In [1]:
```
import os # importing os
os.getcwd()  #getting current directory
```

Out[1]: 'C:\\Users\\sumit\\Data Science\\Live Project\\Diabetes'

In [2]:
```
#os.chdir('D:\\Diabetic_project_own') # changing my directory to d:datasets because my dataset is
```

In [3]:
```
import numpy as np #good for maths(stds)

import pandas as pd #excellent for dataset manupalation

# for data visulization
import matplotlib.pyplot as plt

import seaborn as sns

#Labelencoding to convert categorical data into lowlevel language
from sklearn.preprocessing import LabelEncoder

#scaling data
from sklearn.preprocessing import StandardScaler

#data partions
from sklearn.model_selection import train_test_split

#algorithams
from sklearn.linear_model import LogisticRegression

from sklearn.tree import DecisionTreeClassifier

from sklearn.ensemble import RandomForestClassifier

from xgboost import XGBClassifier


#accuracy confusion matric and classification report
from sklearn.metrics import accuracy_score,confusion_matrix,classification_report


import warnings

# To ignore all warnings
warnings.filterwarnings("ignore")
```

In [4]:
```
df=pd.read_csv("diabetes_prediction_dataset.csv")   #Reding my file
```

In [5]:
```
df.head() #it displace the first 5 rows
```

Out[5]:

	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

In [6]:
```
df.isna().any() #checking is there any null values
```

Out[6]:
```
gender                 False
age                    False
hypertension           False
heart_disease          False
smoking_history        False
bmi                    False
HbA1c_level            False
blood_glucose_level    False
diabetes               False
dtype: bool
```

In [7]:
```
df.corr(numeric_only=True) #correlation
```

Out[7]:

	age	hypertension	heart_disease	bmi	HbA1c_level	blood_glucose_level	diabetes
age	1.000000	0.251171	0.233354	0.337396	0.101354	0.110672	0.258008
hypertension	0.251171	1.000000	0.121262	0.147666	0.080939	0.084429	0.197823
heart_disease	0.233354	0.121262	1.000000	0.061198	0.067589	0.070066	0.171727
bmi	0.337396	0.147666	0.061198	1.000000	0.082997	0.091261	0.214357
HbA1c_level	0.101354	0.080939	0.067589	0.082997	1.000000	0.166733	0.400660
blood_glucose_level	0.110672	0.084429	0.070066	0.091261	0.166733	1.000000	0.419558
diabetes	0.258008	0.197823	0.171727	0.214357	0.400660	0.419558	1.000000

In [8]:
```
df.shape #shape of the dataframe
```

Out[8]:
```
(100000, 9)
```

Checking all unique elements

In [9]:
```
for column in df.columns: # itreating each column in df.columns
    unique_values = df[column].unique() #finding unique values of each column

    #printing unique values
    print('Column "{}" has unique values: {}\n'.format(column, unique_values))
```

```
Column "gender" has unique values: ['Female' 'Male' 'Other']

Column "age" has unique values: [80.   54.   28.   36.   76.   20.   44.   79.   42.   32.   53.   7
8.
 67.   15.   37.   40.    5.   69.   72.    4.   30.   45.   43.   50.
 41.   26.   34.   73.   77.   66.   29.   60.   38.    3.   57.   74.
 19.   46.   21.   59.   27.   13.   56.    2.    7.   11.    6.   55.
  9.   62.   47.   12.   68.   75.   22.   58.   18.   24.   17.   25.
  0.08 33.   16.   61.   31.    8.   49.   39.   65.   14.   70.    0.56
 48.   51.   71.    0.88 64.   63.   52.    0.16 10.   35.   23.    0.64
  1.16  1.64  0.72  1.88  1.32  0.8   1.24  1.    1.8   0.48  1.56  1.08
  0.24  1.4   0.4   0.32  1.72  1.48]

Column "hypertension" has unique values: [0 1]

Column "heart_disease" has unique values: [1 0]

Column "smoking_history" has unique values: ['never' 'No Info' 'current' 'former' 'ever' 'not curren
t']

Column "bmi" has unique values: [25.19 27.32 23.45 ... 59.42 44.39 60.52]

Column "HbA1c_level" has unique values: [6.6 5.7 5.  4.8 6.5 6.1 6.  5.8 3.5 6.2 4.  4.5 9.  7.  8.8
8.2 7.5 6.8]

Column "blood_glucose_level" has unique values: [140  80 158 155  85 200 145 100 130 160 126 159  90
260 220 300 280 240]

Column "diabetes" has unique values: [0 1]
```

In [10]:
```
df["smoking_history"].value_counts() #Value count of smoling _history parameter
```

Out[10]:
```
smoking_history
No Info        35816
never          35095
former          9352
current         9286
not current     6447
ever            4004
Name: count, dtype: int64
```

In [11]:
```
# Replacing No Info columns with pd.NA
df['smoking_history'] = df['smoking_history'].replace('No Info', pd.NA)
```

In [12]:
```
# Replace missing values with the mode
mode_value = df['smoking_history'].mode()[0]
df['smoking_history'] = df['smoking_history'].fillna(mode_value)
```

In [13]:
```
# Printing the updated value counts
print(df['smoking_history'].value_counts())
```

```
smoking_history
never          70911
former          9352
current         9286
not current     6447
ever            4004
Name: count, dtype: int64
```

In [14]:
```
df.info() #information of the dataframe
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 100000 entries, 0 to 99999
Data columns (total 9 columns):
 #   Column               Non-Null Count   Dtype  
---  ------               --------------   -----  
 0   gender               100000 non-null  object 
 1   age                  100000 non-null  float64
 2   hypertension         100000 non-null  int64  
 3   heart_disease        100000 non-null  int64  
 4   smoking_history      100000 non-null  object 
 5   bmi                  100000 non-null  float64
 6   HbA1c_level          100000 non-null  float64
 7   blood_glucose_level  100000 non-null  int64  
 8   diabetes             100000 non-null  int64  
dtypes: float64(3), int64(4), object(2)
memory usage: 6.9+ MB
```

In [15]:
```
df.gender.value_counts() #Gdender value_counts
```

Out[15]:
```
gender
Female    58552
Male      41430
Other        18
Name: count, dtype: int64
```

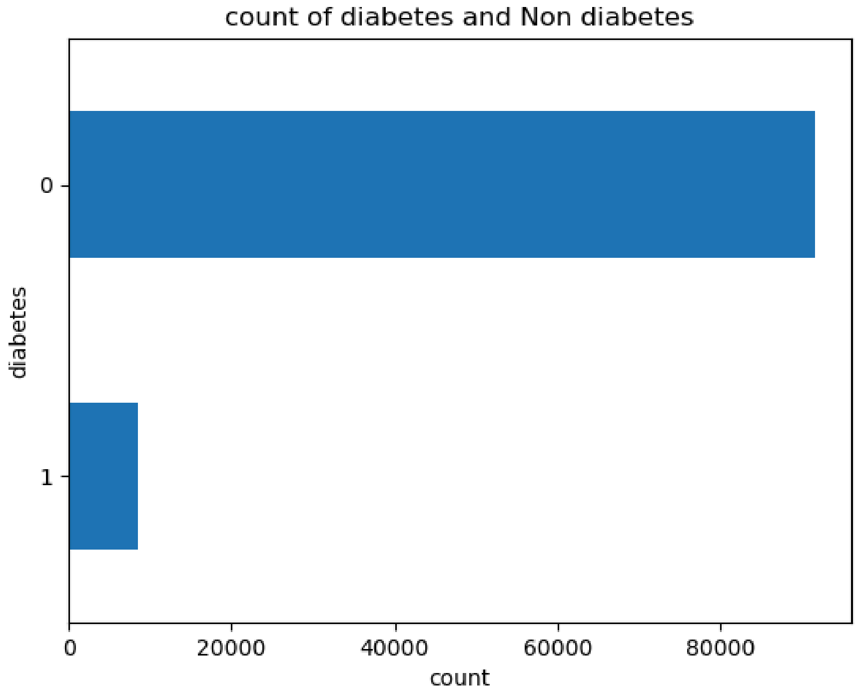
In [16]:
```
df.describe() #describetions
```

Out[16]:

	age	hypertension	heart_disease	bmi	HbA1c_level	blood_glucose_level	diabetes
count	100000.000000	100000.00000	100000.000000	100000.000000	100000.000000	100000.000000	100000.000000
mean	41.885856	0.07485	0.039420	27.320767	5.527507	138.058060	0.085000
std	22.516840	0.26315	0.194593	6.636783	1.070672	40.708136	0.278883
min	0.080000	0.00000	0.000000	10.010000	3.500000	80.000000	0.000000
25%	24.000000	0.00000	0.000000	23.630000	4.800000	100.000000	0.000000
50%	43.000000	0.00000	0.000000	27.320000	5.800000	140.000000	0.000000
75%	60.000000	0.00000	0.000000	29.580000	6.200000	159.000000	0.000000
max	80.000000	1.00000	1.000000	95.690000	9.000000	300.000000	1.000000

In [17]:
```
#removing , in bmi parameter
df["bmi"] = [float(str(i).replace(",", "")) for i in df["bmi"]]

```

In [18]:
```
#ploting value_counts of diabetes in graphcial representatio
df['diabetes'].value_counts().plot(kind='barh')

#Xlabel name
plt.xlabel('count')

#ylabel name
plt.ylabel('diabetes')

#title of the plot
plt.title('count of diabetes and Non diabetes')

#invert ylabes to no diabetes on top
plt.gca().invert_yaxis()

#printing the plot
plt.show()
```



In [19]:
```
df['diabetes'].value_counts()/len(df) #percentage of diabetes and no diabetes
```

Out[19]:
```
diabetes
0    0.915
1    0.085
Name: count, dtype: float64
```

In [20]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 100000 entries, 0 to 99999
Data columns (total 9 columns):
 #   Column               Non-Null Count   Dtype  
---  ------               --------------   -----  
 0   gender               100000 non-null  object 
 1   age                  100000 non-null  float64
 2   hypertension         100000 non-null  int64  
 3   heart_disease        100000 non-null  int64  
 4   smoking_history      100000 non-null  object 
 5   bmi                  100000 non-null  float64
 6   HbA1c_level          100000 non-null  float64
 7   blood_glucose_level  100000 non-null  int64  
 8   diabetes             100000 non-null  int64  
dtypes: float64(3), int64(4), object(2)
memory usage: 6.9+ MB
```

In [21]:
```
le=LabelEncoder() #activating label encoder function

le
```

Out[21]:
```
▾ LabelEncoder
LabelEncoder()
```

In [22]:
```
Label_encod_columns=['gender','smoking_history']  #selecting columns to apply labelencoder in next

df[Label_encod_columns]=df[Label_encod_columns].apply(le.fit_transform) #applying label encoding
```

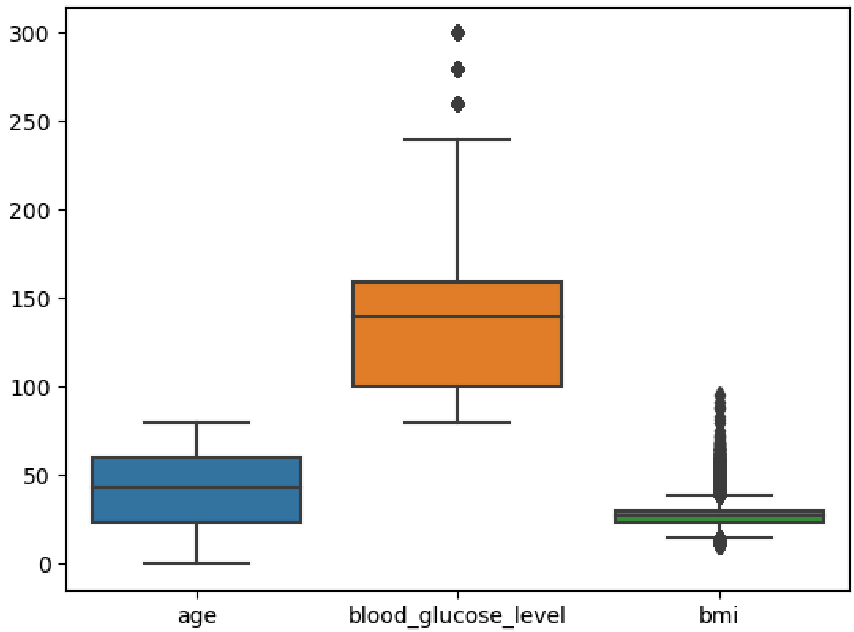
In [23]:
```
df.head(3) # printing top 3 columns to confirm to check labelencoder
```

Out[23]:

	gender	age	hypertension	heart_disease	smoking_history	bmi	HbA1c_level	blood_glucose_level	diabetes
0	0	80.0	0	1	3	25.19	6.6	140	0
1	0	54.0	0	0	3	27.32	6.6	80	0
2	1	28.0	0	0	3	27.32	5.7	158	0

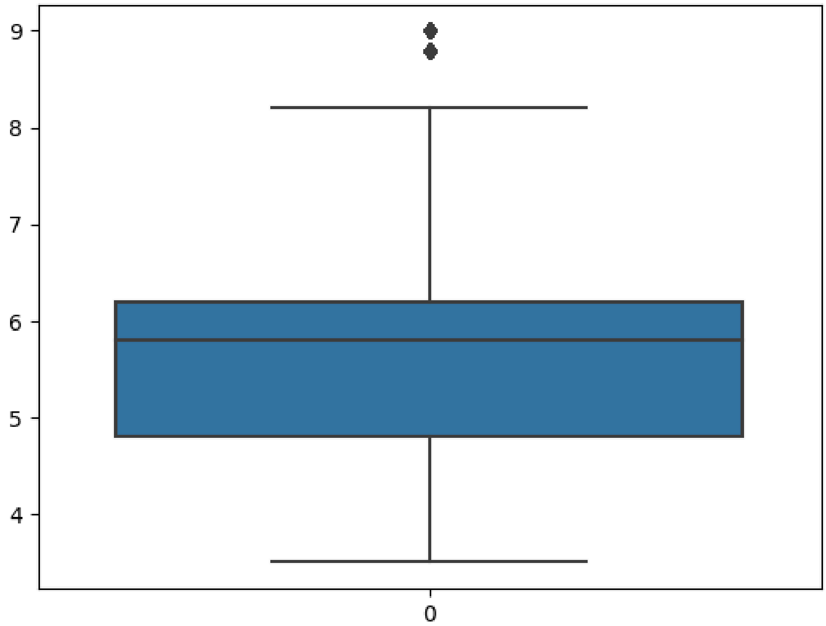
In [24]:
```
sns.boxplot(data=df[['age','blood_glucose_level','bmi']]) #checking outliers using boxplot
```

Out[24]: <Axes: >



In [25]:
```
sns.boxplot(data=df['HbA1c_level']) #checking outlayers using boxplot
```

Out[25]: <Axes: >

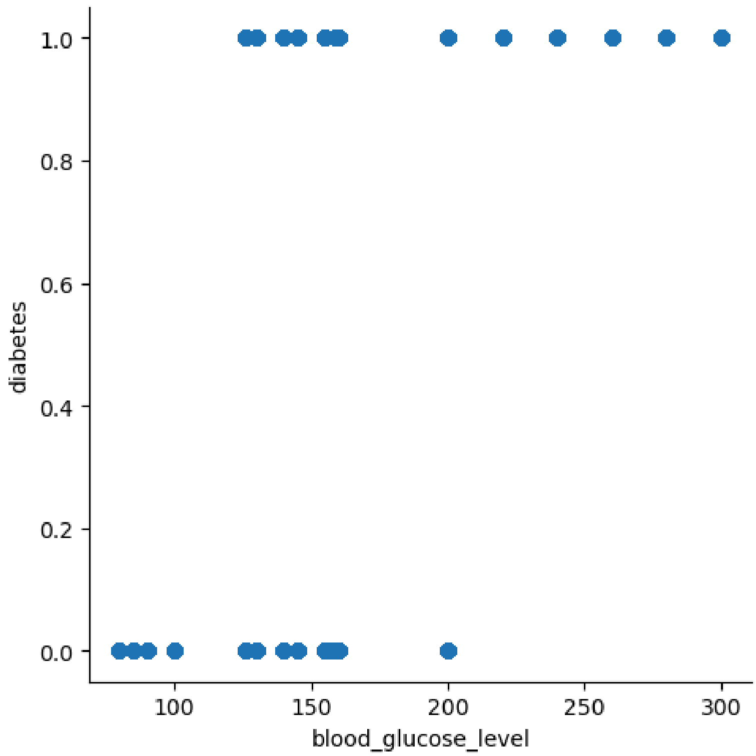


In [26]:
```
''' it is always good to ignore outliers in medical data '''
```

Out[26]: ' it is always good to ignore outliers in medical data '

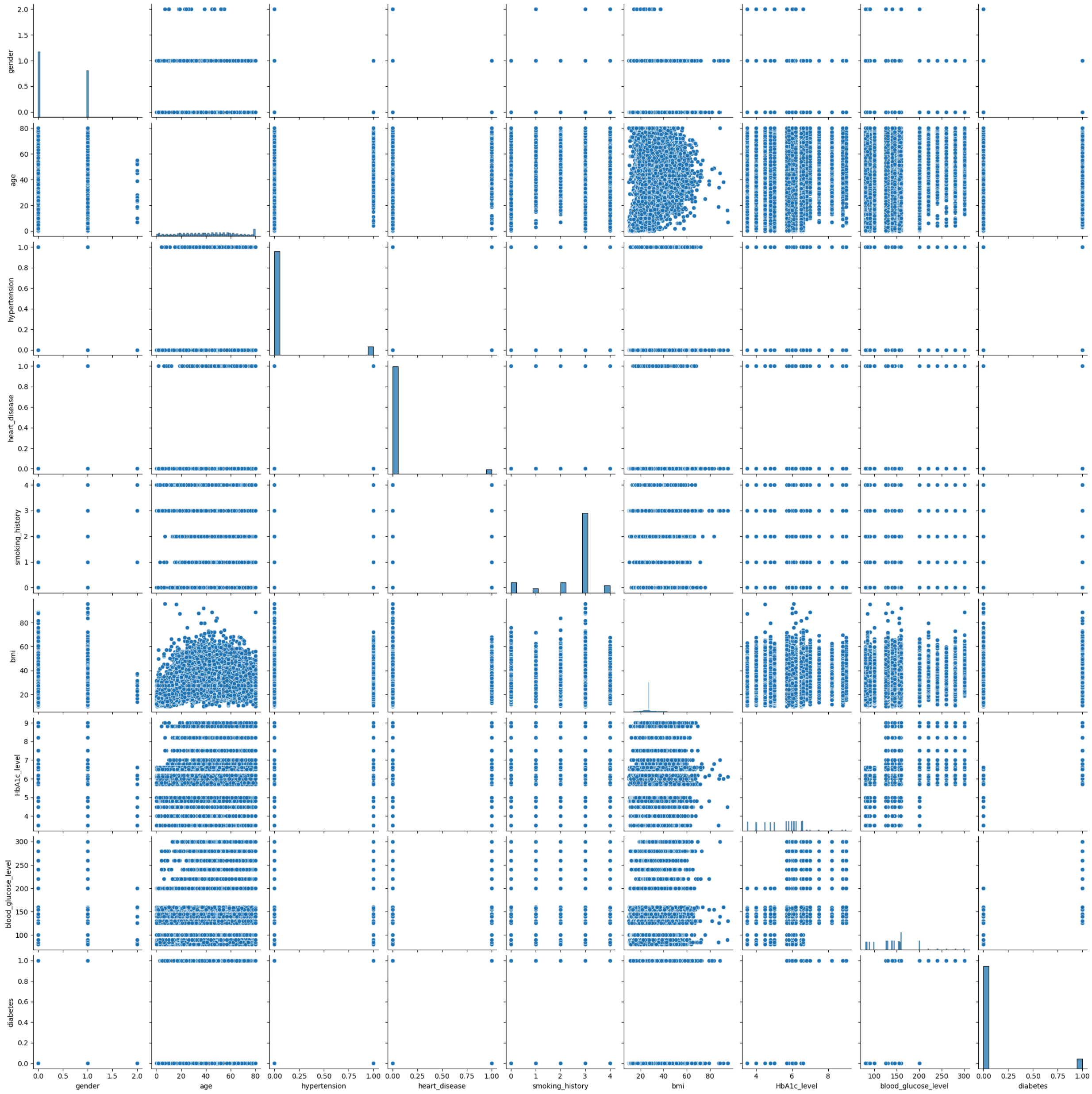
In [27]:
```
sns.lmplot(data=df, x='blood_glucose_level', y='diabetes', fit_reg=False)#implot plot
```

Out[27]: <seaborn.axisgrid.FacetGrid at 0x20a81dc7c50>



In [28]:

```
sns.pairplot(df) #using pairplot to check relation between parameters

#print the pairplot
plt.show()
```




```
'''when age increase hypertension and hert disease ,blood_glucose_level and diabetes and age  and also the is a
   relationship between them

    *bmi

    *HbA1c_level

    *blood_glucose_level

    these four paramers have relationship between each other

    *gender and smokling history it doesnot effect on diabetes

'''
```

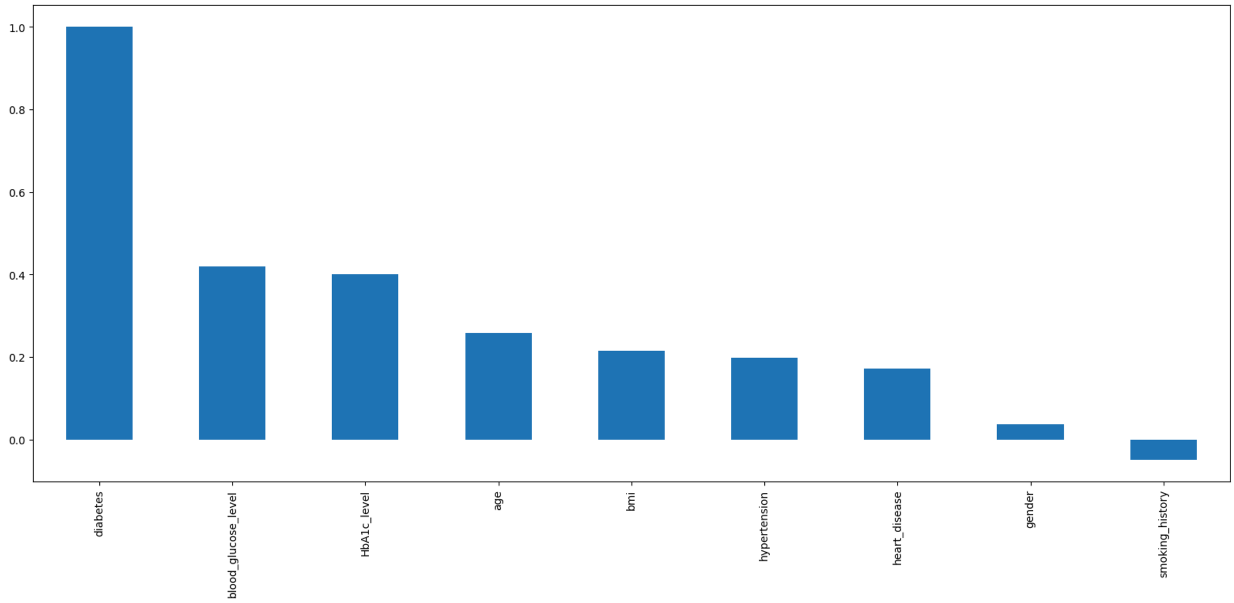
In [29]:
```python
df.corr()
```

Out[29]:

	gender	age	hypertension	heart_disease	smoking_history	bmi	HbA1c_level	blood_glucose
gender	1.000000	-0.030656	0.014203	0.077696	-0.044081	-0.022994	0.019957	0.0
age	-0.030656	1.000000	0.251171	0.233354	-0.098969	0.337396	0.101354	0.1
hypertension	0.014203	0.251171	1.000000	0.121262	-0.048631	0.147666	0.080939	0.0
heart_disease	0.077696	0.233354	0.121262	1.000000	-0.048253	0.061198	0.067589	0.0
smoking_history	-0.044081	-0.098969	-0.048631	-0.048253	1.000000	-0.087735	-0.017534	-0.0
bmi	-0.022994	0.337396	0.147666	0.061198	-0.087735	1.000000	0.082997	0.0
HbA1c_level	0.019957	0.101354	0.080939	0.067589	-0.017534	0.082997	1.000000	0.1
blood_glucose_level	0.017199	0.110672	0.084429	0.070066	-0.022985	0.091261	0.166733	1.0
diabetes	0.037411	0.258008	0.197823	0.171727	-0.049841	0.214357	0.400660	0.4

In [30]:
```python
plt.figure(figsize=(20,8)) #figsize

#printing graphical representations of
df.corr()['diabetes'].sort_values(ascending=False).plot(kind='bar')
```

Out[30]: <Axes: >



In [31]:
```python
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 100000 entries, 0 to 99999
Data columns (total 9 columns):
 #   Column               Non-Null Count   Dtype  
---  ------               --------------   -----  
 0   gender               100000 non-null  int32  
 1   age                  100000 non-null  float64
 2   hypertension         100000 non-null  int64  
 3   heart_disease        100000 non-null  int64  
 4   smoking_history      100000 non-null  int32  
 5   bmi                  100000 non-null  float64
 6   HbA1c_level          100000 non-null  float64
 7   blood_glucose_level  100000 non-null  int64  
 8   diabetes             100000 non-null  int64  
dtypes: float64(3), int32(2), int64(4)
memory usage: 6.1 MB
```

In [32]:
```
#selecting X variables
X = df.loc[:, 'age':'heart_disease'].join(df.loc[:, 'bmi':'blood_glucose_level'])
X
```

Out[32]:

	age	hypertension	heart_disease	bmi	HbA1c_level	blood_glucose_level
0	80.0	0	1	25.19	6.6	140
1	54.0	0	0	27.32	6.6	80
2	28.0	0	0	27.32	5.7	158
3	36.0	0	0	23.45	5.0	155
4	76.0	1	1	20.14	4.8	155
...	...	...	...	...	...	...
99995	80.0	0	0	27.32	6.2	90
99996	2.0	0	0	17.37	6.5	100
99997	66.0	0	0	27.83	5.7	155
99998	24.0	0	0	35.42	4.0	100
99999	57.0	0	0	22.43	6.6	90

100000 rows × 6 columns

In [33]:
```
y=df.loc[:,'diabetes']  #y variable

y #printing y variable
```

Out[33]:
```
0        0
1        0
2        0
3        0
4        0
        ..
99995    0
99996    0
99997    0
99998    0
99999    0
Name: diabetes, Length: 100000, dtype: int64
```

Data partision

In [34]:
```
# spliting trining and testing data in 70 30 rating testing size is 0.3 random_state=42

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)
```

In [35]:
```
X_train.head() #printing X_train data
```

Out[35]:

	age	hypertension	heart_disease	bmi	HbA1c_level	blood_glucose_level
76513	49.0	0	0	27.32	5.0	155
60406	64.0	0	0	27.32	3.5	145
27322	24.0	0	0	27.32	3.5	130
53699	55.0	0	0	27.32	6.5	159
65412	14.0	0	0	20.98	6.2	85

In [36]:
```
print('Shape of Train data')

print(X_train.shape)

print(y_train.shape)

print('Shape of Testing data')

print(X_test.shape)

print(y_test.shape)
```

```
Shape of Train data
(70000, 6)
(70000,)
Shape of Testing data
(30000, 6)
(30000,)
```

In [37]:
```
ss=StandardScaler() #activating StandardScaler()
ss
```

Out[37]:
```
▾ StandardScaler
StandardScaler()
```

In [38]:
```
X_train_scaled = ss.fit_transform(X_train) #scaling X_train data
```

In [39]:
```
if len(X_test.shape) == 1:   #if x is 1d array
    X_test = X_test.values.reshape(-1, 1) #converting to 2d array

X_test_scaled = ss.fit_transform(X_test) #scaling X_test data
```

In [41]:
```
model_lr = LogisticRegression()  #activating Logistic Regression
model_lr = model_lr.fit(X_train_scaled,y_train) #training logistic regression model
model_lr
```

Out[41]:
```
▾ LogisticRegression
LogisticRegression()
```

In [ ]:
```

```

In [42]:
```
y_pred=model_lr.predict(X_test_scaled) #predecting y_test data
y_pred[:10]
```

Out[42]:
```
array([0, 0, 0, 0, 0, 1, 0, 0, 0, 0], dtype=int64)
```

In [43]:
```
y_test[:10] # actual y_test data
```

Out[43]:
```
75721    0
80184    0
19864    0
76699    0
92991    1
76434    0
84004    0
80917    0
60767    0
50074    0
Name: diabetes, dtype: int64
```

In [44]:
```
accuracy_score(y_pred,y_test) #accuracy_score
```

Out[44]:
```
0.9587333333333333
```

In [45]:
```
print(classification_report(y_pred,y_test)) #classifiaction_report
```

```
              precision    recall  f1-score   support

           0       0.99      0.97      0.98     28183
           1       0.61      0.86      0.72      1817

    accuracy                           0.96     30000
   macro avg       0.80      0.91      0.85     30000
weighted avg       0.97      0.96      0.96     30000
```

''' As you can see that the accuracy is quite low, and as it's an imbalanced dataset, we shouldn't consider Accuracy as our metrics to measure the model, as Accuracy is cursed in imbalanced datasets. Hence, we need to check recall, precision & f1 score for the minority class, and it's quite evident that the precision, recall & f1 score is too low for Class 1, i.e. churned customers. Hence, moving ahead to call SMOTEENN (UpSampling + ENN)'''

'''main advantage of using SMOTEENN is that it addresses both overfitting and underfitting issues that can arise from class imbalance. By generating synthetic samples and removing noisy ones'''

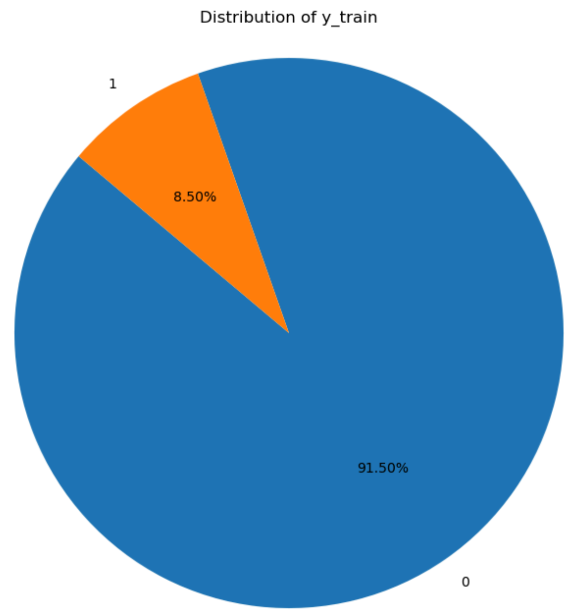
In [46]:
```
confusion_matrix(y_pred,y_test) #confusion_matrix
```

Out[46]:
```
array([[27199,   984],
       [  254,  1563]], dtype=int64)
```

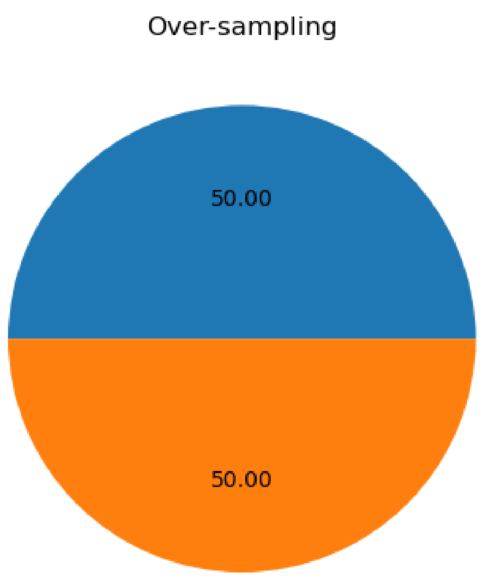
In [47]:
```
y_train.value_counts() #data is highly imblancing
```

Out[47]:
```
diabetes
0    64047
1     5953
Name: count, dtype: int64
```

In [48]:
```
value_counts=y_train.value_counts()

plt.figure(figsize=(16, 8))

plt.pie(value_counts, labels=value_counts.index, autopct='%1.2f%%', startangle=140)

plt.title('Distribution of y_train')

plt.axis('equal')  # Equal aspect ratio ensures that pie is drawn as a circle.

plt.show()
```



In [49]:
```
from imblearn.over_sampling import SMOTE # using smote function to balance our set

smote=SMOTE()

X_ovs,y_ovs=smote.fit_resample(X,y) #passing X and y variables to it to balance out data to 50 50

fig, oversp = plt.subplots()

oversp.pie( y_ovs.value_counts(), autopct='%.2f')

oversp.set_title("Over-sampling")

plt.show()
```



In [50]:
```
# Dividing our resampling data into 70 30 ratio

Xr_train, Xr_test, yr_train, yr_test = train_test_split(X_ovs,y_ovs,train_size=0.7,random_state=42
```

In [51]:
```
print('train data shape')

print(Xr_train.shape)

print(yr_train.shape)

print('test data shape')

print(Xr_test.shape)

print(yr_test.shape)
```

```
train data shape
(128099, 6)
(128099,)
test data shape
(54901, 6)
(54901,)
```

In [52]:
```python
print('y_train and y_test value_count')
print(yr_train.value_counts())
print(yr_test.value_counts())

```

```
y_train and y_test value_count
diabetes
0    64131
1    63968
Name: count, dtype: int64
diabetes
1    27532
0    27369
Name: count, dtype: int64
```

In [53]:
```python
ss=StandardScaler()

ss
```

Out[53]:
```
▾ StandardScaler
StandardScaler()
```

In [55]:
```python
data = Xr_train,Xr_test

Xr_train_sc = ss.fit_transform(Xr_train)            # scaling our resampling data xr train

Xr_test_sc = ss.fit_transform(Xr_test)              # scaling our resamplig xr_test data
```

In [56]:
```python
Xr_train_scaled = pd.DataFrame(Xr_train_sc) #Xr_train_scaled converting into the data frame

print(Xr_train_scaled.shape)
print(yr_train.shape)
```

```
(128099, 6)
(128099,)
```

In [57]:
```python
Xr_train_scaled.head()
```

Out[57]:

	0	1	2	3	4	5
0	-0.752938	-0.293224	-0.204063	0.793742	-0.073425	0.988984
1	-1.513996	-0.293224	-0.204063	-0.669494	0.369006	-0.590454
2	0.487276	-0.293224	4.900454	-0.035747	-0.932747	-1.116933
3	1.176239	-0.293224	-0.204063	-0.295612	-0.036453	0.988984
4	0.580358	3.410359	-0.204063	1.486063	-0.037792	-0.099073

In [58]:
```python
Xr_test_scaled=pd.DataFrame(Xr_test_sc) #Xr_test converting into the dataframe

print(Xr_test_scaled.shape)
Xr_test_scaled.head()
```

```
(54901, 6)
```

Out[58]:

	0	1	2	3	4	5
0	-1.699575	-0.293565	-0.204606	-0.813969	0.370709	-0.077812
1	-1.095207	-0.293565	-0.204606	-0.404864	0.370709	-0.060273
2	-1.467126	-0.293565	-0.204606	-0.287256	0.370709	-1.463333
3	-0.769778	3.406396	-0.204606	0.292576	0.370709	-1.375641
4	-1.374146	-0.293565	-0.204606	-0.287256	-2.151794	-1.112568

In [59]:
```
model_lk = LogisticRegression()
model_lk = model_lk.fit(Xr_train_scaled,yr_train)  #trining the model
model_lk
```

Out[59]:
```
▾ LogisticRegression
LogisticRegression()
```

In [60]:
```
y_pred_lr = model_lk.predict(Xr_test_scaled) #predecting yr_test data
y_pred_lr[:10]
```

Out[60]:
```
array([0, 0, 0, 0, 0, 1, 0, 0, 0, 1], dtype=int64)
```

In [61]:
```
yr_test[:10]
```

Out[61]:
```
180328    1
573       0
13494     0
93981     0
75389     0
180973    1
71021     0
19293     0
16393     0
121419    1
Name: diabetes, dtype: int64
```

In [62]:
```
#classification_report for predict value and orginal value

print(classification_report(y_pred_lr,yr_test))
```

```
              precision    recall  f1-score   support

           0       0.88      0.88      0.88     27429
           1       0.88      0.88      0.88     27472

    accuracy                           0.88     54901
   macro avg       0.88      0.88      0.88     54901
weighted avg       0.88      0.88      0.88     54901
```

after using smote function now our model is good precision , recall , f1-score, support is good we got excate results for all the matrics lets perform with other algo

In [63]:
```
#confusion_matrix for predict value and orginal value

confusion_matrix(y_pred_lr,yr_test)
```

Out[63]:
```
array([[24174,  3255],
       [ 3195, 24277]], dtype=int64)
```

DecisionTreeClassifier

In [64]:
```
# activating DecisionTree Classifier
model_dtc = DecisionTreeClassifier()

# passing xr_train_scaled, yr_train to trining the model
model_dtc = model_dtc.fit(Xr_train_scaled,yr_train)

model_dtc
```

Out[64]:
```
▾ DecisionTreeClassifier
DecisionTreeClassifier()
```

In [65]:
```
y_pred_dtc = model_dtc.predict(Xr_test_scaled) # predicting yr_test data
```

In [66]:
```
# classification report for decisionTreeclassifier

print(classification_report(y_pred_dtc,yr_test))
```

```
              precision    recall  f1-score   support

           0       0.63      1.00      0.77     17278
           1       1.00      0.73      0.84     37623

    accuracy                           0.81     54901
   macro avg       0.81      0.86      0.81     54901
weighted avg       0.88      0.81      0.82     54901
```

In [67]:
```
confusion_matrix(y_pred_dtc,yr_test)
```

Out[67]:
```
array([[17222,    56],
       [10147, 27476]], dtype=int64)
```

RandomForestClassifier()

In [68]:
```
model_rfc = RandomForestClassifier() #activating the fuction

model_rfc = model_rfc.fit(Xr_train_scaled,yr_train)
model_rfc
```

Out[68]:
```
▾ RandomForestClassifier
RandomForestClassifier()
```

In [69]:
```
y_pred_rfc = model_rfc.predict(Xr_test_scaled)
y_pred_rfc
```

Out[69]:
```
array([1, 1, 1, ..., 1, 1, 1], dtype=int64)
```

In [70]:
```
print(classification_report(y_pred_rfc,yr_test))
```

```
              precision    recall  f1-score   support

           0       0.78      0.99      0.87     21685
           1       0.99      0.82      0.90     33216

    accuracy                           0.89     54901
   macro avg       0.89      0.91      0.89     54901
weighted avg       0.91      0.89      0.89     54901
```

In [71]:
```
confusion_matrix(y_pred_rfc,yr_test)
```

Out[71]:
```
array([[21456,   229],
       [ 5913, 27303]], dtype=int64)
```

XGBOOST

In [72]:
```
model_xgb = XGBClassifier()
model_xgb = model_xgb.fit(Xr_train_scaled,yr_train)
model_xgb
```

Out[72]:
```
XGBClassifier
colsample_bylevel=None, colsample_bynode=None,
colsample_bytree=None, device=None, early_stopping_rounds=None,
enable_categorical=False, eval_metric=None, feature_types=None,
gamma=None, grow_policy=None, importance_type=None,
interaction_constraints=None, learning_rate=None, max_bin=None,
max_cat_threshold=None, max_cat_to_onehot=None,
max_delta_step=None, max_depth=None, max_leaves=None,
min_child_weight=None, missing=nan, monotone_constraints=None,
multi_strategy=None, n_estimators=None, n_jobs=None,
num_parallel_tree=None, random_state=None, ...)
```

In [74]:
```
y_pred_xgb = model_xgb.predict(Xr_test_scaled)
y_pred_xgb
```

Out[74]:
```
array([0, 0, 0, ..., 1, 1, 1])
```

In [75]:
```
print(classification_report(y_pred_xgb,yr_test))
```

```
              precision    recall  f1-score   support

           0       0.89      0.98      0.93     24804
           1       0.98      0.90      0.94     30097

    accuracy                           0.93     54901
   macro avg       0.93      0.94      0.93     54901
weighted avg       0.94      0.93      0.93     54901
```

In [76]:
```
confusion_matrix(y_pred_xgb,yr_test)
```

Out[76]:
```
array([[24292,   512],
       [ 3077, 27020]], dtype=int64)
```

finding the hyperparameter tuning and best param grid

In [77]:

```
from sklearn.model_selection import GridSearchCV, cross_val_score
from sklearn.linear_model import LogisticRegression

# Define the parameter grid to search over
param_grid = {
    'C': [0.001, 0.01, 0.1, 1, 10, 100],  # Regularization parameter
    'penalty': ['l1', 'l2']                # Penalty type
}

# Create a Logistic Regression model
logistic = LogisticRegression()

# Create a GridSearchCV object
grid_search = GridSearchCV(estimator=logistic, param_grid=param_grid, cv=10)

# Initialize an empty list to store the accuracy scores
accuracy_scores = []

# Perform cross-validation 10 times
for _ in range(10):
    # Fit the GridSearchCV object to the training data
    grid_search.fit(Xr_train_scaled, yr_train)

    # Get the best parameters
    best_params = grid_search.best_params_

    # Perform cross-validation with the best model
    cv_scores = cross_val_score(grid_search.best_estimator_, Xr_train_scaled, yr_train, cv=10)

    # Store the mean accuracy score
    accuracy_scores.append(cv_scores.mean())

# Print the accuracy scores obtained over 10 iterations
#print("Accuracy scores over 10 iterations:", accuracy_scores)
print("Accuracy scores over 10 iterations:", ["{:.2f}".format(score) for score in accuracy_scores]


# Get the best parameters and best score
best_params = grid_search.best_params_
best_score = grid_search.best_score_

print("Best parameters found:", best_params)
print("Best cross-validation score:", best_score)

```

```
Accuracy scores over 10 iterations: ['0.89', '0.89', '0.89', '0.89', '0.89', '0.89', '0.89', '0.89',
'0.89', '0.89']
Best parameters found: {'C': 0.001, 'penalty': 'l2'}
Best cross-validation score: 0.8858148547606524
```

FINAL MODEL

In [78]:

```
from sklearn.linear_model import LogisticRegression

# Create a Logistic Regression model with the best parameters
final_model = LogisticRegression(C=0.001, penalty='l2')

# Fit the final model to the entire training dataset
final_model.fit(Xr_train_scaled, yr_train)

```

Out[78]:

```
LogisticRegression
LogisticRegression(C=0.001)
```

In [79]:

```python
import pickle

# Save the final model to a pickle file
with open('final_model.pkl', 'wb') as file:
    pickle.dump(final_model, file)

```

In [80]:

```python
import pickle
import numpy as np

# Load the model from the pickle file
with open('final_model.pkl', 'rb') as file:
    loaded_model = pickle.load(file)

# Define the mean and standard deviation of the training data
mean_values = [41.885856, 0.07485, 0.03942, 27.320767, 5.527507, 138.058060]
std_values = [22.516840, 0.26315, 0.194593, 6.636783, 1.070672, 40.708136]

# Define the input features for prediction
age = 30
hypertension = 0
heart_disease = 0
bmi = 100.0
HbA1c_level = 5.0
blood_glucose_level = 90

# Scale the input features manually
scaled_features = [(x - mean) / std for x, mean, std in zip(
    [age, hypertension, heart_disease, bmi, HbA1c_level, blood_glucose_level],
    mean_values, std_values
)]

# Make predictions on the scaled data
prediction = loaded_model.predict([scaled_features])

# Print the prediction
if prediction[0] == 1:
    print("Diabetic")
else:
    print("Not Diabetic")

```

```
Diabetic
```