In [ ]:

```
import pandas as pd
import numpy as np
import scipy.optimize as opt
import statsmodels.api as sm
from sklearn import preprocessing
import matplotlib.pyplot as plt
import seaborn as sns

df=pd.read_csv("/content/diabetes_prediction_dataset.csv")
df.head()
```

Out[ ]:

	gender	age	hypertension	heart_disease	smoking_history	bmi	HbA1c_level	blooc
0	Female	80.0	0	1	never	25.19	6.6	
1	Female	54.0	0	0	No Info	27.32	6.6	
2	Male	28.0	0	0	never	27.32	5.7	
3	Female	36.0	0	0	current	23.45	5.0	
4	Male	76.0	1	1	current	20.14	4.8	

INFORMATION OF THE DATASET

In [ ]:

```
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 [ ]:

```
df.shape
```

Out[ ]:

```
(100000, 9)
```

In [ ]:

```
df.describe()
```

Out[ ]:

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

```
In [ ]: df.isnull()
```

Out[ ]:

	gender	age	hypertension	heart_disease	smoking_history	bmi	HbA1c_level
0	False	False	False	False	False	False	False
1	False	False	False	False	False	False	False
2	False	False	False	False	False	False	False
3	False	False	False	False	False	False	False
4	False	False	False	False	False	False	False
...	...	...	...	...	...	...	...
99995	False	False	False	False	False	False	False
99996	False	False	False	False	False	False	False
99997	False	False	False	False	False	False	False
99998	False	False	False	False	False	False	False
99999	False	False	False	False	False	False	False

100000 rows × 9 columns

```
Warning: total number of rows (100000) exceeds max_rows (20000). Limiting to
(20000) rows.
```

CHECKING OF DUPLICATE VALUES

```
In [ ]: df.duplicated().sum()
```

```
Out[ ]: 3854
```

REMOVAL OF DUPLICATE VALUES

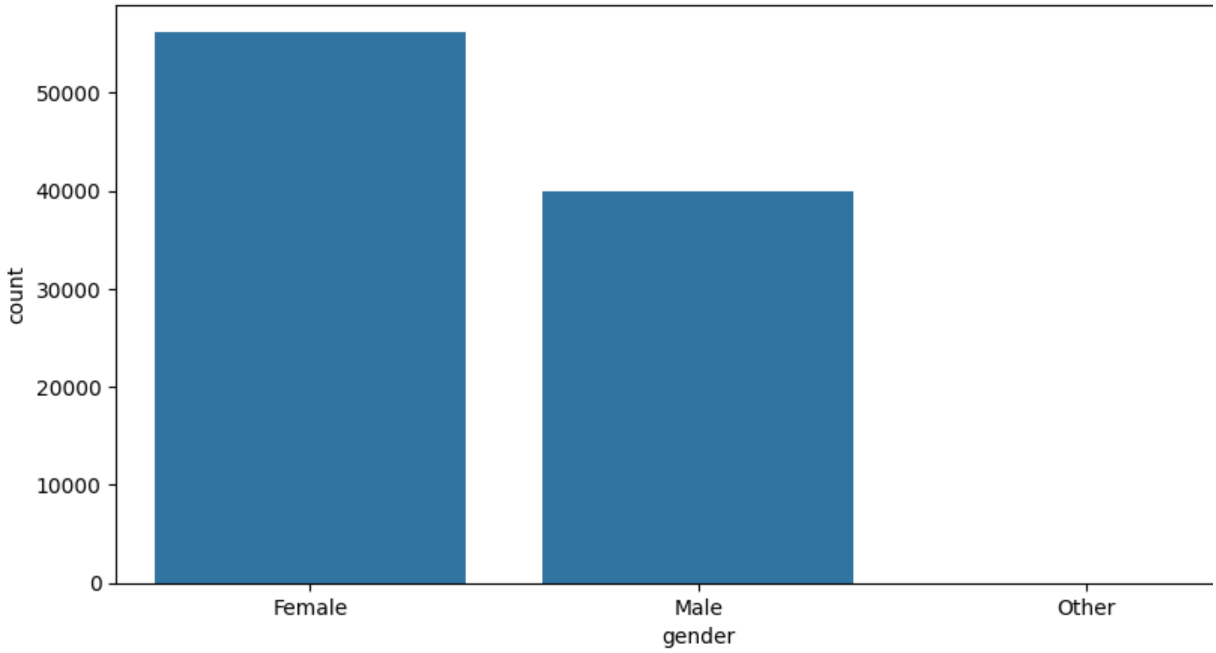
```
In [ ]: df.drop_duplicates(inplace=True)
        df.duplicated().sum()
```

```
Out[ ]: 0
```

GENDER DISTRIBUTION INFORMATION

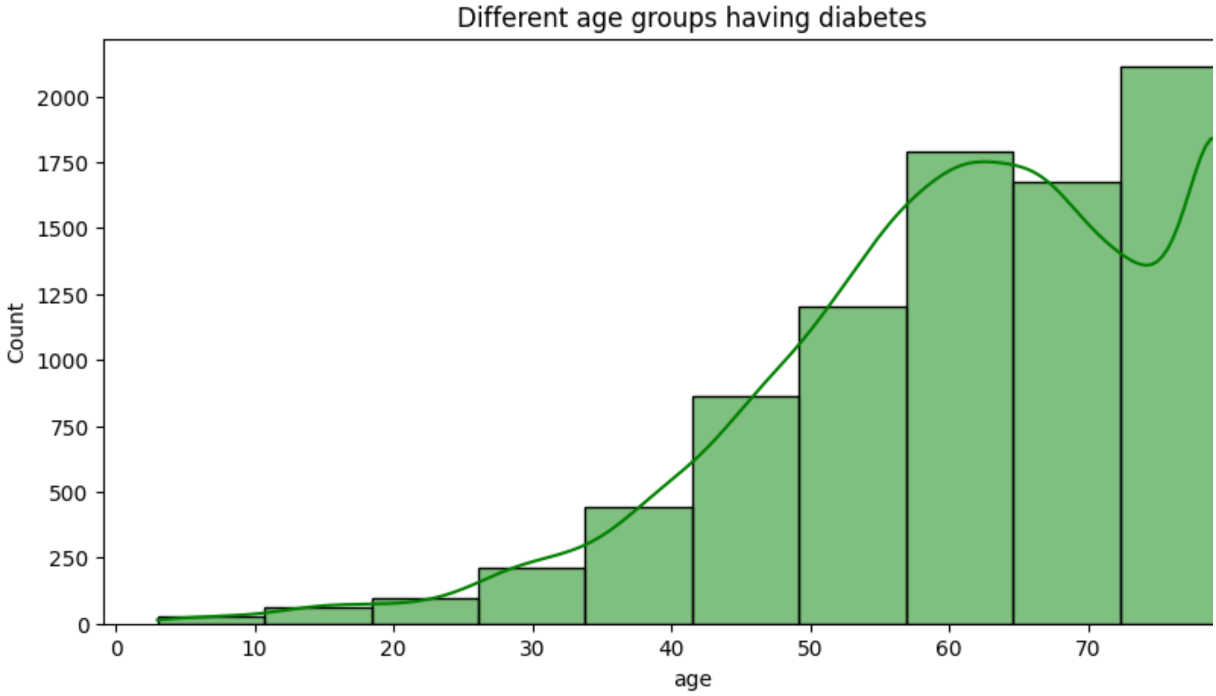
```
In [ ]: plt.figure(figsize=(10,5))
        sns.countplot(x='gender',data=df)
```

```
Out[ ]: <Axes: xlabel='gender', ylabel='count'>
```



DIFFERENT AGE GROUPS HAVING DIABETES

```
In [ ]: plt.figure(figsize=(10,5))
        sns.histplot(df['age'][df['diabetes']==1],bins=10,color='green',kde=True)
        plt.title('Different age groups having diabetes')
        plt.show()
```



PEOPLE INVOLVED IN SMOKING

```
In [ ]: df['smoking_history'].value_counts()
```

```
Out[ ]:                       count
        smoking_history
                  never       34398
                No Info       32887
                 former        9299
                current        9197
            not current        6367
                   ever        3998


        dtype: int64
```

PEOPLE SUFFERING FROM HEART DISEASE

```
In [ ]: df['heart_disease'].value_counts()
```

```
Out[ ]:                  count
        heart_disease
                    0    92223
                    1     3923


        dtype: int64
```

PEOPLE SUFFERING FROM HYPERTENSION

```
In [ ]: df['hypertension'].value_counts()
```

```
Out[ ]:                 count
        hypertension
                   0    88685
                   1     7461


        dtype: int64
```

```
In [ ]: df.drop(columns=['hypertension'],inplace=True)
```

```
In [ ]: df.head()
```

Out[ ]:

	gender	age	heart_disease	smoking_history	bmi	HbA1c_level	blood_glucose_level
0	Female	80.0	1	never	25.19	6.6	140
1	Female	54.0	0	No Info	27.32	6.6	80
2	Male	28.0	0	never	27.32	5.7	158
3	Female	36.0	0	current	23.45	5.0	155
4	Male	76.0	1	current	20.14	4.8	155

```
In [ ]: x=df.drop(columns=['diabetes'])
        y=df['diabetes']
```

```
In [ ]: from sklearn.model_selection import train_test_split
        x_train, x_test, train_y, test_y = train_test_split(x, y, test_size=0.2,
        train_y = np.nan_to_num(train_y)
```

```
In [ ]: df.head()
```

Out[ ]:

	gender	age	heart_disease	smoking_history	bmi	HbA1c_level	blood_glucose_level
0	Female	80.0	1	never	25.19	6.6	140
1	Female	54.0	0	No Info	27.32	6.6	80
2	Male	28.0	0	never	27.32	5.7	158
3	Female	36.0	0	current	23.45	5.0	155
4	Male	76.0	1	current	20.14	4.8	155

LINEAR REGRESSION

```
In [ ]: from sklearn.model_selection import train_test_split
        from sklearn.linear_model import LinearRegression
        # Instead of recreating dummy variables, select the relevant columns for
        x = df[['age','HbA1c_level','blood_glucose_level']]  # Features
        y = df['diabetes']  # Target
        x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.2,
        model = LinearRegression()
        model.fit(x_train, y_train)
        y_pred = model.predict(x_test)
```

```
In [ ]: model.score(x_train,y_train)
```

```
Out[ ]: 0.3294808573465473
```

```
In [ ]: model.score(x_test,y_test)
```

```
Out[ ]: 0.33316792290875474
```

LOGISTIC REGRESSION

```
In [ ]: from sklearn.linear_model import LogisticRegression
        from sklearn.metrics import accuracy_score
        log_reg = LogisticRegression()
        log_reg.fit(x_train, y_train)
```

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

```
In [ ]: log_reg.score(x_train,y_train)
```

```
Out[ ]:  0.9571740600135212
```

```
In [ ]: log_reg.score(x_test,y_test)
```

```
Out[ ]:  0.9551742069682787
```

ACCURACY, PRECISION, RECALL, F1 SCORE, CONFUSION MATRIX

```
In [ ]: from sklearn.metrics import accuracy_score, precision_score, recall_score

        def evaluate_model(model, X_test, y_test):

            y_pred = model.predict(X_test)

            print("Accuracy:", accuracy_score(y_test, y_pred))
            print("Precision:", precision_score(y_test, y_pred))
            print("Recall:", recall_score(y_test, y_pred))
            print("F1 Score:", f1_score(y_test, y_pred))
            print("\nConfusion Matrix:\n", confusion_matrix(y_test, y_pred))


        evaluate_model(log_reg, x_test, y_test)
```

```
Accuracy: 0.9551742069682787
Precision: 0.8731537793223284
Recall: 0.5839628123184195
F1 Score: 0.6998607242339833

Confusion Matrix:
 [[17363   146]
 [  716  1005]]
```

DECISION TREE

```
In [ ]: from sklearn.tree import DecisionTreeClassifier  # Import DecisionTreeCla

        dt = DecisionTreeClassifier()
        dt.fit(x_train, y_train)
```

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

```
In [ ]: dt.score(x_train, y_train)
```

```
Out[ ]:  0.9720604295595194
```

```
In [ ]: dt.score(x_test, y_test)
```

```
Out[ ]:  0.9682267290691627
```

ACCURACY, PRECISION, RECALL, F1 SCORE, CONFUSION MATRIX

```
In [ ]: from sklearn.metrics import accuracy_score, precision_score, recall_score

        def evaluate_model(model, X_test, y_test):

            y_pred = model.predict(X_test)

            print("Accuracy:", accuracy_score(y_test, y_pred))
            print("Precision:", precision_score(y_test, y_pred))
            print("Recall:", recall_score(y_test, y_pred))
            print("F1 Score:", f1_score(y_test, y_pred))
            print("\nConfusion Matrix:\n", confusion_matrix(y_test, y_pred))


        evaluate_model(dt, x_test, y_test)
```

```
Accuracy: 0.9682267290691627
Precision: 0.9497568881685575
Recall: 0.6809994189424753
F1 Score: 0.7932318104906937

Confusion Matrix:
 [[17447    62]
 [  549  1172]]
```

TESTING OF THE MODEL

```
In [ ]: import numpy as np
        from sklearn.preprocessing import StandardScaler # Import StandardScaler

        # Example new patient data (replace with actual values)
        new_patient = np.array([[67,6.5,200]])  # Sample feature values

        scaler = StandardScaler()
        scaler.fit(x_train)

        new_patient = scaler.transform(new_patient)

        # Predict the outcome
        prediction = model.predict(new_patient)
        print("Diabetes Prediction:", "Diabetic" if prediction[0] == 1 else "Non-I
```

```
Diabetes Prediction: Non-Diabetic
/usr/local/lib/python3.11/dist-packages/sklearn/utils/validation.py:2739:
UserWarning: X does not have valid feature names, but StandardScaler was fitt
with feature names
  warnings.warn(
/usr/local/lib/python3.11/dist-packages/sklearn/utils/validation.py:2739:
UserWarning: X does not have valid feature names, but LinearRegression was fi
with feature names
  warnings.warn(
```

FOR MULTIPLE PATIENTS

In [ ]:

```
import numpy as np
from sklearn.preprocessing import StandardScaler # Import StandardScaler

# Example new patient data (replace with actual values)
new_patient = np.array([[70,6.6,140],[73,6.5,200]])  # Sample feature val

scaler = StandardScaler()
scaler.fit(x_train)


# Scale input (if you used scaling)
new_patient = scaler.transform(new_patient)

# Predict the outcome
prediction = model.predict(new_patient)

for i, pred in enumerate(prediction):
    print(f"Patient {i+1}: {'Diabetic' if pred == 1 else 'Non-Diabetic'}"
```

```
Patient 1: Non-Diabetic
Patient 2: Non-Diabetic
```

```
/usr/local/lib/python3.11/dist-packages/sklearn/utils/validation.py:2739:
UserWarning: X does not have valid feature names, but StandardScaler was fitt
with feature names
  warnings.warn(
/usr/local/lib/python3.11/dist-packages/sklearn/utils/validation.py:2739:
UserWarning: X does not have valid feature names, but LinearRegression was fi
with feature names
  warnings.warn(
```