Diabetes Prediction Using Machine Learning

Overview

we will be predicting that whether the patient has diabetes or not on the basis of the features

we will provide to our machine learning model, and for that, we will be using the famous Pima Indians Diabetes Database.

Data analysis: Here one will get to know about how the data analysis part is done in a data science life cycle. Exploratory data analysis: EDA is one of the most important steps in the data science project life cycle and here one will need to know that how to make inferences from the visualizations and data analysis Model building: Here we will be using 4 ML models and then we will choose the best performing model. Saving model: Saving the best model using pickle to make the prediction from real data.

In [1]:
```
# Importing Libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

sns.set()

from mlxtend.plotting import plot_decision_regions
import missingno as msno
from pandas.plotting import scatter_matrix
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier

from sklearn.metrics import confusion_matrix
from sklearn import metrics
from sklearn.metrics import classification_report
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score
import warnings
warnings.filterwarnings('ignore')
%matplotlib inline
```

In [2]:
```
# Here we will be reading the dataset which is in the CSV format

diabetes_df = pd.read_csv('diabetes.csv')
diabetes_df.head()
```

Out[2]:

	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)

In [3]:
```
diabetes_df.columns
```

Out[3]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

In [4]:
```
# Information about the dataset

diabetes_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 [5]:
```
# To know the more about dataset

diabetes_df.describe()
```

Out[5]:

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

In [6]:
```
# To know more about the dataset with transpose - here T is for the transpose

diabetes_df.describe().T
```

Out[6]:

	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

In [7]:
```
# Now let's check that if our dataset have null values or not

diabetes_df.isnull().sum()
```

Out[7]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

Here from the above code we first checked that is there any null values from the IsNull() function then we are going to take the sum of all those missing values from the sum() function and the inference we now get is that there are no missing values but that is actually not a true story as in this particular dataset all the missing values were given the 0 as a value which is not good for the authenticity of the dataset. Hence we will first replace the 0 value with the NAN value then start the imputation process.

In [8]:
```
diabetes_df_copy = diabetes_df.copy(deep = True)
diabetes_df_copy[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']] = \
                            diabetes_df_copy[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']]
```

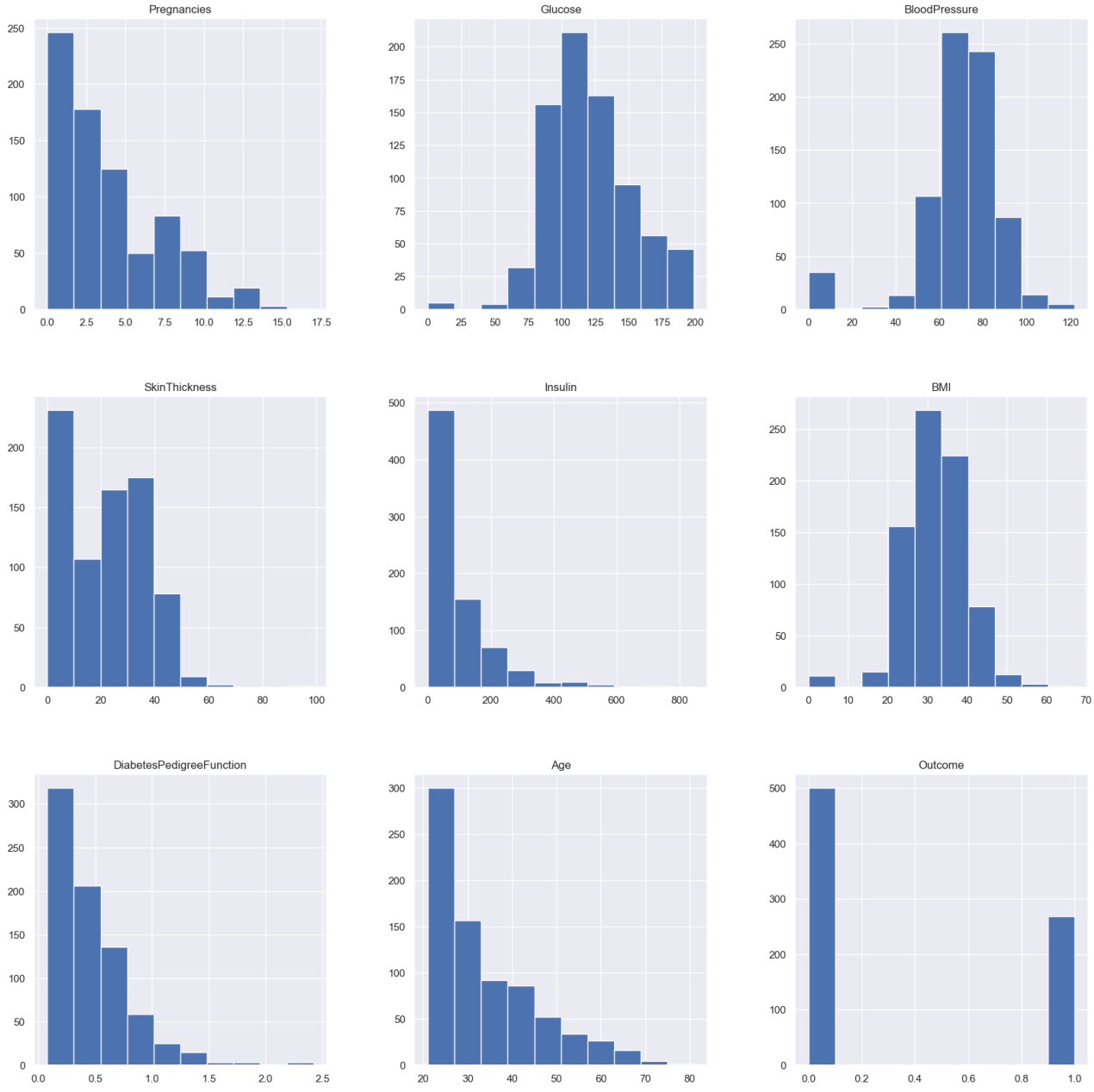
In [9]:
```
# Showing the count of NaNs
print(diabetes_df_copy.isnull().sum())
```

```
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 Visualization

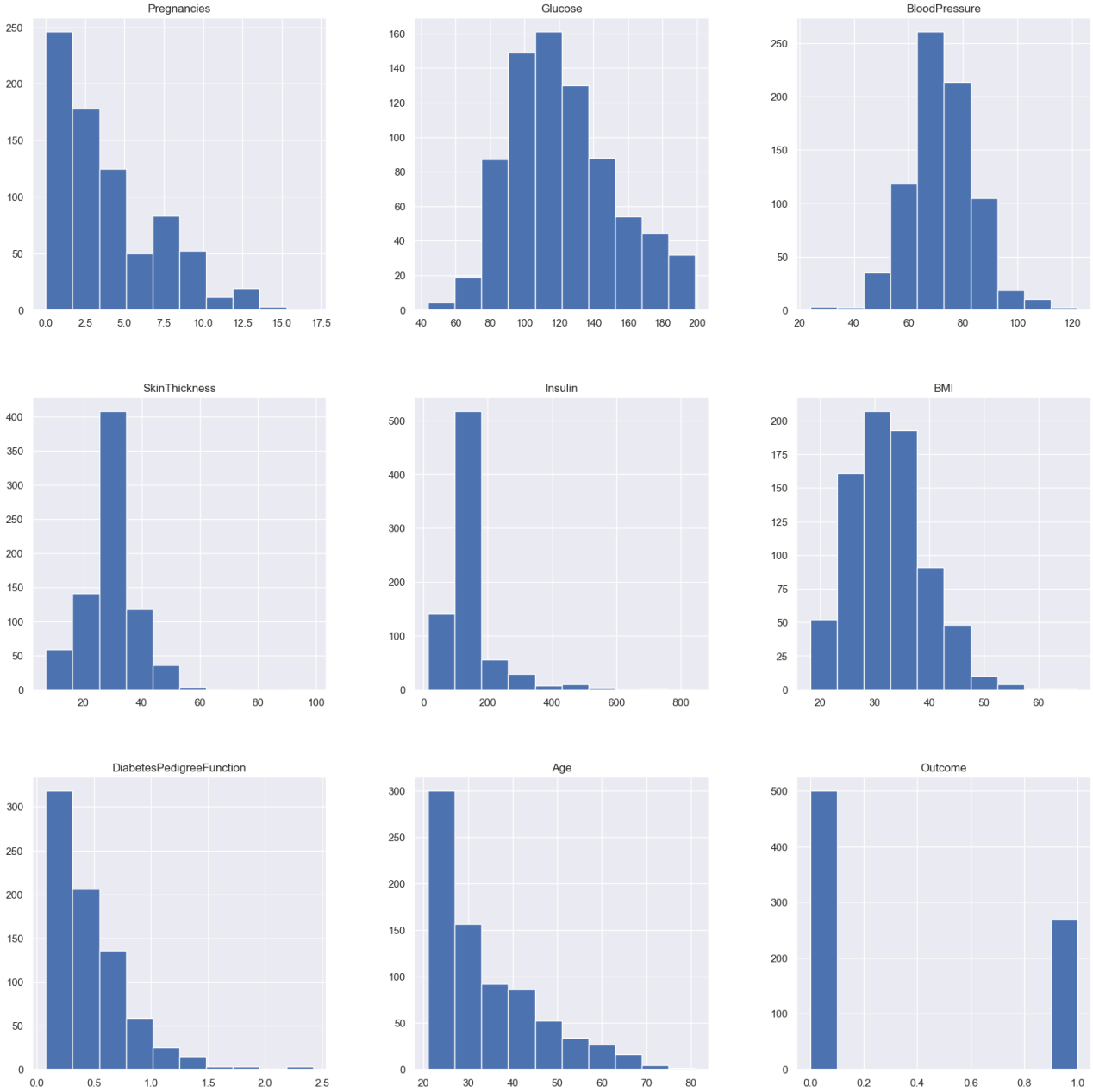
In [10]:
```
#Plotting the data distrubution plots before removing null values

p = diabetes_df.hist(figsize=(20,20))
```



Inference: So here we have seen the distribution of each features whether it is dependent data or independent data and one thing which could always strike that why do we need to see the distribution of data? So the answer is simple it is the best way to start the analysis of the dataset as it shows the occurrence of every kind of value in the graphical structure which in turn lets us know the range of the data.

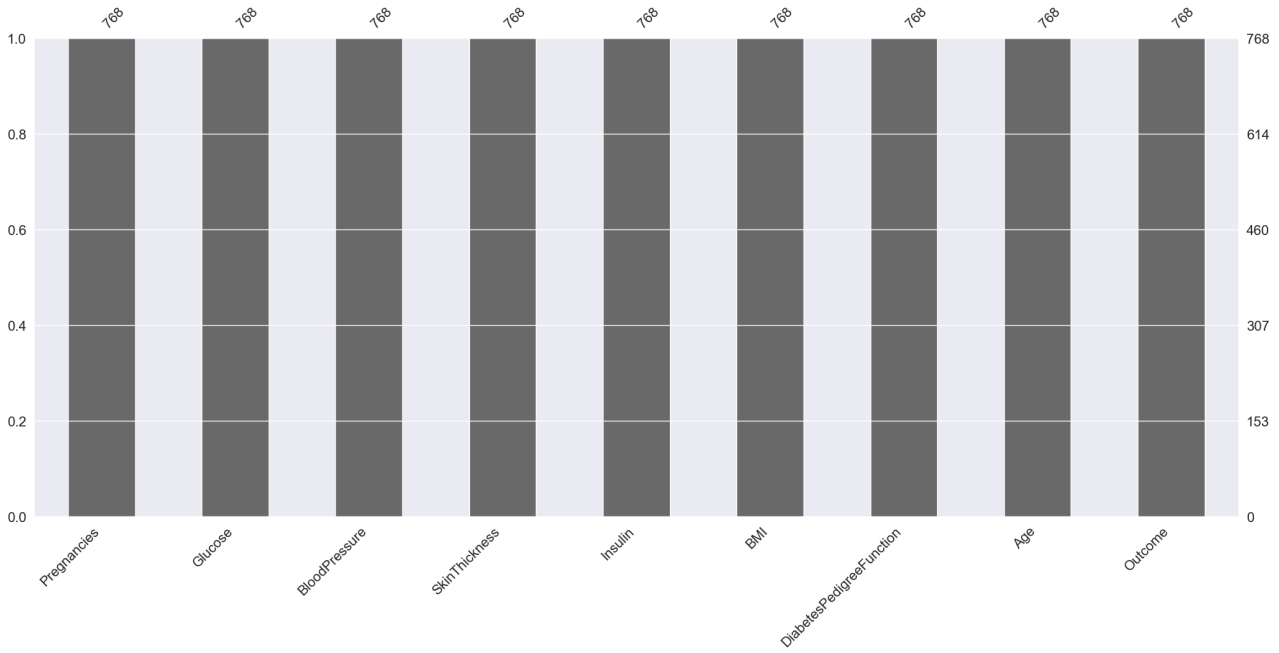
In [11]:
```
#Now we will be imputing the mean value of the column to each missing value of that particular column.

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

In [12]:
```
# Plotting the distrubution after  removing NAN values.

p = diabetes_df_copy.hist(figsize=(20,20))
```



Inference: Here we are again using the hist plot to see the distribution of the dataset but this time we are using this visualization to see the changes that we can see after those null values are removed from the dataset and we can clearly see the difference for example – In age column after removal of the null values, we can see that there is a spike at the range of 50 to 100 which is quite logical as well.

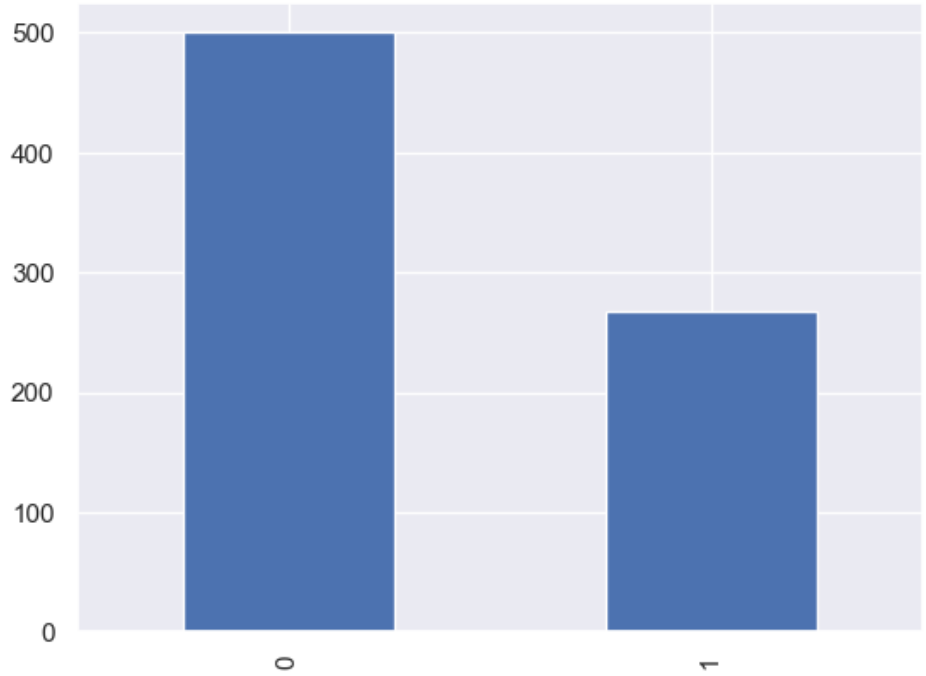
In [13]:
```
# Plotting Null Count Analysis Plot

p = msno.bar(diabetes_df)
```



Inference: Now in the above graph also we can clearly see that there are no null values in the dataset.

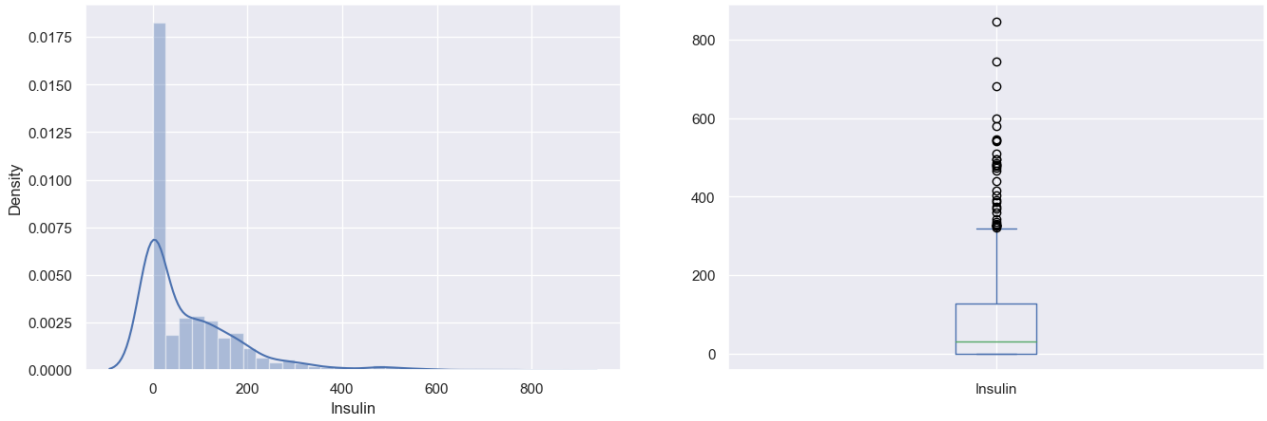
In [19]:
```
#Now, Let's check that how well our outcome column is balanced

color_wheel = {1: "#0392cf", 2: "#7bc043"}
#colors = diabetes_df["Outcome"]
print(diabetes_df.Outcome.value_counts())
p = diabetes_df.Outcome.value_counts().plot(kind='bar')
```

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



Here from the 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.

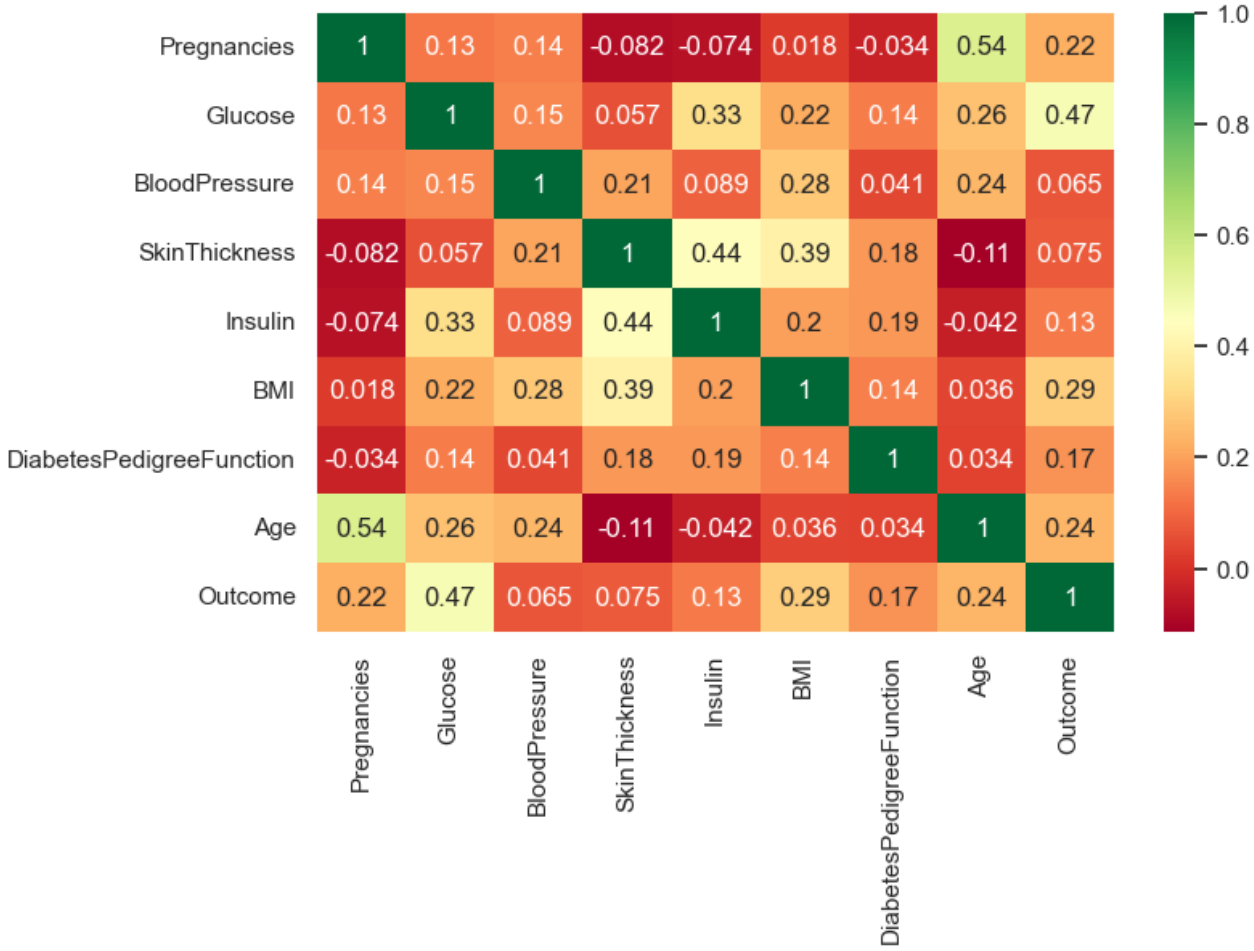
In [22]:
```
plt.subplot(121), sns.distplot(diabetes_df['Insulin'])
plt.subplot(122), diabetes_df['Insulin'].plot.box(figsize=(16,5))
plt.show()
```



That's how Distplot can be helpful where one will able to see the distribution of the data as well as with the help of boxplot one can see the outliers in that column and other information too which can be derived by the box and whiskers plot.

Correlation between all the features

In [23]:
```
#Correlation between all the features before clearning

plt.figure(figsize=(8,5))
# seaborn has an easy method to showcase heatmap
p = sns.heatmap(diabetes_df.corr(), annot=True, cmap='RdYlGn')
```



Scalling the Data

In [24]:
```
# Before scaling down the data let's have a look into it

diabetes_df_copy.head()
```

Out[24]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.0	35.0	125.0	33.6	0.627	50	1
1	1	85.0	66.0	29.0	125.0	26.6	0.351	31	0
2	8	183.0	64.0	29.0	125.0	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]:
```
#After Standard scaling

sc_X = StandardScaler()
X =  pd.DataFrame(sc_X.fit_transform(diabetes_df_copy.drop(["Outcome"],axis = 1),), columns=['Pregnancie
'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age'])
X.head()
```

Out[25]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
0	0.639947	0.865108	-0.033518	0.670643	-0.181541	0.166619	0.468492	1.425995
1	-0.844885	-1.206162	-0.529859	-0.012301	-0.181541	-0.852200	-0.365061	-0.190672
2	1.233880	2.015813	-0.695306	-0.012301	-0.181541	-1.332500	0.604397	-0.105584
3	-0.844885	-1.074652	-0.529859	-0.695245	-0.540642	-0.633881	-0.920763	-1.041549
4	-1.141852	0.503458	-2.680669	0.670643	0.316566	1.549303	5.484909	-0.020496

That's how our dataset will be looking like when it is scaled down or we can see every value now is on the same scale which will help our ML model to give a better result.

Model Building

In [26]:
```
#Splitting the dataset

X = diabetes_df.drop('Outcome', axis=1)
y = diabetes_df['Outcome']
```

In [28]:
```
#Now we will split the data into training and testing data using the train test split function

from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X,y,test_size=0.33,random_state=7)
```

Random Forest

In [31]:
```
# Building the model using RandomForest

from sklearn.ensemble import RandomForestClassifier

rfc = RandomForestClassifier(n_estimators=200)
rfc.fit(X_train,y_train)
```

Out[31]:
```
RandomForestClassifier(n_estimators=200)
```

In [32]:
```
#Now after building the model let's check the accuracy of the model on the training dataset.

rfc_train = rfc.predict(X_train)
from sklearn import metrics

print("Accuracy_Score =", format(metrics.accuracy_score(y_train, rfc_train)))
```

```
Accuracy_Score = 1.0
```

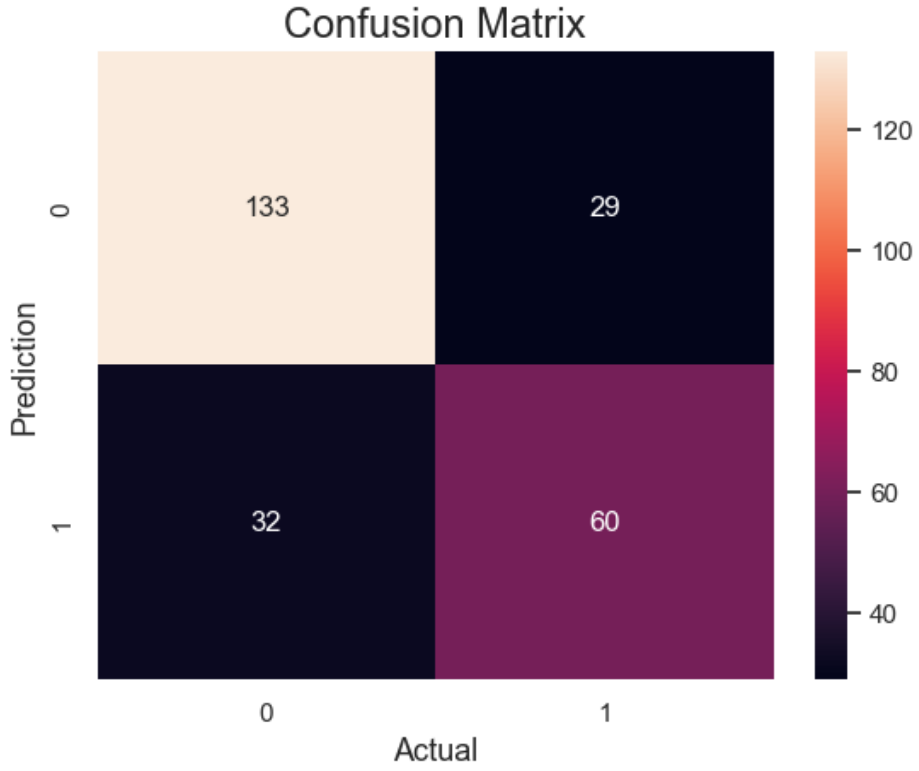
So here we can see that on the training dataset our model is overfitted. Getting the accuracy score for Random Forest

In [33]:
```
from sklearn import metrics

predictions = rfc.predict(X_test)
print("Accuracy_Score =", format(metrics.accuracy_score(y_test, predictions)))
```

```
Accuracy_Score = 0.7795275590551181
```

In [34]:
```
#Classification report and confusion matrix of random forest model
# Train the model
clf = RandomForestClassifier(random_state=23)
```

```
clf.fit(X_train, y_train)

# prediction
y_pred = clf.predict(X_test)

# compute the confusion matrix
cm = confusion_matrix(y_test,y_pred)

#Plot the confusion matrix.
sns.heatmap(cm,
            annot=True,
            fmt='g')
plt.ylabel('Prediction',fontsize=13)
plt.xlabel('Actual',fontsize=13)
plt.title('Confusion Matrix',fontsize=17)
plt.show()


# Finding precision and recall
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy   :", accuracy)
```




```
Accuracy   : 0.7598425196850394
```

In [35]:

```
# Finding precision and recall
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy   :", accuracy)
precision = precision_score(y_test, y_pred)
print("Precision :", precision)
recall = recall_score(y_test, y_pred)
print("Recall    :", recall)
F1_score = f1_score(y_test, y_pred)
print("F1-score  :", F1_score)
```

```
Accuracy   : 0.7598425196850394
Precision : 0.6741573033707865
Recall    : 0.6521739130434783
F1-score  : 0.6629834254143646
```

Decision Tree

In [36]:
```
#Building the model using DecisionTree

from sklearn.tree import DecisionTreeClassifier

dtree = DecisionTreeClassifier()
dtree.fit(X_train, y_train)

#Now we will be making the predictions on the testing data directly as it is of more importance.
```

Out[36]:
```
DecisionTreeClassifier()
```

In [37]:
```
#Getting the accuracy score for Decision Tree

from sklearn import metrics

predictions = dtree.predict(X_test)
print("Accuracy Score =", format(metrics.accuracy_score(y_test,predictions)))
```

```
Accuracy Score = 0.7086614173228346
```

In [38]:
```
#Classification report and confusion matrix of the decision tree model

from sklearn.metrics import classification_report, confusion_matrix

print(confusion_matrix(y_test, predictions))
print(classification_report(y_test,predictions))
```

```
[[128  34]
 [ 40  52]]
              precision    recall  f1-score   support

           0       0.76      0.79      0.78       162
           1       0.60      0.57      0.58        92

    accuracy                           0.71       254
   macro avg       0.68      0.68      0.68       254
weighted avg       0.70      0.71      0.71       254
```

XgBoost classifier

In [41]:
```
#Building model using XGBoost

from xgboost import XGBClassifier

xgb_model = XGBClassifier(gamma=0)
xgb_model.fit(X_train, y_train)
```

Out[41]:
```
XGBClassifier(base_score=None, booster=None, callbacks=None,
              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=0, 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 [42]:
```
#Now we will be making the predictions on the testing data directly as it is of more importance.
#Getting the accuracy score for the XgBoost classifier

from sklearn import metrics

xgb_pred = xgb_model.predict(X_test)
print("Accuracy Score =", format(metrics.accuracy_score(y_test, xgb_pred)))
```

```
Accuracy Score = 0.7283464566929134
```

In [43]:
```
#Classification report and confusion matrix of the XgBoost classifier
```

In [44]:
```
#Support Vector Machine (SVM)

#Building the model using Support Vector Machine (SVM)

from sklearn.svm import SVC

svc_model = SVC()
svc_model.fit(X_train, y_train)

#Prediction from support vector machine model on the testing data

svc_pred = svc_model.predict(X_test)

#Accuracy score for SVM

from sklearn import metrics

print("Accuracy Score =", format(metrics.accuracy_score(y_test, svc_pred)))
```

```
Accuracy Score = 0.7480314960629921
```

In [45]:
```
# Classification report and confusion matrix of the SVM classifier

from sklearn.metrics import classification_report, confusion_matrix

print(confusion_matrix(y_test, svc_pred))
print(classification_report(y_test,svc_pred))
```

```
[[145  17]
 [ 47  45]]
              precision    recall  f1-score   support

           0       0.76      0.90      0.82       162
           1       0.73      0.49      0.58        92

    accuracy                           0.75       254
   macro avg       0.74      0.69      0.70       254
weighted avg       0.74      0.75      0.73       254
```

The Conclusion from Model Building

Therefore Random forest is the best model for this prediction since it has an accuracy_score of 0.76.

Feature Importance

Knowing about the feature importance is quite necessary as it shows that how much weightage each feature provides in the model building phase.

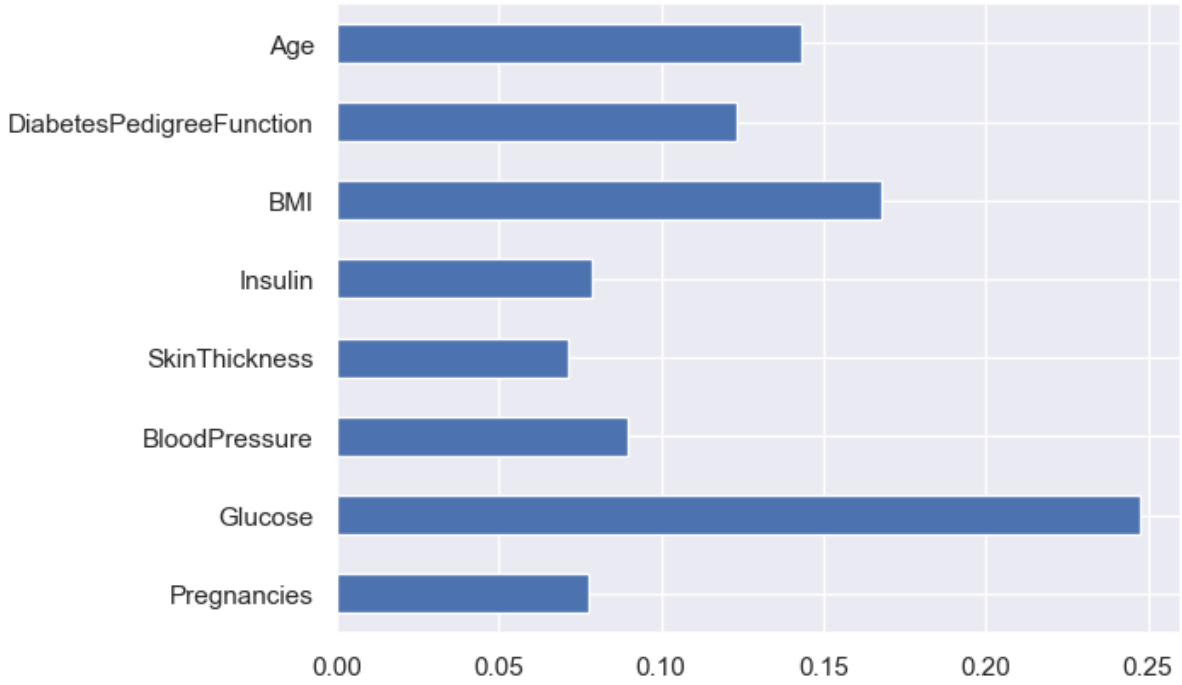
In [46]:
```
#Getting feature importances

rfc.feature_importances_
```

Out[46]:
```
array([0.07785196, 0.24783368, 0.089465  , 0.07157293, 0.07866362,
       0.16799742, 0.12326635, 0.14334905])
```

From the above output, it is not much clear that which feature is important for that reason we will now make a visualization of the same.

In [47]:
```
#Plotting feature importances

(pd.Series(rfc.feature_importances_, index=X.columns).plot(kind='barh'))
```

Out[47]:
```
<Axes: >
```



Here from the above graph, it is clearly visible that Glucose as a feature is the most important in this dataset.

Saving Model – Random Forest

In [48]:
```
import pickle

# Firstly we will be using the dump() function to save the model using pickle
saved_model = pickle.dumps(rfc)

# Then we will be loading that saved model
rfc_from_pickle = pickle.loads(saved_model)

# lastly, after loading that model we will use this to make predictions
rfc_from_pickle.predict(X_test)
```

Out[48]:
```
array([0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0,
       1, 1, 0, 0, 0, 0, 1, 0, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 1, 1, 0,
       0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1,
       0, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0,
       1, 0, 1, 0, 1, 0, 0, 1, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1,
       0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1,
       0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0,
       0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0,
       1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 1, 1, 0, 0, 1, 0,
       0, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 0,
       0, 1, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 1, 1,
       1, 0, 1, 0, 1, 0, 0, 0, 0, 1, 1, 1], dtype=int64)
```

Now for the last time, I'll be looking at the head and tail of the dataset so that we can take any random set of features from both the head and tail of the data to test that if our model is good enough to give the right prediction.

In [49]:
```
diabetes_df.head()
```

Out[49]:

	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 [50]:
```
diabetes_df.tail()
```

Out[50]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
763	10	101	76	48	180	32.9	0.171	63	0
764	2	122	70	27	0	36.8	0.340	27	0
765	5	121	72	23	112	26.2	0.245	30	0
766	1	126	60	0	0	30.1	0.349	47	1
767	1	93	70	31	0	30.4	0.315	23	0

In [51]:
```
#Putting data points in the model will either return 0 or 1 i.e. person suffering from diabetes or not.

rfc.predict([[0,137,40,35,168,43.1,2.228,33]]) #4th patient
```

Out[51]:
```
array([1], dtype=int64)
```

In [52]:
```
#Another one

rfc.predict([[10,101,76,48,180,32.9,0.171,63]])  # 763 th patient
```

Out[52]:
```
array([0], dtype=int64)
```

Conclusion

After using all these patient records, we are able to build a machine learning model (random forest – best one) to accurately

predict whether or not the patients in the dataset have diabetes or not along with that we were able to draw some insights from

the data via data analysis and visualization.