Diabetes Prediction using Machine Learning¶

Diabetes, is a group of metabolic disorders in which there are high blood sugar levels over a prolonged period. Symptoms of high blood sugar include frequent urination, increased thirst, and increased hunger. If left untreated, diabetes can cause many complications. Acute complications can include diabetic ketoacidosis, hyperosmolar hyperglycemic state, or death. Serious long-term complications include cardiovascular disease, stroke, chronic kidney disease, foot ulcers, and damage to the eyes.

This dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases. The objective of the dataset is to diagnostically predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. Several constraints were placed on the selection of these instances from a larger database. In particular, all patients here are females at least 21 years old of Pima Indian heritage.

Objective

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

Details about the dataset:

The datasets consists of several medical predictor variables and one target variable, Outcome. Predictor variables includes the number of pregnancies the patient has had, their BMI, insulin level, age, and so on.

- **Pregnancies**: Number of times pregnant
- **Glucose**: Plasma glucose concentration a 2 hours in an oral glucose tolerance test
- **BloodPressure**: Diastolic blood pressure (mm Hg)
- **SkinThickness**: Triceps skin fold thickness (mm)
- **Insulin**: 2-Hour serum insulin (mu U/ml)
- **BMI**: Body mass index (weight in kg/(height in m)^2)
- **DiabetesPedigreeFunction**: Diabetes pedigree function
- **Age**: Age (years)
- **Outcome**: Class variable (0 or 1)

Number of Observation Units: 768

Variable Number: 9

Result; The model created as a result of XGBoost hyperparameter optimization became the model with the lowest Cross Validation Score value. (0.90)

1) Exploratory Data Analysis

In [1]:

```
#Installation of required libraries
import numpy as np
import pandas as pd
import statsmodels.api as sm
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.preprocessing import scale, StandardScaler
from sklearn.model_selection import train_test_split, GridSearchCV, cross_v
al_score
from sklearn.metrics import confusion_matrix, accuracy_score, mean_squared_
error, r2_score, roc_auc_score, roc_curve, classification_report
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
from sklearn.neural_network import MLPClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import GradientBoostingClassifier
from lightgbm import LGBMClassifier
from sklearn.model_selection import KFold
import warnings
warnings.simplefilter(action = "ignore")
```

In [2]:

```
#Reading the dataset
df = pd.read_csv("../input/pima-indians-diabetes-database/diabetes.csv")
```

In [3]:

```
# The first 5 observation units of the data set were accessed.
df.head()
```

Out[3]:

	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

In [4]:

```
# The size of the data set was examined. It consists of 768 observation unit
s and 9 variables.
df.shape
```

Out[4]:

```
(768, 9)
```

In [5]:

```
#Feature information
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
```

In [6]:

```
# Descriptive statistics of the data set accessed.
df.describe([0.10,0.25,0.50,0.75,0.90,0.95,0.99]).T
```

Out[6]:

	count	mean	std	min	10%	25%	50%	75%	90%	95%	99%	max
Pregnancies	768.0	3.845052	3.369578	0.000	0.000	1.00000	3.0000	6.00000	9.0000	10.00000	13.00000	17.00
Glucose	768.0	120.894531	31.972618	0.000	85.000	99.00000	117.0000	140.25000	167.0000	181.00000	196.00000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	54.000	62.00000	72.0000	80.00000	88.0000	90.00000	106.00000	122.00
SkinThickness	768.0	20.536458	15.952218	0.000	0.000	0.00000	23.0000	32.00000	40.0000	44.00000	51.33000	99.00

	count	mean	std	min	10%	25%	50%	75%	90%	95%	99%	max
Insulin	768.0	79.799479	115.244002	0.000	0.000	0.00000	30.5000	127.25000	210.0000	293.00000	519.90000	846.00
BMI	768.0	31.992578	7.884160	0.000	23.600	27.30000	32.0000	36.60000	41.5000	44.39500	50.75900	67.10
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.165	0.24375	0.3725	0.62625	0.8786	1.13285	1.69833	2.42
Age	768.0	33.240885	11.760232	21.000	22.000	24.00000	29.0000	41.00000	51.0000	58.00000	67.00000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.000	0.00000	0.0000	1.00000	1.0000	1.00000	1.00000	1.00

In [7]:

```python
# The distribution of the Outcome variable was examined.
df["Outcome"].value_counts()*100/len(df)
```

Out[7]:

```
0    65.104167
1    34.895833
Name: Outcome, dtype: float64
```

In [8]:

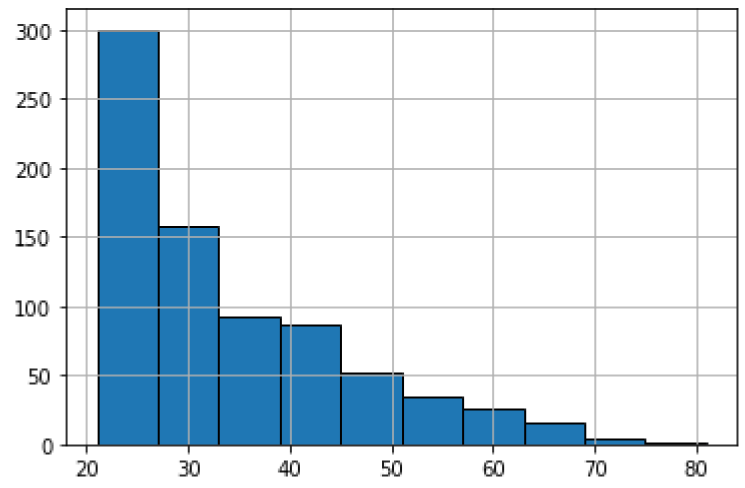
```python
# The classes of the outcome variable were examined.
df.Outcome.value_counts()
```

Out[8]:

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

In [9]:

```python
# The histagram of the Age variable was reached.
df["Age"].hist(edgecolor = "black");
```



In [10]:

```
print("Max Age: " + str(df["Age"].max()) + " Min Age: " + str(df["Age"].min
()))
```

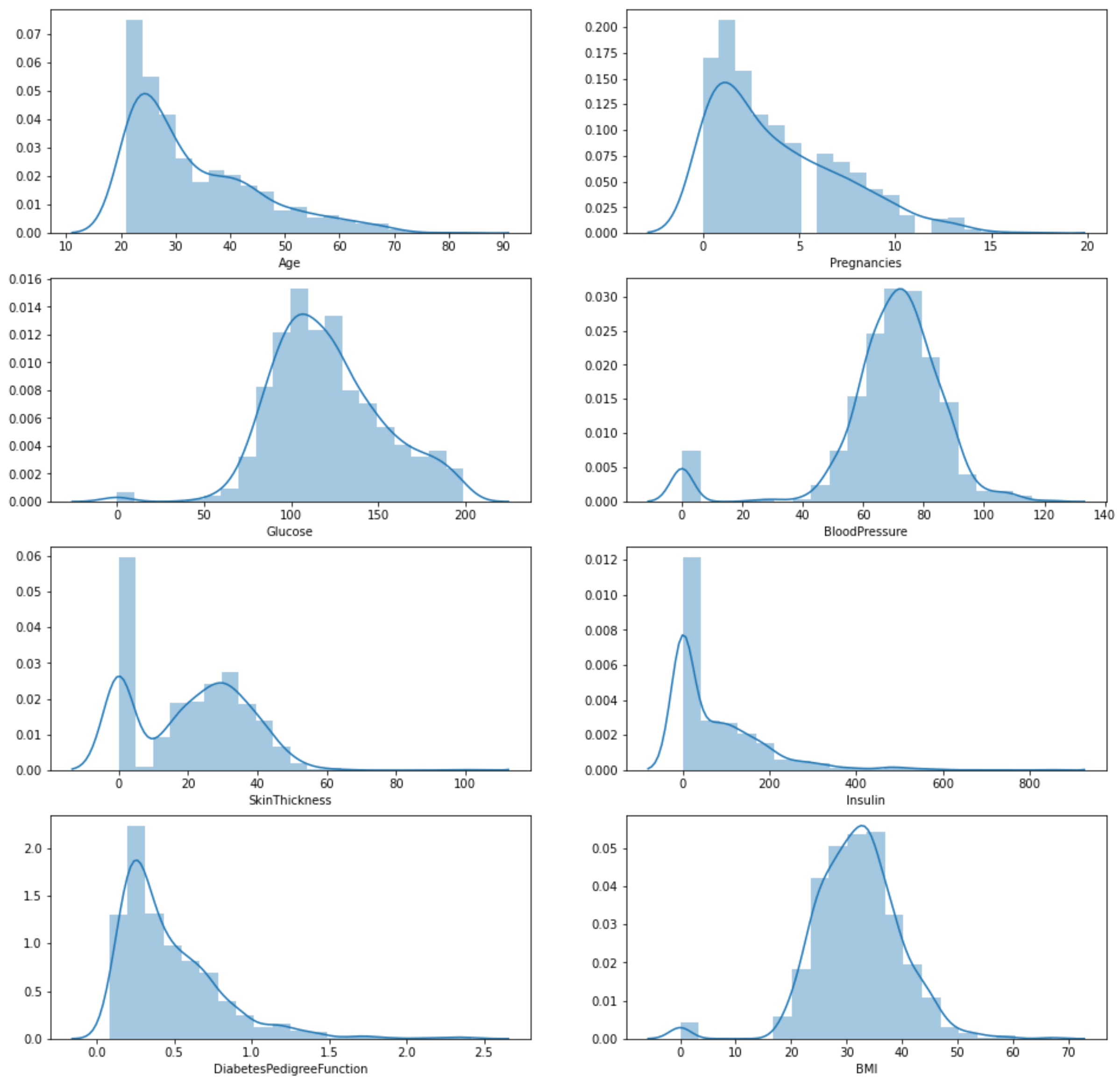
```
Max Age: 81 Min Age: 21
```

In [11]:

```
# Histogram and density graphs of all variables were accessed.
fig, ax = plt.subplots(4,2, figsize=(16,16))
sns.distplot(df.Age, bins = 20, ax=ax[0,0])
sns.distplot(df.Pregnancies, bins = 20, ax=ax[0,1])
sns.distplot(df.Glucose, bins = 20, ax=ax[1,0])
sns.distplot(df.BloodPressure, bins = 20, ax=ax[1,1])
sns.distplot(df.SkinThickness, bins = 20, ax=ax[2,0])
sns.distplot(df.Insulin, bins = 20, ax=ax[2,1])
sns.distplot(df.DiabetesPedigreeFunction, bins = 20, ax=ax[3,0])
sns.distplot(df.BMI, bins = 20, ax=ax[3,1])
```

Out[11]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f77b83d5950>
```



In [12]:

```
df.groupby("Outcome").agg({"Pregnancies":"mean"})
```

Out[12]:

	Pregnancies
Outcome	
0	3.298000
1	4.865672

In [13]:

```
df.groupby("Outcome").agg({"Age":"mean"})
```

```
Out[13]:
```

	Age
Outcome	
0	31.190000
1	37.067164

```
In [14]:
```

```
df.groupby("Outcome").agg({"Age":"max"})
```

```
Out[14]:
```

	Age
Outcome	
0	81
1	70

```
In [15]:
```

```
df.groupby("Outcome").agg({"Insulin": "mean"})
```

```
Out[15]:
```

	Insulin
Outcome	
0	68.792000

	Insulin
Outcome	
1	100.335821

In [16]:

```
df.groupby("Outcome").agg({"Insulin": "max"})
```

Out[16]:

	Insulin
Outcome	
0	744
1	846

In [17]:

```
df.groupby("Outcome").agg({"Glucose": "mean"})
```

Out[17]:

	Glucose
Outcome	
0	109.980000
1	141.257463

In [18]:

```
df.groupby("Outcome").agg({"Glucose": "max"})
```

Out[18]:

	Glucose
Outcome	
0	197
1	199

In [19]:

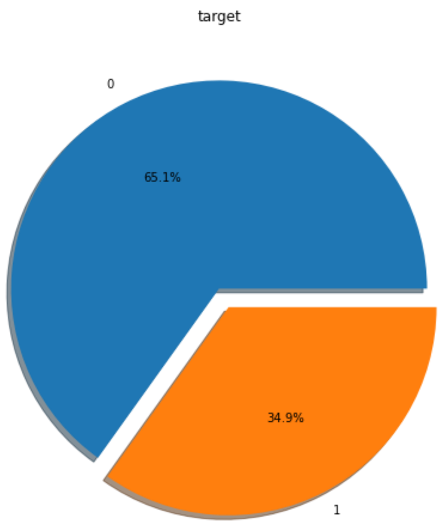
```
df.groupby("Outcome").agg({"BMI": "mean"})
```

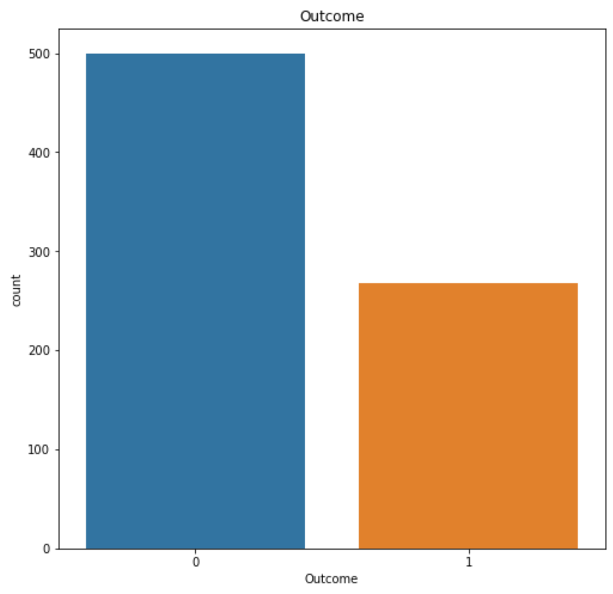
Out[19]:

	BMI
Outcome	
0	30.304200
1	35.142537

In [20]:

```
# The distribution of the outcome variable in the data was examined and visu
alized.
f,ax=plt.subplots(1,2,figsize=(18,8))
df['Outcome'].value_counts().plot.pie(explode=[0,0.1],autopct='%1.1f%%',ax=
ax[0],shadow=True)
ax[0].set_title('target')
ax[0].set_ylabel('')
sns.countplot('Outcome',data=df,ax=ax[1])
ax[1].set_title('Outcome')
plt.show()
```





In [21]:

```
# Access to the correlation of the data set was provided. What kind of relat
ionship is examined between the variables.
# If the correlation value is> 0, there is a positive correlation. While the
value of one variable increases, the value of the other variable also increa
ses.
# Correlation = 0 means no correlation.
# If the correlation is <0, there is a negative correlation. While one varia
ble increases, the other variable decreases.
# When the correlations are examined, there are 2 variables that act as a po
sitive correlation to the Salary dependent variable.
# These variables are Glucose. As these increase, Outcome variable increases
.
df.corr()
```

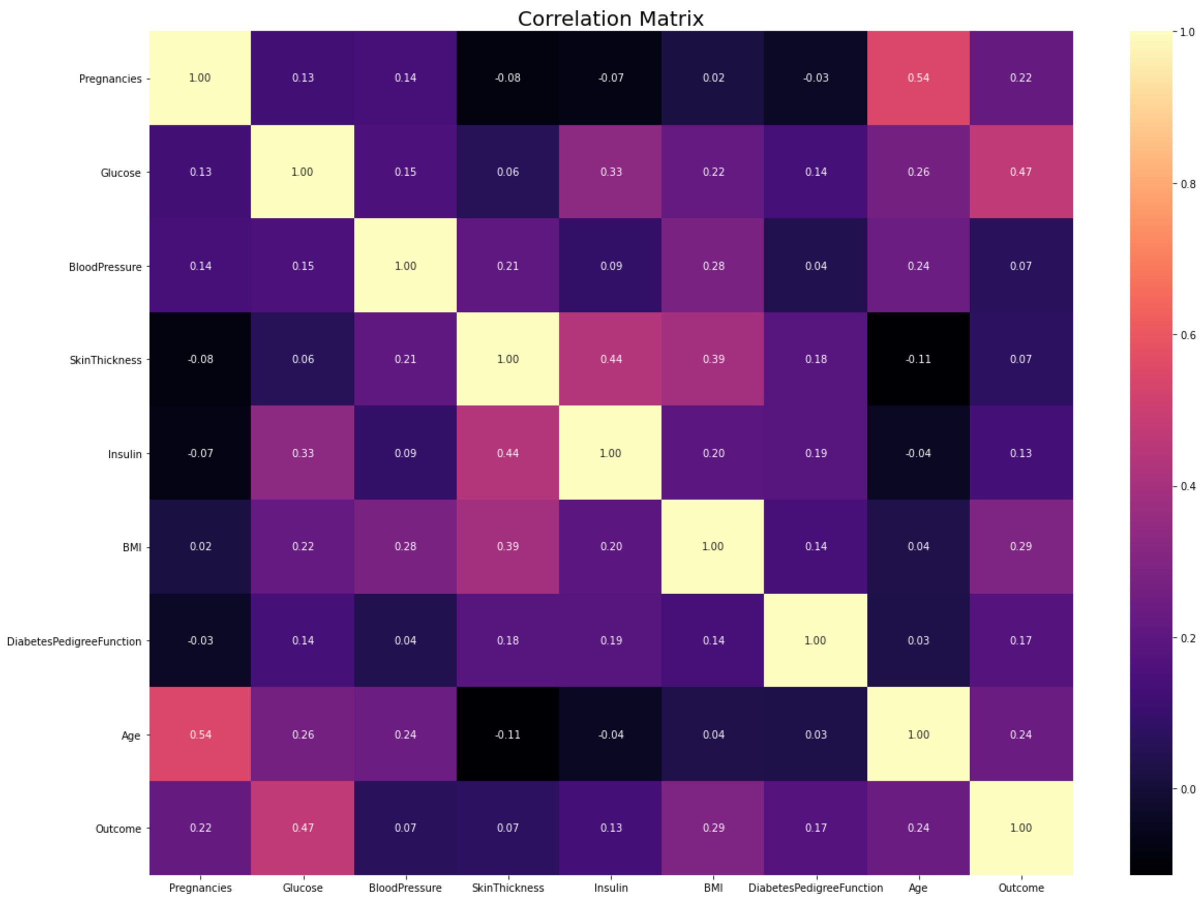
Out[21]:

	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

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
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

In [22]:

```
# Correlation matrix graph of the data set
f, ax = plt.subplots(figsize= [20,15])
sns.heatmap(df.corr(), annot=True, fmt=".2f", ax=ax, cmap = "magma" )
ax.set_title("Correlation Matrix", fontsize=20)
plt.show()
```



2) Data Preprocessing

2.1) Missing Observation Analysis

We saw on df.head() that some features contain 0, it doesn't make sense here and this indicates missing value Below we replace 0 value by NaN:

In [23]:

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

In [24]:

```
df.head()
```

Out[24]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.0	35.0	NaN	33.6	0.627	50	1
1	1	85.0	66.0	29.0	NaN	26.6	0.351	31	0

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
2	8	183.0	64.0	NaN	NaN	23.3	0.672	32	1
3	1	89.0	66.0	23.0	94.0	28.1	0.167	21	0
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33	1

In [25]:

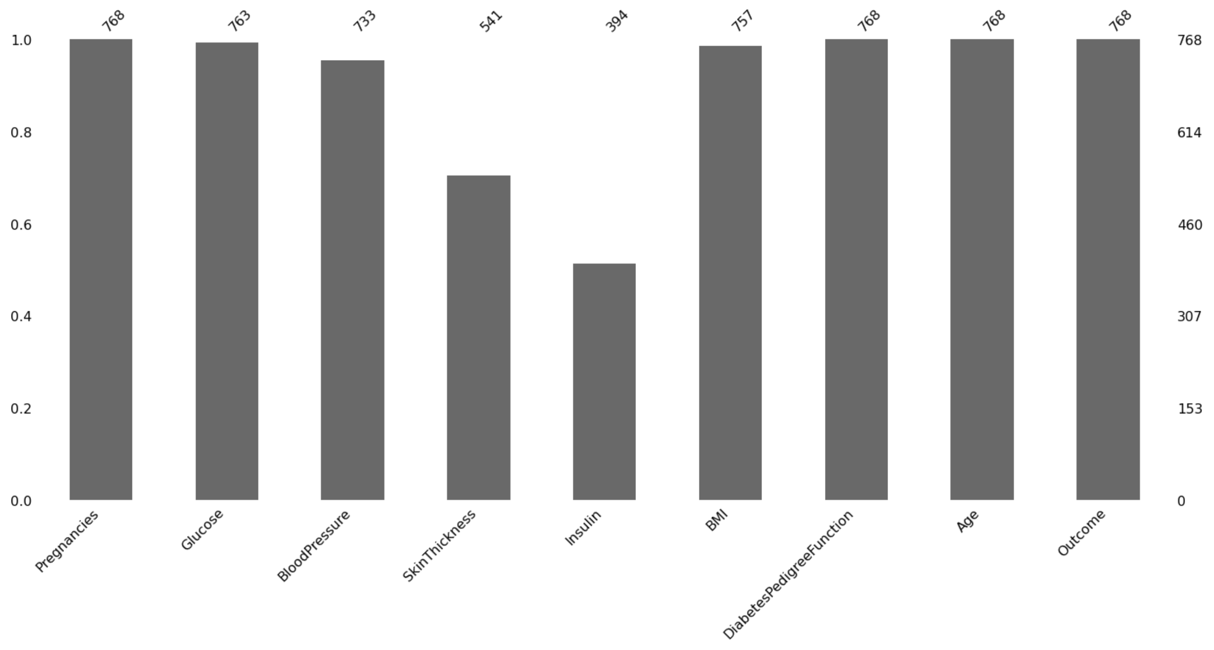
```
# Now, we can look at where are missing values
df.isnull().sum()
```

Out[25]:

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

In [26]:

```
# Have been visualized using the missingno library for the visualization of missing observations.
# Plotting
import missingno as msno
msno.bar(df);
```



In [27]:

```
# The missing values will be filled with the median values of each variable.
def median_target(var):
    temp = df[df[var].notnull()]
    temp = temp[[var, 'Outcome']].groupby(['Outcome'])[[var]].median().rese
t_index()
    return temp
```

In [28]:

```
# The values to be given for incomplete observations are given the median va
lue of people who are not sick and the median values of people who are sick.
columns = df.columns
columns = columns.drop("Outcome")
for i in columns:
    median_target(i)
    df.loc[(df['Outcome'] == 0 ) & (df[i].isnull()), i] = median_target(i)[
i][0]
    df.loc[(df['Outcome'] == 1 ) & (df[i].isnull()), i] = median_target(i)[
i][1]
```

In [29]:

```
df.head()
```

Out[29]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.0	35.0	169.5	33.6	0.627	50	1

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
1	1	85.0	66.0	29.0	102.5	26.6	0.351	31	0
2	8	183.0	64.0	32.0	169.5	23.3	0.672	32	1
3	1	89.0	66.0	23.0	94.0	28.1	0.167	21	0
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33	1

In [30]:

```
# Missing values were filled.
df.isnull().sum()
```

Out[30]:

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

2.2) Outlier Observation Analysis

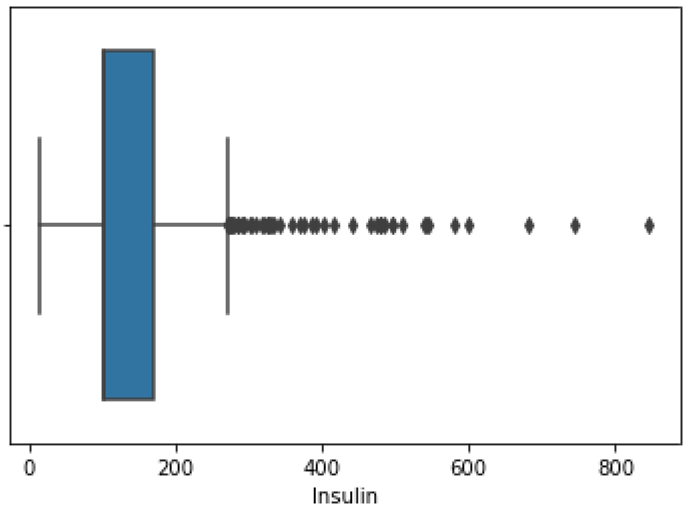
In [31]:

```
# In the data set, there were asked whether there were any outlier observati
ons compared to the 25% and 75% quarters.
# It was found to be an outlier observation.
for feature in df:

    Q1 = df[feature].quantile(0.25)
    Q3 = df[feature].quantile(0.75)
    IQR = Q3-Q1
    lower = Q1- 1.5*IQR
    upper = Q3 + 1.5*IQR

    if df[(df[feature] > upper)].any(axis=None):
        print(feature,"yes")
    else:
        print(feature, "no")
```

```
Pregnancies yes
Glucose no
BloodPressure yes
SkinThickness yes
Insulin yes
BMI yes
DiabetesPedigreeFunction yes
Age yes
Outcome no
```

In [32]:

```
# The process of visualizing the Insulin variable with boxplot method was do
ne. We find the outlier observations on the chart.
import seaborn as sns
sns.boxplot(x = df["Insulin"]);
```

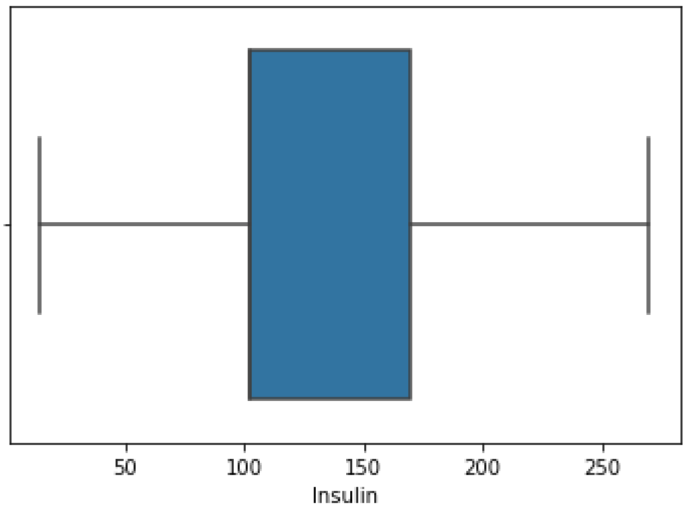


In [33]:

```
#We conduct a stand alone observation review for the Insulin variable
#We suppress contradictory values
Q1 = df.Insulin.quantile(0.25)
Q3 = df.Insulin.quantile(0.75)
IQR = Q3-Q1
lower = Q1 - 1.5*IQR
upper = Q3 + 1.5*IQR
df.loc[df["Insulin"] > upper,"Insulin"] = upper
```

In [34]:

```
import seaborn as sns
sns.boxplot(x = df["Insulin"]);
```



2.3) Local Outlier Factor (LOF)

In [35]:

```
# We determine outliers between all variables with the LOF method
from sklearn.neighbors import LocalOutlierFactor
lof =LocalOutlierFactor(n_neighbors= 10)
lof.fit_predict(df)
```

Out[35]:

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

In [36]:

```
df_scores = lof.negative_outlier_factor_
np.sort(df_scores)[0:30]
```

Out[36]:

```
array([-3.05893469, -2.37289269, -2.15297995, -2.09708735, -2.0772561 ,
       -1.95255968, -1.86384019, -1.74003158, -1.72703492, -1.71674689,
       -1.70343883, -1.6688722 , -1.64296768, -1.64190437, -1.61620872,
       -1.61369917, -1.60057603, -1.5988774 , -1.59608032, -1.57027568,
       -1.55876022, -1.55674614, -1.51852389, -1.50843907, -1.50280943,
       -1.50160698, -1.48391514, -1.4752983 , -1.4713427 , -1.47006248]
)
```

In [37]:

```
#We choose the threshold value according to lof scores
threshold = np.sort(df_scores)[7]
threshold
```

Out[37]:

```
-1.740031580305444
```

In [38]:

```
#We delete those that are higher than the threshold
outlier = df_scores > threshold
df = df[outlier]
```

In [39]:

```
# The size of the data set was examined.
df.shape
```

Out[39]:

```
(760, 9)
```

3) Feature Engineering

Creating new variables is important for models. But you need to create a logical new variable. For this data set, some new variables were created according to BMI, Insulin and glucose variables.

In [40]:

```
# According to BMI, some ranges were determined and categorical variables we
re assigned.
```

```
NewBMI = pd.Series(["Underweight", "Normal", "Overweight", "Obesity 1", "Ob
esity 2", "Obesity 3"], dtype = "category")
df["NewBMI"] = NewBMI
df.loc[df["BMI"] < 18.5, "NewBMI"] = NewBMI[0]
df.loc[(df["BMI"] > 18.5) & (df["BMI"] <= 24.9), "NewBMI"] = NewBMI[1]
df.loc[(df["BMI"] > 24.9) & (df["BMI"] <= 29.9), "NewBMI"] = NewBMI[2]
df.loc[(df["BMI"] > 29.9) & (df["BMI"] <= 34.9), "NewBMI"] = NewBMI[3]
df.loc[(df["BMI"] > 34.9) & (df["BMI"] <= 39.9), "NewBMI"] = NewBMI[4]
df.loc[df["BMI"] > 39.9 ,"NewBMI"] = NewBMI[5]
```

In [41]:

```
df.head()
```

Out[41]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome	NewBMI
0	6	148.0	72.0	35.0	169.5	33.6	0.627	50	1	Obesity 1
1	1	85.0	66.0	29.0	102.5	26.6	0.351	31	0	Overweight
2	8	183.0	64.0	32.0	169.5	23.3	0.672	32	1	Normal
3	1	89.0	66.0	23.0	94.0	28.1	0.167	21	0	Overweight
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33	1	Obesity 3

In [42]:

```
# A categorical variable creation process is performed according to the insu
lin value.
def set_insulin(row):
    if row["Insulin"] >= 16 and row["Insulin"] <= 166:
        return "Normal"
    else:
        return "Abnormal"
```

In [43]:

```
# The operation performed was added to the dataframe.
df = df.assign(NewInsulinScore=df.apply(set_insulin, axis=1))
```

```
df.head()
```

Out[43]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome	NewBMI	NewInsulinScore
0	6	148.0	72.0	35.0	169.5	33.6	0.627	50	1	Obesity 1	Abnormal
1	1	85.0	66.0	29.0	102.5	26.6	0.351	31	0	Overweight	Normal
2	8	183.0	64.0	32.0	169.5	23.3	0.672	32	1	Normal	Abnormal
3	1	89.0	66.0	23.0	94.0	28.1	0.167	21	0	Overweight	Normal
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33	1	Obesity 3	Abnormal

In [44]:

```
# Some intervals were determined according to the glucose variable and these
were assigned categorical variables.
NewGlucose = pd.Series(["Low", "Normal", "Overweight", "Secret", "High"], d
type = "category")
df["NewGlucose"] = NewGlucose
df.loc[df["Glucose"] <= 70, "NewGlucose"] = NewGlucose[0]
df.loc[(df["Glucose"] > 70) & (df["Glucose"] <= 99), "NewGlucose"] = NewGlu
cose[1]
df.loc[(df["Glucose"] > 99) & (df["Glucose"] <= 126), "NewGlucose"] = NewGl
ucose[2]
df.loc[df["Glucose"] > 126 ,"NewGlucose"] = NewGlucose[3]
```

In [45]:

```
df.head()
```

Out[45]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome	NewBMI	NewInsulinScore	NewGlucose
0	6	148.0	72.0	35.0	169.5	33.6	0.627	50	1	Obesity 1	Abnormal	Secret
1	1	85.0	66.0	29.0	102.5	26.6	0.351	31	0	Overweight	Normal	Normal
2	8	183.0	64.0	32.0	169.5	23.3	0.672	32	1	Normal	Abnormal	Secret
3	1	89.0	66.0	23.0	94.0	28.1	0.167	21	0	Overweight	Normal	Normal
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33	1	Obesity 3	Abnormal	Secret

4) One Hot Encoding

Categorical variables in the data set should be converted into numerical values. For this reason, these transformation processes are performed with Label Encoding and One Hot Encoding method.

In [46]:

```
# Here, by making One Hot Encoding transformation, categorical variables were converted into numerical values. It is also protected from the Dummy variable trap.
df = pd.get_dummies(df, columns =["NewBMI","NewInsulinScore", "NewGlucose"], drop_first = True)
```

In [47]:

```
df.head()
```

Out[47]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome	NewBMI_Obesity 1	NewBMI_Obesity 2	NewBMI_Obesity 3	NewBMI_Overweight	NewBMI_Underweight	NewInsulinScore_Normal	NewGlucose_Low	NewGlucose_Normal	NewGlucose_Overweight	NewGlucose_Secret
0	6	148.0	72.0	35.0	169.5	33.6	0.627	50	1	1	0	0	0	0	0	0	0	0	1
1	1	85.0	66.0	29.0	102.5	26.6	0.351	31	0	0	0	0	1	0	1	0	1	0	0
2	8	183.0	64.0	32.0	169.5	23.3	0.672	32	1	0	0	0	0	0	0	0	0	0	1
3	1	89.0	66.0	23.0	94.0	28.1	0.167	21	0	0	0	0	1	0	1	0	1	0	0
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33	1	0	0	1	0	0	0	0	0	0	1

In [48]:

```
categorical_df = df[['NewBMI_Obesity 1','NewBMI_Obesity 2', 'NewBMI_Obesity
3', 'NewBMI_Overweight','NewBMI_Underweight',
                     'NewInsulinScore_Normal','NewGlucose_Low','NewGlucose_
Normal', 'NewGlucose_Overweight', 'NewGlucose_Secret']]
```

In [49]:

```
categorical_df.head()
```

Out[49]:

	NewBMI_Obesity 1	NewBMI_Obesity 2	NewBMI_Obesity 3	NewBMI_Overweight	NewBMI_Underweight	NewInsulinScore_Normal	NewGlucose_Low	NewGlucose_Normal	NewGlucose_Overweight	NewGlucose_Secret
0	1	0	0	0	0	0	0	0	0	1
1	0	0	0	1	0	1	0	1	0	0
2	0	0	0	0	0	0	0	0	0	1
3	0	0	0	1	0	1	0	1	0	0
4	0	0	1	0	0	0	0	0	0	1

In [50]:

```
y = df["Outcome"]
X = df.drop(["Outcome",'NewBMI_Obesity 1','NewBMI_Obesity 2', 'NewBMI_Obesity 3', 'NewBMI_Overweight','NewBMI_Underweight',
                    'NewInsulinScore_Normal','NewGlucose_Low','NewGlucose_Normal', 'NewGlucose_Overweight', 'NewGlucose_Secret'], axis = 1)
cols = X.columns
index = X.index
```

In [51]:

```
X.head()
```

Out[51]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
0	6	148.0	72.0	35.0	169.5	33.6	0.627	50
1	1	85.0	66.0	29.0	102.5	26.6	0.351	31
2	8	183.0	64.0	32.0	169.5	23.3	0.672	32

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
3	1	89.0	66.0	23.0	94.0	28.1	0.167	21
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33

In [52]:

```
# The variables in the data set are an effective factor in increasing the pe
rformance of the models by standardization.
# There are multiple standardization methods. These are methods such as" Nor
malize"," MinMax"," Robust" and "Scale".
from sklearn.preprocessing import RobustScaler
transformer = RobustScaler().fit(X)
X = transformer.transform(X)
X = pd.DataFrame(X, columns = cols, index = index)
```

In [53]:

```
X.head()
```

Out[53]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
0	0.6	0.775	0.000	1.000000	1.000000	0.177778	0.669707	1.235294
1	-0.4	-0.800	-0.375	0.142857	0.000000	-0.600000	-0.049511	0.117647
2	1.0	1.650	-0.500	0.571429	1.000000	-0.966667	0.786971	0.176471
3	-0.4	-0.700	-0.375	-0.714286	-0.126866	-0.433333	-0.528990	-0.470588
4	-0.6	0.500	-2.000	1.000000	0.977612	1.233333	4.998046	0.235294

In [54]:

```
X = pd.concat([X,categorical_df], axis = 1)
```

In [55]:

```
X.head()
```

Out[55]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	NewBMI_Obesity 1	NewBMI_Obesity 2	NewBMI_Obesity 3	NewBMI_Overweight	NewBMI_Underweight	NewInsulinScore_Normal	NewGlucose_Low	NewGlucose_Normal	NewGlucose_Overweight	NewGlucose_Secret
0	0.6	0.775	0.000	1.000000	1.000000	0.177778	0.669707	1.235294	1	0	0	0	0	0	0	0	0	1
1	-0.4	-0.800	-0.375	0.142857	0.000000	-0.600000	-0.049511	0.117647	0	0	0	1	0	1	0	1	0	0
2	1.0	1.650	-0.500	0.571429	1.000000	-0.966667	0.786971	0.176471	0	0	0	0	0	0	0	0	0	1
3	-0.4	-0.700	-0.375	-0.714286	-0.1268	-0.4333	-0.528990	-0.4705	0	0	0	1	0	1	0	1	0	0

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	NewBMI_Obesity 1	NewBMI_Obesity 2	NewBMI_Obesity 3	NewBMI_Overweight	NewBMI_Underweight	NewInsulinScore_Normal	NewGlucose_Low	NewGlucose_Normal	NewGlucose_Overweight	NewGlucose_Secret
					66	33		88										
4	-0.6	0.500	-2.000	1.000000	0.977612	1.233333	4.998046	0.235294	0	0	1	0	0	0	0	0	0	1

In [56]:

```
y.head()
```

Out[56]:

```
0    1
1    0
2    1
3    0
4    1
Name: Outcome, dtype: int64
```

5) Base Models

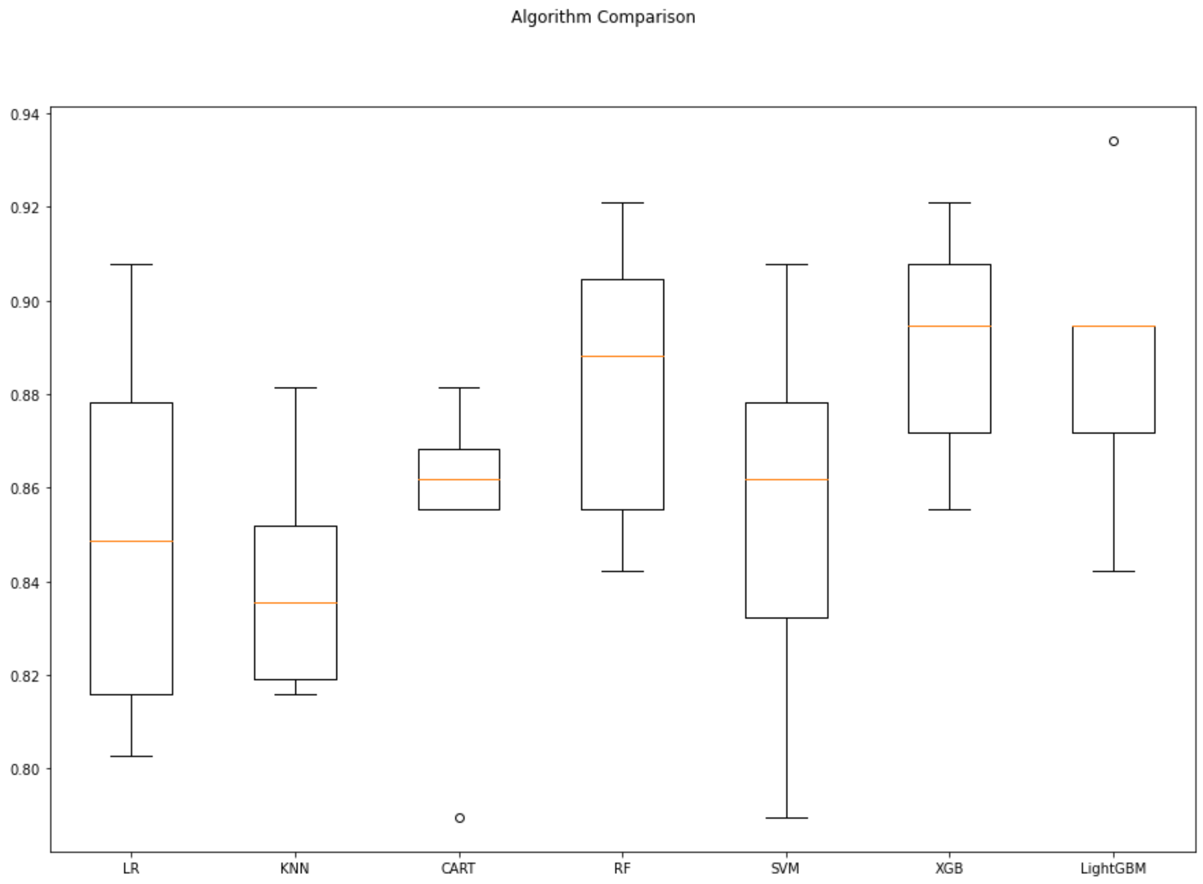
In [57]:

```
# Validation scores of all base models

models = []
models.append(('LR', LogisticRegression(random_state = 12345)))
models.append(('KNN', KNeighborsClassifier()))
models.append(('CART', DecisionTreeClassifier(random_state = 12345)))
models.append(('RF', RandomForestClassifier(random_state = 12345)))
models.append(('SVM', SVC(gamma='auto', random_state = 12345)))
models.append(('XGB', GradientBoostingClassifier(random_state = 12345)))
models.append(("LightGBM", LGBMClassifier(random_state = 12345)))

# evaluate each model in turn
results = []
names = []
```

In [58]:

```
for name, model in models:
        kfold = KFold(n_splits = 10, random_state = 12345)
        cv_results = cross_val_score(model, X, y, cv = 10, scoring= "accura
cy")
        results.append(cv_results)
        names.append(name)
        msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
        print(msg)

# boxplot algorithm comparison
fig = plt.figure(figsize=(15,10))
fig.suptitle('Algorithm Comparison')
ax = fig.add_subplot(111)
plt.boxplot(results)
ax.set_xticklabels(names)
plt.show()
```

```
LR: 0.848684 (0.036866)
KNN: 0.840789 (0.023866)
CART: 0.857895 (0.024826)
RF: 0.881579 (0.026316)
SVM: 0.853947 (0.036488)
XGB: 0.890789 (0.020427)
LightGBM: 0.885526 (0.024298)
```



6) Model Tuning

1) Random Forests Tuning

In [59]:

```
rf_params = {"n_estimators" :[100,200,500,1000],
             "max_features": [3,5,7],
             "min_samples_split": [2,5,10,30],
            "max_depth": [3,5,8,None]}
```

In [60]:

```
rf_model = RandomForestClassifier(random_state = 12345)
```

In [61]:

```
gs_cv = GridSearchCV(rf_model,
                    rf_params,
                    cv = 10,
                    n_jobs = -1,
                    verbose = 2).fit(X, y)
```

```
Fitting 10 folds for each of 192 candidates, totalling 1920 fits
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 4 concurrent work
ers.
[Parallel(n_jobs=-1)]: Done  33 tasks      | elapsed:   10.4s
[Parallel(n_jobs=-1)]: Done 154 tasks      | elapsed:   48.2s
[Parallel(n_jobs=-1)]: Done 357 tasks      | elapsed:  1.9min
[Parallel(n_jobs=-1)]: Done 640 tasks      | elapsed:  3.5min
[Parallel(n_jobs=-1)]: Done 1005 tasks      | elapsed:  5.7min
[Parallel(n_jobs=-1)]: Done 1450 tasks      | elapsed:  8.4min
[Parallel(n_jobs=-1)]: Done 1920 out of 1920 | elapsed: 11.4min finishe
d
```

In [62]:

```
gs_cv.best_params_
```

Out[62]:

```
{'max_depth': 8,
 'max_features': 7,
 'min_samples_split': 2,
 'n_estimators': 500}
```

1.1) Final Model Installation

In [63]:

```
rf_tuned = RandomForestClassifier(**gs_cv.best_params_)
```

In [64]:

```
rf_tuned = rf_tuned.fit(X,y)
```

In [65]:

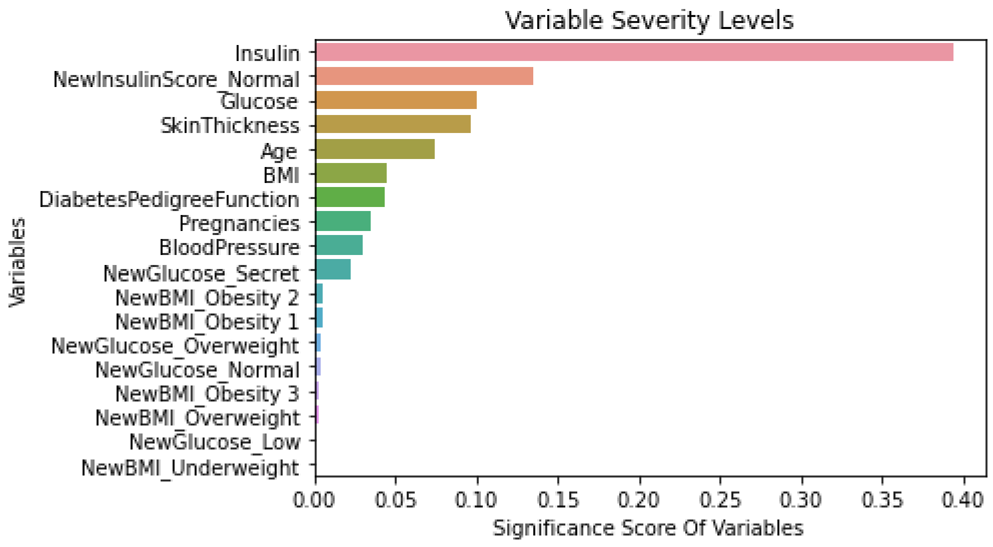
```
cross_val_score(rf_tuned, X, y, cv = 10).mean()
```

Out[65]:

```
0.8921052631578947
```

In [66]:

```
feature_imp = pd.Series(rf_tuned.feature_importances_,
                        index=X.columns).sort_values(ascending=False)

sns.barplot(x=feature_imp, y=feature_imp.index)
plt.xlabel('Significance Score Of Variables')
plt.ylabel('Variables')
plt.title("Variable Severity Levels")
plt.show()
```



2) LightGBM Tuning

In [67]:

```
lgbm = LGBMClassifier(random_state = 12345)
```

In [68]:

```
lgbm_params = {"learning_rate": [0.01, 0.03, 0.05, 0.1, 0.5],
              "n_estimators": [500, 1000, 1500],
              "max_depth":[3,5,8]}
```

In [69]:

```
gs_cv = GridSearchCV(lgbm,
                     lgbm_params,
                     cv = 10,
                     n_jobs = -1,
                     verbose = 2).fit(X, y)
```

```
Fitting 10 folds for each of 45 candidates, totalling 450 fits
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 4 concurrent work
ers.
[Parallel(n_jobs=-1)]: Done  33 tasks      | elapsed:    3.7s
[Parallel(n_jobs=-1)]: Done 154 tasks      | elapsed:   25.3s
[Parallel(n_jobs=-1)]: Done 357 tasks      | elapsed:   57.4s
[Parallel(n_jobs=-1)]: Done 450 out of 450 | elapsed:  1.1min finished
```

In [70]:

```
gs_cv.best_params_
```

Out[70]:

```
{'learning_rate': 0.01, 'max_depth': 3, 'n_estimators': 1000}
```

2.1) Final Model Installation

In [71]:

```
lgbm_tuned = LGBMClassifier(**gs_cv.best_params_).fit(X,y)
```

In [72]:

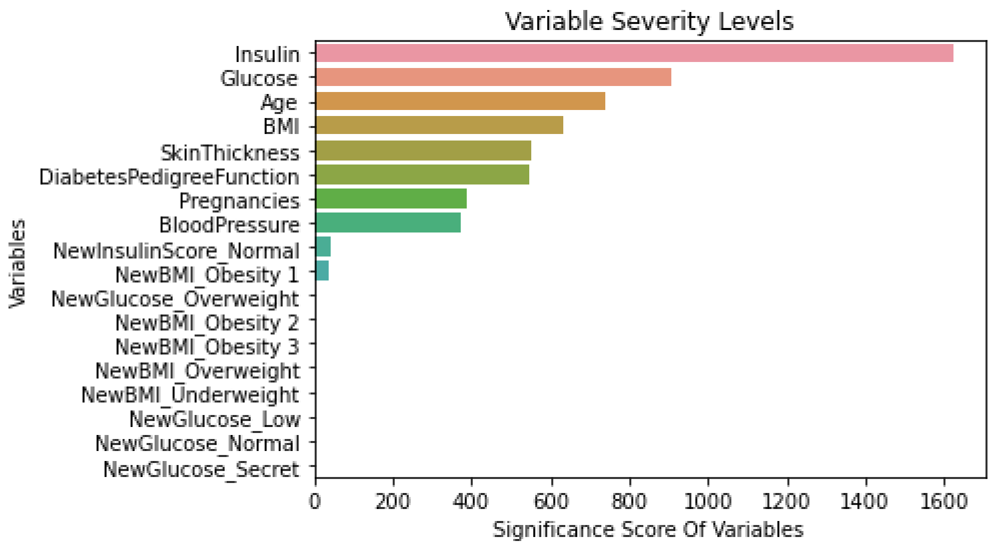
```
cross_val_score(lgbm_tuned, X, y, cv = 10).mean()
```

Out[72]:

```
0.8960526315789474
```

In [73]:

```
feature_imp = pd.Series(lgbm_tuned.feature_importances_,
                        index=X.columns).sort_values(ascending=False)

sns.barplot(x=feature_imp, y=feature_imp.index)
plt.xlabel('Significance Score Of Variables')
plt.ylabel('Variables')
plt.title("Variable Severity Levels")
plt.show()
```



3) XGBoost Tuning

In [74]:

```
xgb = GradientBoostingClassifier(random_state = 12345)
```

In [75]:

```
xgb_params = {
    "learning_rate": [0.01, 0.1, 0.2, 1],
    "min_samples_split": np.linspace(0.1, 0.5, 10),
    "max_depth":[3,5,8],
    "subsample":[0.5, 0.9, 1.0],
    "n_estimators": [100,1000]}
```

In [76]:

```
xgb_cv_model  = GridSearchCV(xgb,xgb_params, cv = 10, n_jobs = -1, verbose
= 2).fit(X, y)
```

```
Fitting 10 folds for each of 720 candidates, totalling 7200 fits
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 4 concurrent work
ers.
[Parallel(n_jobs=-1)]: Done  33 tasks      | elapsed:    4.0s
[Parallel(n_jobs=-1)]: Done 154 tasks      | elapsed:   42.3s
[Parallel(n_jobs=-1)]: Done 357 tasks      | elapsed:  1.9min
[Parallel(n_jobs=-1)]: Done 640 tasks      | elapsed:  3.1min
[Parallel(n_jobs=-1)]: Done 1005 tasks      | elapsed:  5.4min
[Parallel(n_jobs=-1)]: Done 1450 tasks      | elapsed:  8.4min
[Parallel(n_jobs=-1)]: Done 1977 tasks      | elapsed: 11.6min
```

```
[Parallel(n_jobs=-1)]: Done 2584 tasks      | elapsed: 14.8min
[Parallel(n_jobs=-1)]: Done 3273 tasks      | elapsed: 19.3min
[Parallel(n_jobs=-1)]: Done 4042 tasks      | elapsed: 23.6min
[Parallel(n_jobs=-1)]: Done 4893 tasks      | elapsed: 28.7min
[Parallel(n_jobs=-1)]: Done 5824 tasks      | elapsed: 34.5min
[Parallel(n_jobs=-1)]: Done 6837 tasks      | elapsed: 40.9min
[Parallel(n_jobs=-1)]: Done 7200 out of 7200 | elapsed: 43.2min finishe
d
```

In [77]:

```
xgb_cv_model.best_params_
```

Out[77]:

```
{'learning_rate': 0.1,
 'max_depth': 5,
 'min_samples_split': 0.1,
 'n_estimators': 100,
 'subsample': 1.0}
```

3.1) Final Model Installation

In [78]:

```
xgb_tuned = GradientBoostingClassifier(**xgb_cv_model.best_params_).fit(X,y
)
```

In [79]:

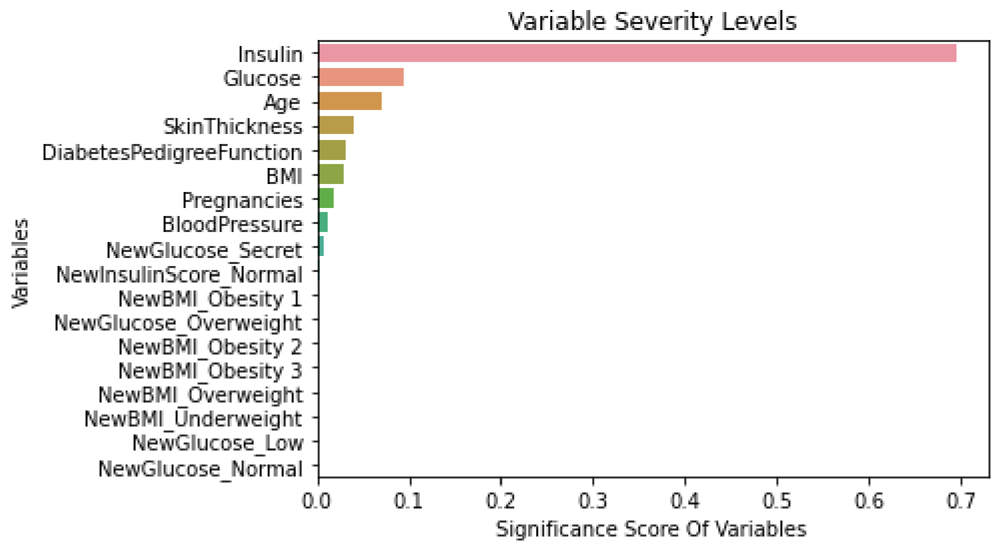
```
cross_val_score(xgb_tuned, X, y, cv = 10).mean()
```

Out[79]:

```
0.9013157894736843
```

In [80]:

```
feature_imp = pd.Series(xgb_tuned.feature_importances_,
                        index=X.columns).sort_values(ascending=False)

sns.barplot(x=feature_imp, y=feature_imp.index)
plt.xlabel('Significance Score Of Variables')
plt.ylabel('Variables')
plt.title("Variable Severity Levels")
plt.show()
```



7) Comparison of Final Models

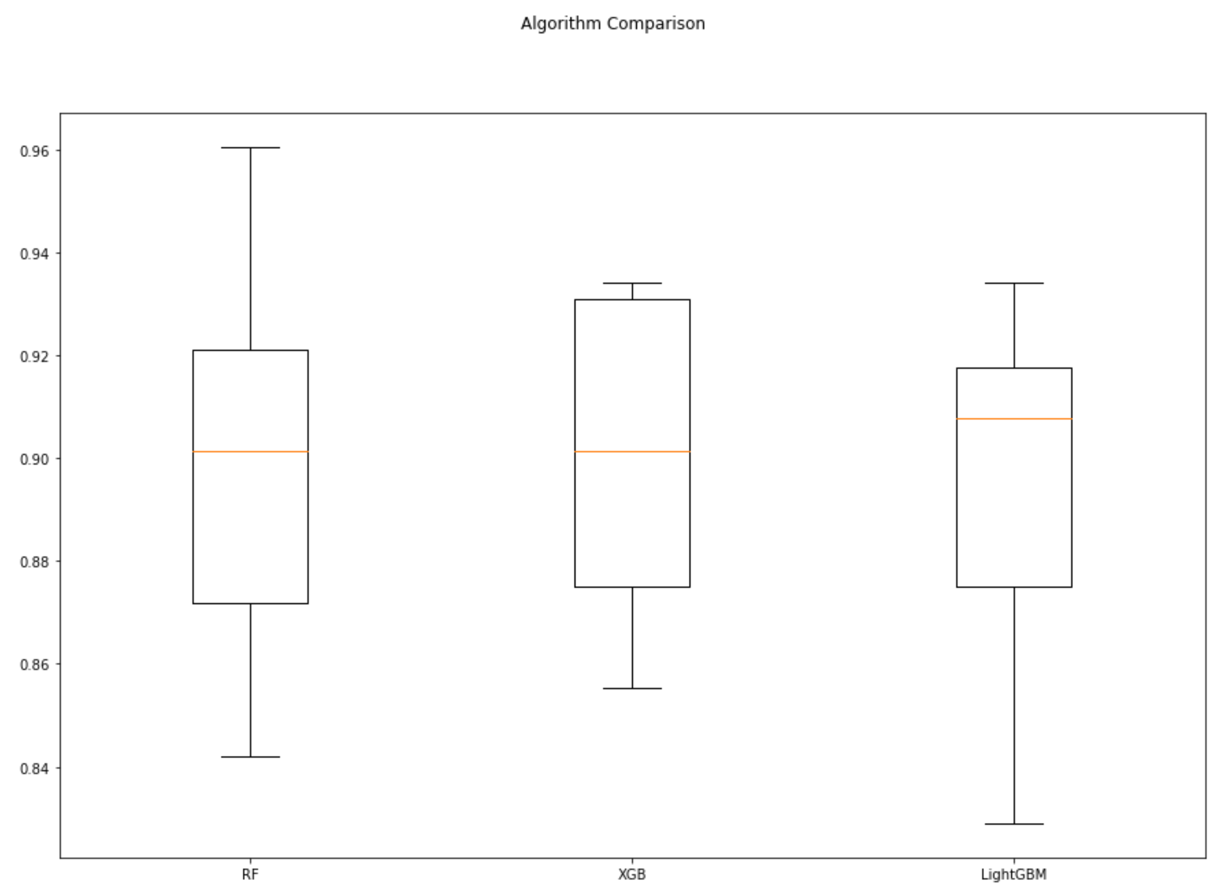
In [81]:

```
models = []

models.append(('RF', RandomForestClassifier(random_state = 12345, max_depth
= 8, max_features = 7, min_samples_split = 2, n_estimators = 500)))
models.append(('XGB', GradientBoostingClassifier(random_state = 12345, lear
ning_rate = 0.1, max_depth = 5, min_samples_split = 0.1, n_estimators = 100
, subsample = 1.0)))
models.append(("LightGBM", LGBMClassifier(random_state = 12345, learning_ra
te = 0.01,  max_depth = 3, n_estimators = 1000)))

# evaluate each model in turn
results = []
names = []
```

In [82]:

```
for name, model in models:

        kfold = KFold(n_splits = 10, random_state = 12345)
        cv_results = cross_val_score(model, X, y, cv = 10, scoring= "accura
cy")
        results.append(cv_results)
        names.append(name)
        msg = "%s: %f (%f)" % (name, cv_results.mean(), cv_results.std())
        print(msg)

# boxplot algorithm comparison
fig = plt.figure(figsize=(15,10))
fig.suptitle('Algorithm Comparison')
ax = fig.add_subplot(111)
plt.boxplot(results)
ax.set_xticklabels(names)
plt.show()
```

```
RF: 0.897368 (0.034211)
XGB: 0.901316 (0.028373)
LightGBM: 0.896053 (0.033000)
```



8) Reporting

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 validation scores in the established models. The work done is as follows:

1) Diabetes Data Set read.

2) With Exploratory Data Analysis; The data set's structural data were checked. The types of variables in the dataset were examined. Size information of the dataset was accessed. The 0 values in the data set are missing values. Primarily these 0 values were replaced with NaN values. Descriptive statistics of the data set were examined.

3) Data Preprocessing section; df for: The NaN values missing observations were filled with the median values of whether each variable was sick or not. The outliers were determined by LOF and dropped. The X variables were standardized with the rubost method..

4) During Model Building; Logistic Regression, KNN, SVM, CART, Random Forests, XGBoost, LightGBM like using machine learning models Cross Validation Score were calculated. Later Random Forests, XGBoost, LightGBM hyperparameter optimizations optimized to increase Cross Validation value.

5) Result; The model created as a result of XGBoost hyperparameter optimization became the model with the lowest Cross Validation Score value. (0.90)