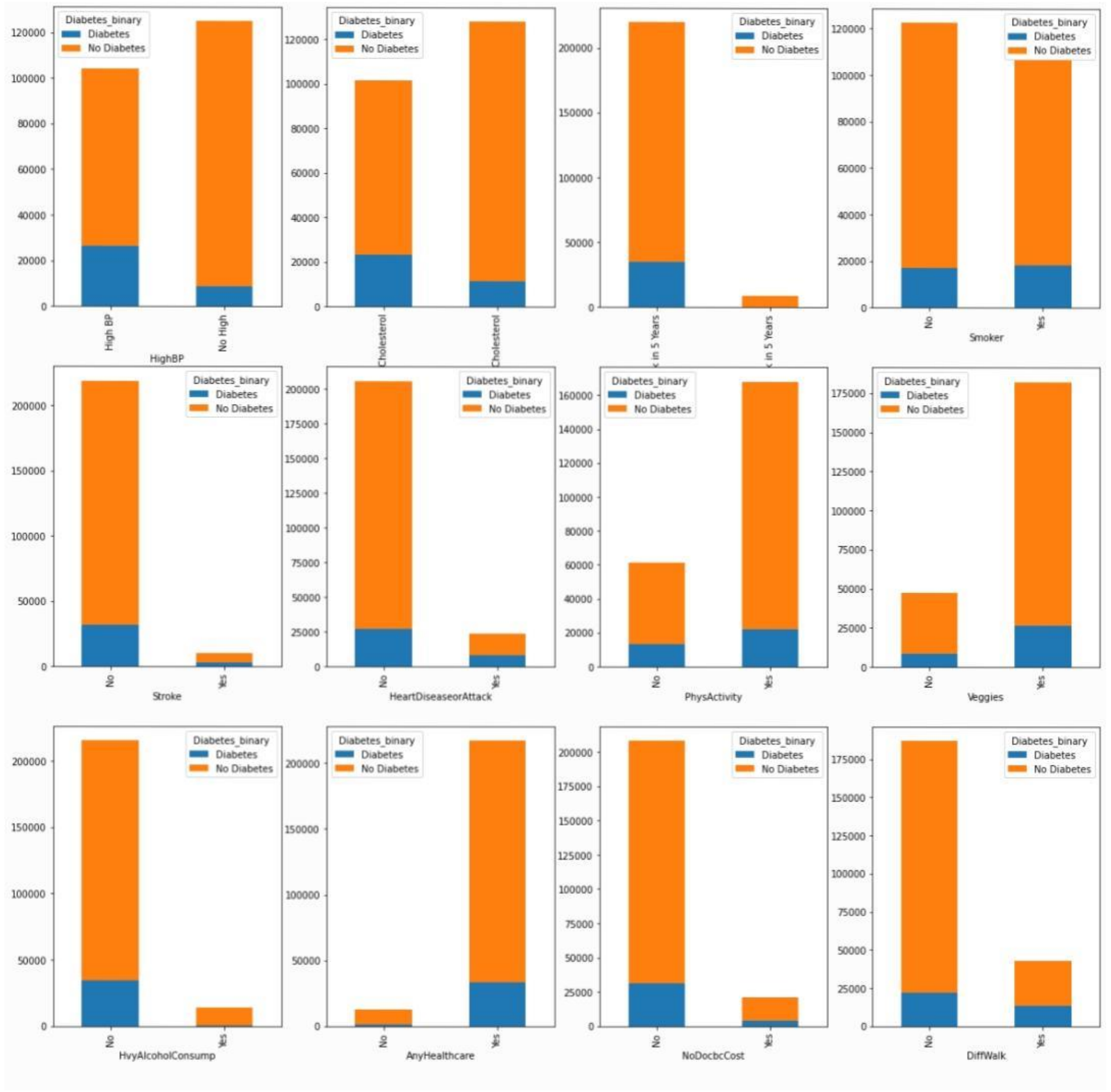


Visualization Of [Yes – NO] Columns and their relation with the target:

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:



Diabetes_binary
Diabetes
No Diabetes
High BP
No High
HighBP
Cholesterol
k in 5 Years
No
Yes
Smoker
Stroke
HeartDiseaseorAttack
PhysActivity
Veggies
HvyAlcoholConsump
AnyHealthcare
NoDocbcCost
DiffWalk

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()
```

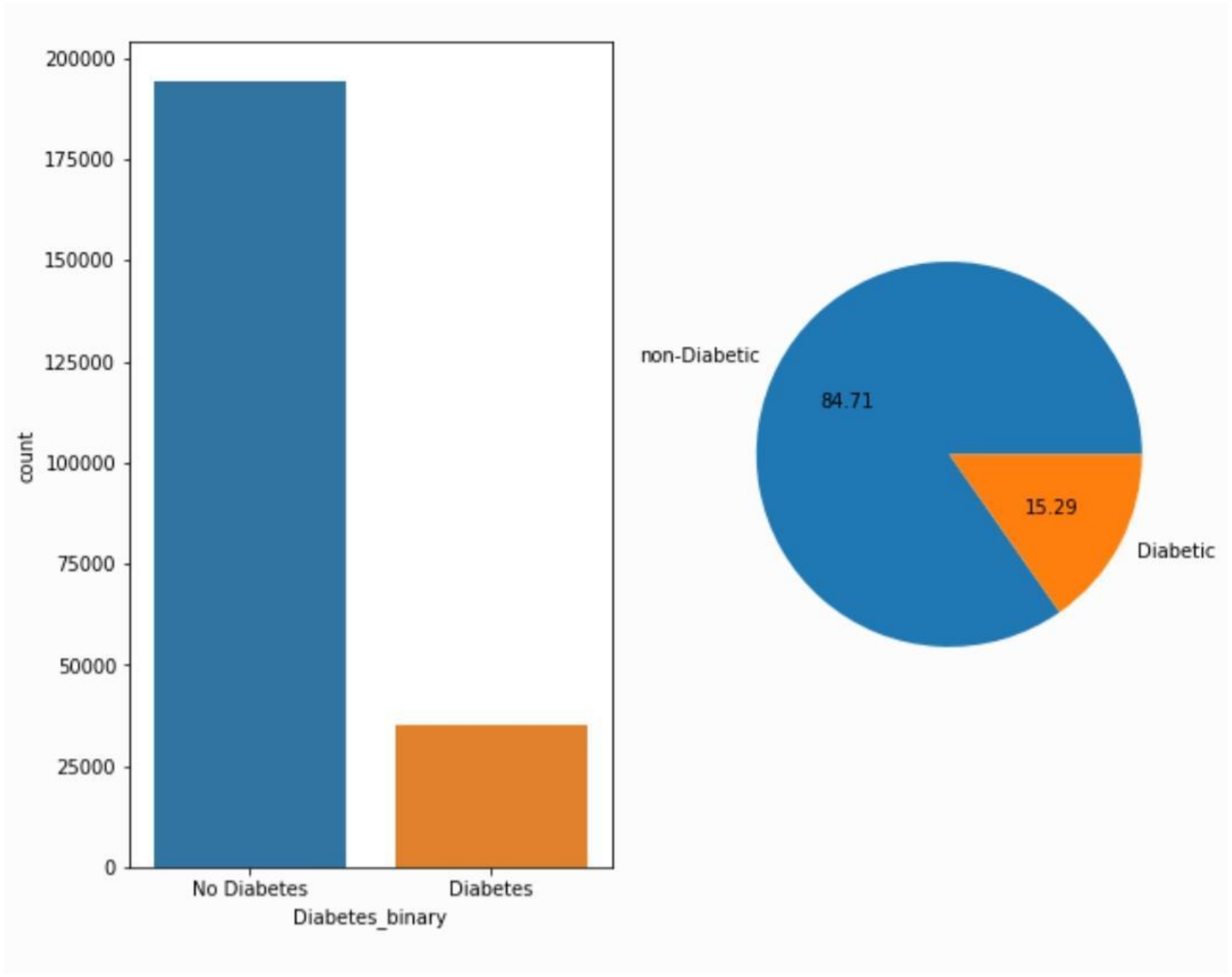
Output:

```
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:


count
200000
175000
150000
125000
100000
75000
50000
25000
0
No Diabetes
Diabetes
Diabetes_binary
non-Diabetic
84.71
15.29
Diabetic

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.