Diabetes Prediction using Machine Learning

Diabetes refers to a collection of metabolic disorders characterized by elevated blood sugar levels persisting over an extended period. Symptoms associated with high blood sugar levels include frequent urination, heightened thirst, and increased appetite. Without proper treatment, diabetes can lead to various complications. Acute complications may involve conditions such as diabetic ketoacidosis, hyperosmolar hyperglycemic state, or even mortality. Furthermore, severe long-term consequences encompass cardiovascular ailments, strokes, chronic kidney ailments, foot ulcers, and vision impairment.

We will try to build a machine learning model to accurately predict whether or not the patients in the dataset have diabetes or not?

Number of Observation Units: 768

Variable Number: 9

```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
import pandas as pd
from google.colab import files
uploaded = files.upload()
```

```
Choose Files No file chosen    Upload widget is only available when the cell has been executed in the current browser session. Please rerun this cell to enable.
Saving diabetes.csv to diabetes.csv
```

Reading the dataset which is the CSV format

```
df = pd.read_csv('diabetes.csv')
```

```
df.head()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

Exploratory Data Analysis (EDA)

```
df.shape
```

```
(768, 9)
```

```
df.columns
```

```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

```
df.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
```

```
df.describe()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

```
df.describe().T
```

	count	mean	std	min	25%	50%	75%	max
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	99.00
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	846.00
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	67.10
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

let's check that if our dataset have null values or not

```
df.isnull().head(6)
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	False	False	False	False	False	False	False	False	False
1	False	False	False	False	False	False	False	False	False
2	False	False	False	False	False	False	False	False	False
3	False	False	False	False	False	False	False	False	False
4	False	False	False	False	False	False	False	False	False
5	False	False	False	False	False	False	False	False	False

```
df.isnull().sum()
```

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

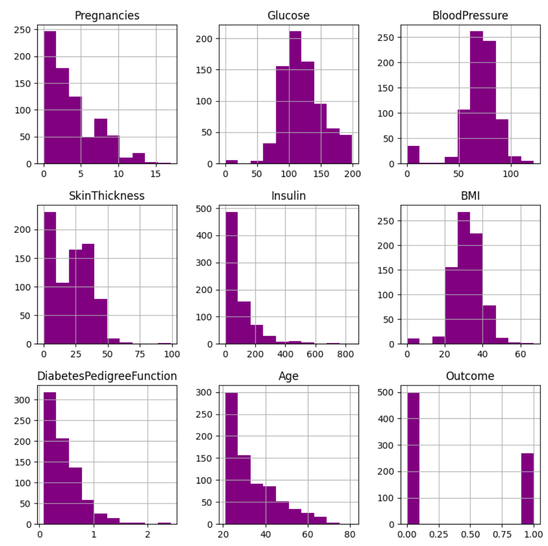
```
df_copy = df.copy(deep = True)
df_copy[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']] = df_copy[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']].replace(0,np.NaN)

# Showing the Count of NANs
print(df_copy.isnull().sum())
```

```
Pregnancies                   0
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
DiabetesPedigreeFunction      0
Age                           0
Outcome                       0
dtype: int64
```

As mentioned above that now we will be replacing the zeros with the NAN values so that we can impute it later to maintain the authenticity of the dataset as well as trying to have a better Imputation approach i.e to apply mean values of each column to the null values of the respective columns.

Data Visalization

```
df.hist(figsize=(10, 10), color="purple")

# Show plot
plt.show()
```



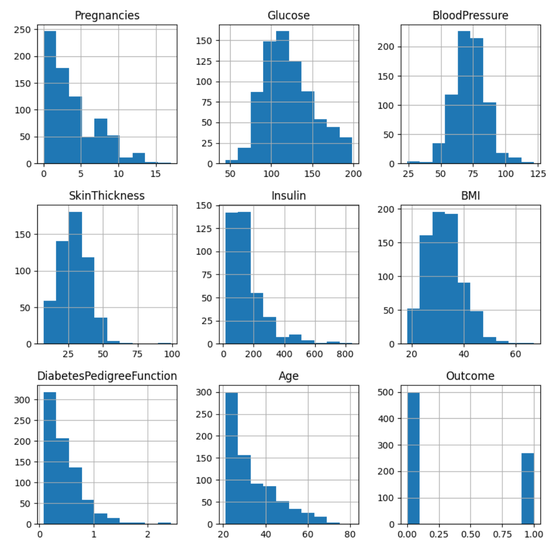
The best way to start the analysis of the dataset is to shows the occurrence of every kind of value in the graphical structure which in turn lets us know the range of the data.

Now we will be imputing the mean value of the column to each missing value of that particular column.

Plotting the distributions after removing the NAN values.

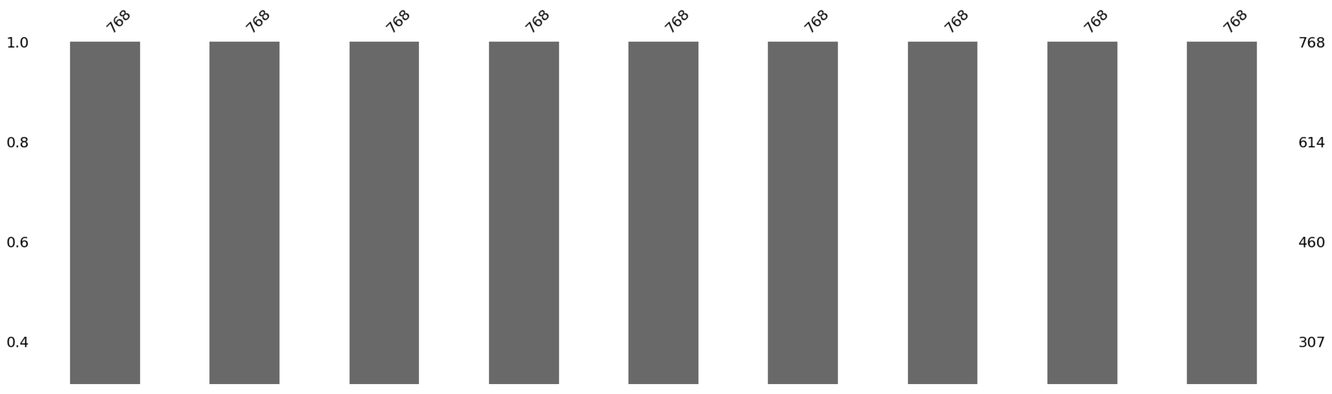
```
df_copy['Glucose'].fillna(df_copy['Glucose'].mean(), inplace = True)
df_copy['BloodPressure'].fillna(df_copy['BloodPressure'].mean(), inplace = True)
df_copy['SkinThickness'].fillna(df_copy['SkinThickness'].median(), inplace = True)
df_copy['Insulin'].fillna(df_copy['Insulin'].median(), inplace = True)
df_copy['BMI'].fillna(df_copy['BMI'].median(), inplace = True)
```

```
p = df_copy.hist(figsize = (10,10))
```



Now we can clearly see that there are no null values in the dataset.

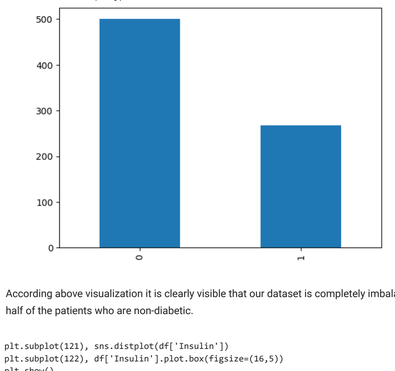
```
import missingno as msno
p = msno.bar(df)
```



Now, let's check that how well our outcome column is balanced

```
color_wheel = {1: "#0392cf", 2: "#7bc043"}
colors = df["Outcome"].map(lambda x: color_wheel.get(x + 1))
print(df.Outcome.value_counts())
p=df.Outcome.value_counts().plot(kind="bar")
```

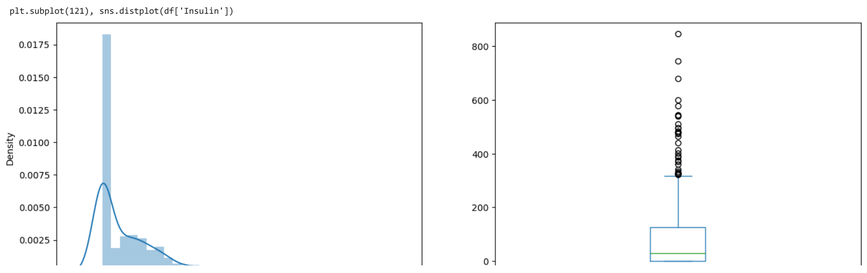
```
0    500
1    268
Name: Outcome, dtype: int64
```



According above visualization it is clearly visible that our dataset is completely imbalanced in fact the number of patients who are diabetic is half of the patients who are non-diabetic.

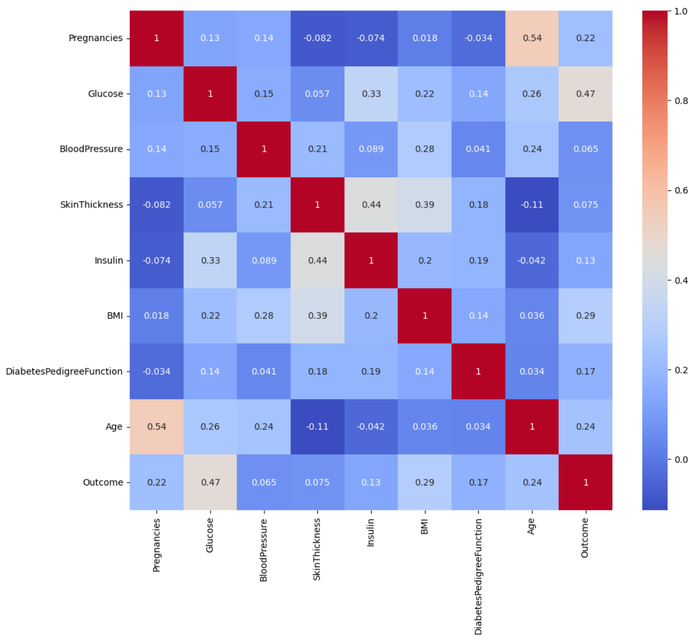
```
plt.subplot(121), sns.distplot(df['Insulin'])
plt.subplot(122), df['Insulin'].plot.box(figsize=(16,5))
plt.show()
```

```
<ipython-input-21-1d062345beba>:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  plt.subplot(121), sns.distplot(df['Insulin'])
```



Correlation between all the features before cleaning

```
plt.figure(figsize=(12, 10))
# Specify the colormap using the cmap parameter
p = sns.heatmap(df.corr(), annot=True, cmap='coolwarm')
plt.show()
```



Model Building

Splitting the dataset

```
x = df.drop('Outcome', axis = 1)
y = df['Outcome']
```

x

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
0	6	148	72	35	0	33.6	0.627	50
1	1	85	66	29	0	26.6	0.351	31
2	8	183	64	0	0	23.3	0.672	32
3	1	89	66	23	94	28.1	0.167	21
4	0	137	40	35	168	43.1	2.288	33
...	...	...	...	...	...	...	...	...
763	10	101	76	48	180	32.9	0.171	63
764	2	122	70	27	0	36.8	0.340	27
765	5	121	72	23	112	26.2	0.245	30
766	1	126	60	0	0	30.1	0.349	47
767	1	93	70	31	0	30.4	0.315	23

768 rows × 8 columns

y

```
0      1
1      0
2      1
3      0
4      1
      ..
763    0
764    0
765    0
766    1
767    0
Name: Outcome, Length: 768, dtype: int64
```

```
x = np.array(x)
y = np.array(y)
```

x

```
array([[  6.   , 148.   ,  72.   , ...,  33.6  ,   0.627,  50.   ],
       [  1.   ,  85.   ,  66.   , ...,  26.6  ,   0.351,  31.   ],
       [  8.   , 183.   ,  64.   , ...,  23.3  ,   0.672,  32.   ],
       ...,
       [  5.   , 121.   ,  72.   , ...,  26.2  ,   0.245,  30.   ],
       [  1.   , 126.   ,  60.   , ...,  30.1  ,   0.349,  47.   ],
       [  1.   ,  93.   ,  70.   , ...,  30.4  ,   0.315,  23.   ]])
```

y

```
array([1, 0, 1, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 1, 0, 1, 0, 0,
       1, 1, 1, 1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 1, 0, 0, 0, 1, 1,
       0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0,
       1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0,
       1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1,
       1, 1, 0, 0, 1, 1, 1, 1, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 1, 1, 1, 1,
       1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0,
       1, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 1, 0, 1, 0, 1,
       0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 1, 0, 1,
       1, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 1, 1, 1, 1, 1, 0, 1, 1,
       1, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 1, 1, 1, 1, 1, 0, 0, 0,
       1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 1, 1, 0, 0,
       1, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 1, 0,
       0, 1, 0, 0, 0, 1, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1, 0, 1, 0, 0, 1, 0,
       1, 1, 0, 0, 1, 0, 1, 0, 0, 1, 0, 1, 0, 1, 1, 1, 0, 0, 1, 0, 1, 0,
       0, 0, 1, 0, 0, 0, 0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0,
       0, 0, 0, 1, 1, 1, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0,
       0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0,
       1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0,
       1, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 1, 0, 1, 0, 1, 0, 1, 0, 1, 0, 0,
       0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 1, 0,
       0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1, 0,
       1, 0, 0, 0, 1, 0, 0, 0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1,
       0, 1, 1, 1, 1, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 0, 0, 1,
       0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 1, 1, 1, 0, 0, 0, 0, 1, 1, 0,
       0, 0, 1, 0, 1, 1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 0, 0,
       0, 0, 0, 0, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0,
       1, 1, 1, 0, 0, 1, 1, 1, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0])
```

Normalize

```
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
x = scaler.fit_transform(x)
```

x

```
array([[ 0.63994726,  0.84832379,  0.14964075, ...,  0.20401277,
         0.46849198,  1.4259954 ],
       [-0.84488505, -1.12339636, -0.16054575, ..., -0.68442195,
        -0.36506078, -0.19067191],
       [ 1.23388019,  1.94372388, -0.26394125, ..., -1.10325546,
         0.60439732, -0.10558415],
       ...,
       [ 0.3429808 ,  0.00330087,  0.14964075, ..., -0.73518964,
```

```
 -0.68519336, -0.27575966],
[-0.84488505,  0.1597866 , -0.47073225, ..., -0.24020459,
 -0.37110101,  1.17073215],
[-0.84488505, -0.8730192 ,  0.04624525, ..., -0.20212881,
 -0.47378505, -0.87137393]])
```

Train / Test

```
from sklearn.model_selection import train_test_split
x_train, x_test, y_train, y_test = train_test_split(x, y, test_size = 0.2)
```

```
x_train.shape, y_train.shape
```

```
((614, 8), (614,))
```

```
x_test.shape, y_test.shape
```

```
((154, 8), (154,))
```

Naive Bayes

Building the model using Naive Bayes

```
from sklearn.naive_bayes import GaussianNB
model = GaussianNB()
model.fit(x_train, y_train)
```

```
GaussianNB()
```

```
y_pred_train = model.predict(x_train)
y_pred_test = model.predict(x_test)
```

```
from sklearn.metrics import accuracy_score
acc_train = accuracy_score(y_true = y_train, y_pred = y_pred_train)
acc_test = accuracy_score(y_true = y_test, y_pred = y_pred_test)
```

```
acc_train, acc_test
```

```
(0.7687296416938111, 0.7467532467532467)
```

```
from sklearn.metrics import confusion_matrix, precision_score, recall_score
```

```
confusion_matrix(y_test, y_pred_test)
```

```
array([[83, 17],
       [22, 32]])
```

```
precision_score(y_test, y_pred_test)
```

```
0.6530612244897959
```

```
precision_score(y_train, y_pred_train)
```

```
0.6855670103092784
```

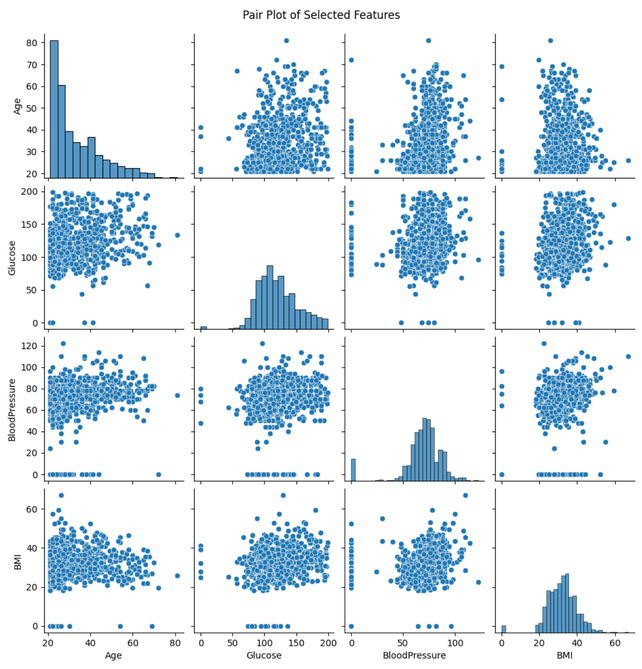
```
recall_score(y_test, y_pred_test)
```

```
0.5925925925925926
```

```
recall_score(y_train, y_pred_train)
```

```
0.6214953271028038
```

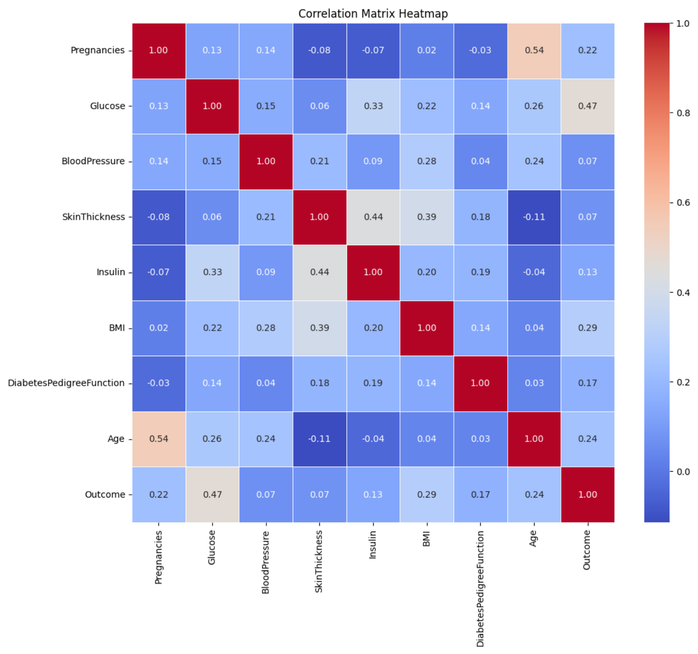
```
selected_features = ['Age', 'Glucose', 'BloodPressure', 'BMI']
# Create a pair plot
sns.pairplot(df[selected_features])
plt.suptitle("Pair Plot of Selected Features", y=1.02)
plt.show()
```




```
df.corr()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.017683	-0.033523	0.544341	0.221898
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.221071	0.137337	0.263514	0.466581
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.281805	0.041265	0.239528	0.065068
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.392573	0.183928	-0.113970	0.074752
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.197859	0.185071	-0.042163	0.130548
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.000000	0.140647	0.036242	0.292695
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.140647	1.000000	0.033561	0.173844
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.036242	0.033561	1.000000	0.238356
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.292695	0.173844	0.238356	1.000000

```
correlation_matrix = df.corr()
# Create a heatmap
plt.figure(figsize=(12, 10))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', fmt=".2f", linewidths=.5)
plt.title("Correlation Matrix Heatmap")
plt.show()
```



KNN

```
from sklearn.neighbors import KNeighborsClassifier

knn = KNeighborsClassifier(n_neighbors=4)
knn.fit(x_train, y_train)
```

```
KNeighborsClassifier(n_neighbors=4)
```

```
y_pred_train = knn.predict(x_train)
y_pred_test = knn.predict(x_test)
```

```
from sklearn.metrics import accuracy_score
acc_train = accuracy_score(y_train, y_pred_train)
acc_test = accuracy_score(y_test, y_pred_test)
acc_train, acc_test
```

```
(0.8094462540716613, 0.7532467532467533)
```

```
from sklearn.metrics import recall_score, precision_score, confusion_matrix
confusion_matrix(y_test, y_pred_test)
```

```
array([[92,  8],
       [30, 24]])
```

```
p = precision_score(y_test, y_pred_test)
p
```

```
0.75
```

```
r = recall_score(y_test, y_pred_test)
r
```

```
0.4444444444444444
```

As evident from the results, the recall_score is unsatisfactory. By augmenting the value of k, we observe an improvement in the recall score. Therefore, increasing the value of k can enhance the recall performance for this dataset.

```
from sklearn.neighbors import KNeighborsClassifier

knn = KNeighborsClassifier(n_neighbors= 8)
knn.fit(x_train, y_train)
y_pred_train = knn.predict(x_train)
y_pred_test = knn.predict(x_test)
from sklearn.metrics import accuracy_score
acc_train = accuracy_score(y_train, y_pred_train)
acc_test = accuracy_score(y_test, y_pred_test)
acc_train, acc_test
```

```
(0.7931596091205212, 0.7532467532467533)
```

```
from sklearn.metrics import recall_score, precision_score, confusion_matrix
confusion_matrix(y_test, y_pred_test)
```

```
array([[91,  9],
       [29, 25]])
```

```
p = precision_score(y_test, y_pred_test)
p
```

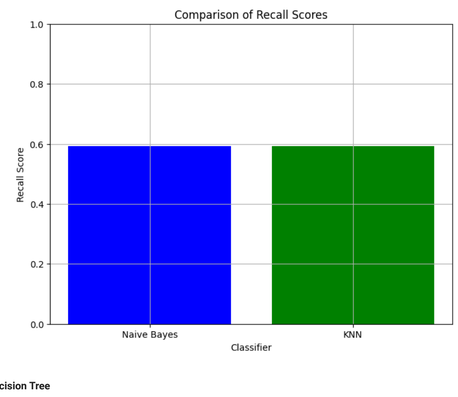
```
0.7352941176470589
```

```
r = recall_score(y_test, y_pred_test)
r
```

```
0.46296296296296297
```

When considering this code, if we contrast the recall metrics between the KNN and Naive Bayes models, it becomes apparent that the Naive Bayes model outperforms KNN on this dataset.

```
import matplotlib.pyplot as plt
from sklearn.naive_bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import recall_score


naive_bayes = GaussianNB()
knn = KNeighborsClassifier()

naive_bayes.fit(x_train, y_train)
knn.fit(x_train, y_train)

# Predictions for Naive Bayes
y_pred_nb = naive_bayes.predict(x_test)
y_pred_knn = knn.predict(x_test)

recall_nb = recall_score(y_test, y_pred_nb)
recall_knn = recall_score(y_test, y_pred_knn)


plt.figure(figsize=(8, 6))


plt.bar(['Naive Bayes', 'KNN'], [recall_nb, recall_knn], color=['blue', 'green'])

plt.title('Comparison of Recall Scores')
plt.xlabel('Classifier')
plt.ylabel('Recall Score')

plt.ylim(0, 1)  # Limiting y-axis from 0 to 1 for better visualization
plt.grid(True)
plt.show()
```



Decision Tree

Building the model using DecisionTree

```
from sklearn.tree import DecisionTreeClassifier
dt = DecisionTreeClassifier(max_depth=8, min_samples_split=4, min_samples_leaf=2)
dt.fit(x_train, y_train)
```

```
DecisionTreeClassifier(max_depth=8, min_samples_leaf=2, min_samples_split=4)
```

Random Forest

Building the model using Random Forest

```
from sklearn.ensemble import RandomForestClassifier

rf = RandomForestClassifier(n_estimators=100)
rf.fit(x_train, y_train)
```

```
RandomForestClassifier()
```

Getting the accuracy score for Decision Tree and Random Forest

```
from sklearn.metrics import accuracy_score
y_pred_train_dt = dt.predict(x_train)
y_pred_train_rf = rf.predict(x_train)
acc_train_dt = accuracy_score(y_train, y_pred_train_dt)
acc_train_rf = accuracy_score(y_train, y_pred_train_rf)
acc_train_dt, acc_train_rf
```

```
(0.9071661237785016, 1.0)
```

```
y_pred_test_dt = dt.predict(x_test)
y_pred_test_rf = rf.predict(x_test)
acc_test_dt = accuracy_score(y_test, y_pred_test_dt)
acc_test_rf = accuracy_score(y_test, y_pred_test_rf)
acc_test_dt, acc_test_rf
```

```
(0.7662337662337663, 0.7402597402597403)
```

Based on the information provided, it's observed that while the Random Forest model achieves a perfect accuracy of 100% on the training data, its accuracy drops to 0.7467 on the test data. This indicates the model's tendency to overfit the training data. By introducing a maximum depth parameter, we anticipate observing alterations in the model's performance.

```
from sklearn.ensemble import RandomForestClassifier

rf = RandomForestClassifier(n_estimators=100, max_depth=8)
rf.fit(x_train, y_train)
from sklearn.metrics import accuracy_score
y_pred_train_dt = dt.predict(x_train)
y_pred_train_rf = rf.predict(x_train)
acc_train_dt = accuracy_score(y_train, y_pred_train_dt)
acc_train_rf = accuracy_score(y_train, y_pred_train_rf)
acc_train_dt, acc_train_rf
```

```
(0.9071661237785016, 0.9625407166123778)
```

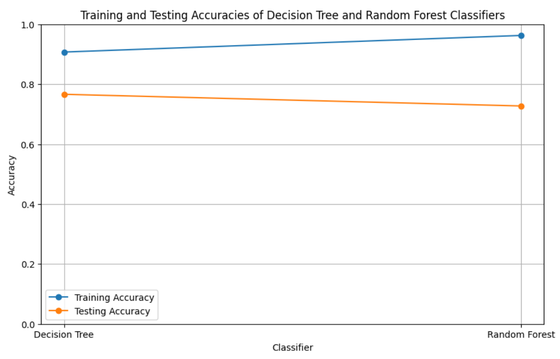
```
y_pred_test_dt = dt.predict(x_test)
y_pred_test_rf = rf.predict(x_test)
acc_test_dt = accuracy_score(y_test, y_pred_test_dt)
acc_test_rf = accuracy_score(y_test, y_pred_test_rf)
acc_test_dt, acc_test_rf
```

```
(0.7662337662337663, 0.7272727272727273)
```

```
from sklearn.metrics import recall_score

r_dt = recall_score(y_test, y_pred_test_dt)
r_rf = recall_score(y_test, y_pred_test_rf)


r_dt, r_rf
```

```
(0.5740740740740741, 0.5370370370370371)
```

```
train_accuracies = [acc_train_dt, acc_train_rf]
test_accuracies = [acc_test_dt, acc_test_rf]

plt.figure(figsize=(10, 6))

plt.plot(['Decision Tree', 'Random Forest'], train_accuracies, marker='o', label='Training Accuracy')

plt.plot(['Decision Tree', 'Random Forest'], test_accuracies, marker='o', label='Testing Accuracy')
plt.title('Training and Testing Accuracies of Decision Tree and Random Forest Classifiers')
plt.xlabel('Classifier')
plt.ylabel('Accuracy')
plt.ylim(0, 1)
plt.legend()

plt.grid(True)
plt.show()
```

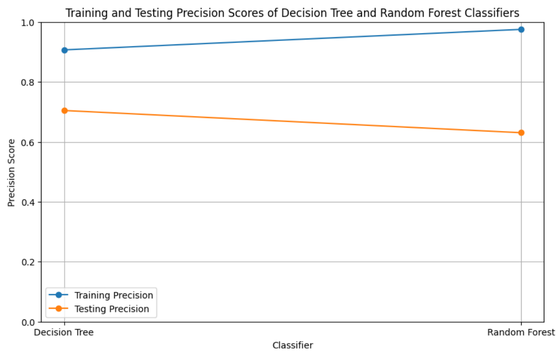



```
# Recall scores for decision tree and random forest classifiers
train_recalls = [recall_score(y_train, dt.predict(x_train)), recall_score(y_train, rf.predict(x_train))]
test_recalls = [recall_score(y_test, dt.predict(x_test)), recall_score(y_test, rf.predict(x_test))]
plt.figure(figsize=(10, 6))
plt.plot(['Decision Tree', 'Random Forest'], train_recalls, marker='o', label='Training Recall')
plt.plot(['Decision Tree', 'Random Forest'], test_recalls, marker='o', label='Testing Recall')
plt.title('Training and Testing Recall Scores of Decision Tree and Random Forest Classifiers')
plt.xlabel('Classifier')
plt.ylabel('Recall Score')
plt.ylim(0, 1)
plt.legend()

# Show plot
plt.grid(True)
plt.show()
```


```
from sklearn.metrics import precision_score

p_dt = precision_score(y_test, y_pred_test_dt)
p_rf = precision_score(y_test, y_pred_test_rf)

p_dt, p_rf
```

```
(0.7045454545454546, 0.6304347826086957)
```

```
train_precisions = [precision_score(y_train, dt.predict(x_train)), precision_score(y_train, rf.predict(x_train))]
test_precisions = [precision_score(y_test, dt.predict(x_test)), precision_score(y_test, rf.predict(x_test))]


plt.figure(figsize=(10, 6))

plt.plot(['Decision Tree', 'Random Forest'], train_precisions, marker='o', label='Training Precision')
plt.plot(['Decision Tree', 'Random Forest'], test_precisions, marker='o', label='Testing Precision')
plt.title('Training and Testing Precision Scores of Decision Tree and Random Forest Classifiers')
plt.xlabel('Classifier')
plt.ylabel('Precision Score')
plt.ylim(0, 1)
plt.legend()

plt.grid(True)
plt.show()
```



Based on the information provided earlier, it is evident that Random Forest outperforms the Decision Tree model on this dataset.

Support Vector Machine (SVM)

Building the model using Support Vector Machine (SVM) with linear kernel

```
from sklearn import svm
model = svm.SVC(kernel = 'linear')
model.fit(x_train, y_train)
```

```
SVC
SVC(kernel='linear')
```

Prediction from support vector machine model on the traing and testing data

```
y_pred_train = model.predict(x_train)
y_pred_test = model.predict(x_test)
```

Accuracy score , recall_score, and precision_score for SVM

```
from sklearn.metrics import accuracy_score, recall_score, precision_score

acc_train = accuracy_score(y_train, y_pred = y_pred_train)
acc_test = accuracy_score(y_test, y_pred = y_pred_test)

acc_train, acc_test
```

```
(0.7785016286644951, 0.7727272727272727)
```

```
p = precision_score(y_test, y_pred_test)
r = recall_score(y_test, y_pred_test)

p, r
```

```
(0.7111111111111111, 0.5925925925925926)
```

Building the model using Support Vector Machine (SVM) with linear rbf

```
from sklearn import svm
model = svm.SVC(kernel = 'rbf')
model.fit(x_train, y_train)
y_pred_train = model.predict(x_train)
y_pred_test = model.predict(x_test)
from sklearn.metrics import accuracy_score, recall_score, precision_score

acc_train = accuracy_score(y_train, y_pred = y_pred_train)
acc_test = accuracy_score(y_test, y_pred = y_pred_test)

acc_train, acc_test
```

```
(0.8306188925081434, 0.7597402597402597)
```

```
p = precision_score(y_test, y_pred_test)
r = recall_score(y_test, y_pred_test)
p, r
```

```
(0.6976744186046512, 0.5555555555555556)
```

Logistic Regression

```
from sklearn.linear_model import LogisticRegression
model = LogisticRegression()
model.fit(x_train, y_train)
```

```
LogisticRegression
LogisticRegression()
```

```
y_pred_train = model.predict(x_train)
y_pred_test = model.predict(x_test)
```

```
from sklearn.metrics import accuracy_score, recall_score, precision_score

acc_train = accuracy_score(y_train, y_pred_train)
acc_test = accuracy_score(y_test, y_pred_test)

acc_train, acc_test
```

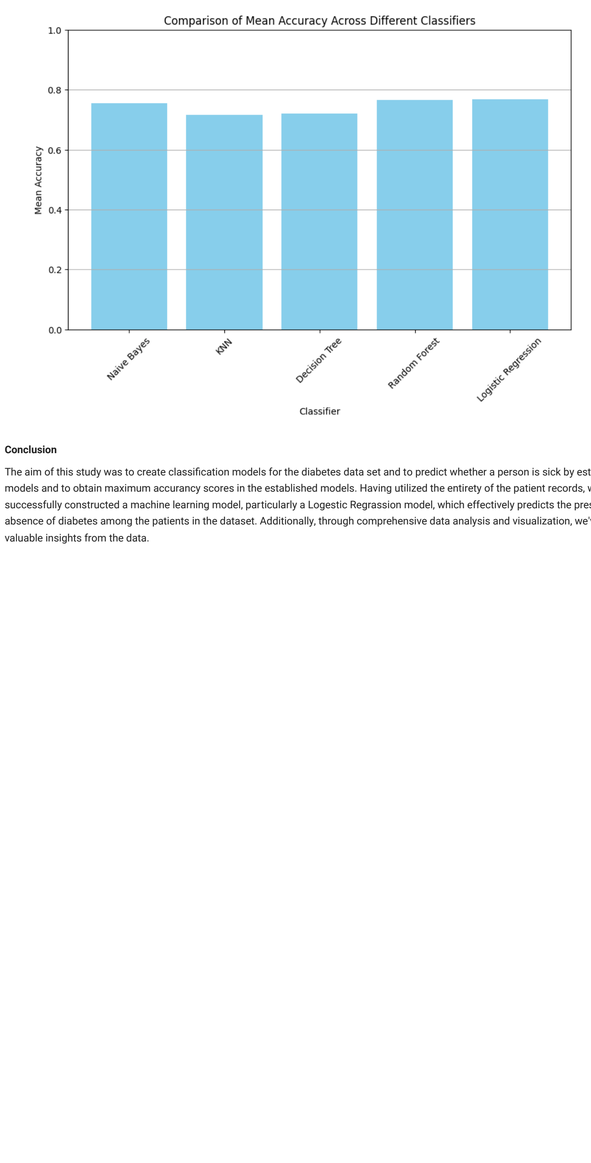
```
(0.8306188925081434, 0.7597402597402597)
```

```
p = precision_score(y_test, y_pred_test)
r = recall_score(y_test, y_pred_test)

p, r
```

```
(0.6976744186046512, 0.5555555555555556)
```

Comparing used models

```
import matplotlib.pyplot as plt
from sklearn.model_selection import cross_val_score
from sklearn.naive_bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression

# Initialize models
models = {
    'Naive Bayes': GaussianNB(),
    'KNN': KNeighborsClassifier(),
    'Decision Tree': DecisionTreeClassifier(),
    'Random Forest': RandomForestClassifier(),
    'Logistic Regression': LogisticRegression()
}

# Cross-validate each model and get accuracy scores
accuracy_scores = {}
for model_name, model in models.items():
    scores = cross_val_score(model, x_train, y_train, cv=5, scoring='accuracy')
    accuracy_scores[model_name] = scores.mean()

# Plotting
plt.figure(figsize=(10, 6))
plt.bar(accuracy_scores.keys(), accuracy_scores.values(), color='skyblue')
plt.xlabel('Classifier')
plt.ylabel('Mean Accuracy')
plt.title('Comparison of Mean Accuracy Across Different Classifiers')
plt.xticks(rotation=45)
plt.ylim(0, 1)  # Limiting y-axis from 0 to 1 for better visualization
plt.grid(axis='y')
plt.show()
```



Conclusion

The aim of this study was to create classification models for the diabetes data set and to predict whether a person is sick by establishing models and to obtain maximum accurancy scores in the established models. Having utilized the entirety of the patient records, we've successfully constructed a machine learning model, particularly a Logestic Regrassion model, which effectively predicts the presence or absence of diabetes among the patients in the dataset. Additionally, through comprehensive data analysis and visualization, we've gleaned valuable insights from the data.