Diabetes Prediction Using Machine Learning

Overview

This project predicts whether a patient has diabetes or not based on the features in the dataset provided to the machine learning model, and for that, the famous Pima Indians Diabetes Database will be used.

1, Importing Libraries

In [22]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import sklearn

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
import warnings
warnings.filterwarnings('ignore')
%matplotlib inline
```

2, Reading the dataset which is in the CSV format

In [19]:
```
diabetes_df = pd.read_csv('diabetes.csv')
diabetes_df.head(10)
```

Out[19]:

	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
5	5	116	74	0	0	25.6	0.201	30	0
6	3	78	50	32	88	31.0	0.248	26	1
7	10	115	0	0	0	35.3	0.134	29	0
8	2	197	70	45	543	30.5	0.158	53	1
9	8	125	96	0	0	0.0	0.232	54	1

3, Exploratory Data Analysis (EDA)

3.1, List all the columns available in the dataset.

In [20]:
```
diabetes_df.columns
```

Out[20]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

3.2, Information about the dataset

In [21]:
```
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
```

3.3, Description about the dataset

In [24]:
```
diabetes_df.describe()
```

Out[24]:

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

3.4, More about the dataset with transpose

In [25]:
```
diabetes_df.describe().T
```

Out[25]:

	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

3.5, Check if the dataset have a null values

In [27]:
```
diabetes_df.isnull().head(10)
```

Out[27]:

	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
6	False	False	False	False	False	False	False	False	False
7	False	False	False	False	False	False	False	False	False
8	False	False	False	False	False	False	False	False	False
9	False	False	False	False	False	False	False	False	False

3.6, Check how many null values do every columns have

In [28]:
```
diabetes_df.isnull().sum()
```

Out[28]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

N.B:- Here from the above code I first checked that is there any null values from the IsNull() function then I am going to take the sum of all those missing values from the sum() function and the inference I now get is that there are no missing values but that is 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 I will first replace the 0 value with the NAN value and then start the imputation process.

3.7, Showing the Count of NANs

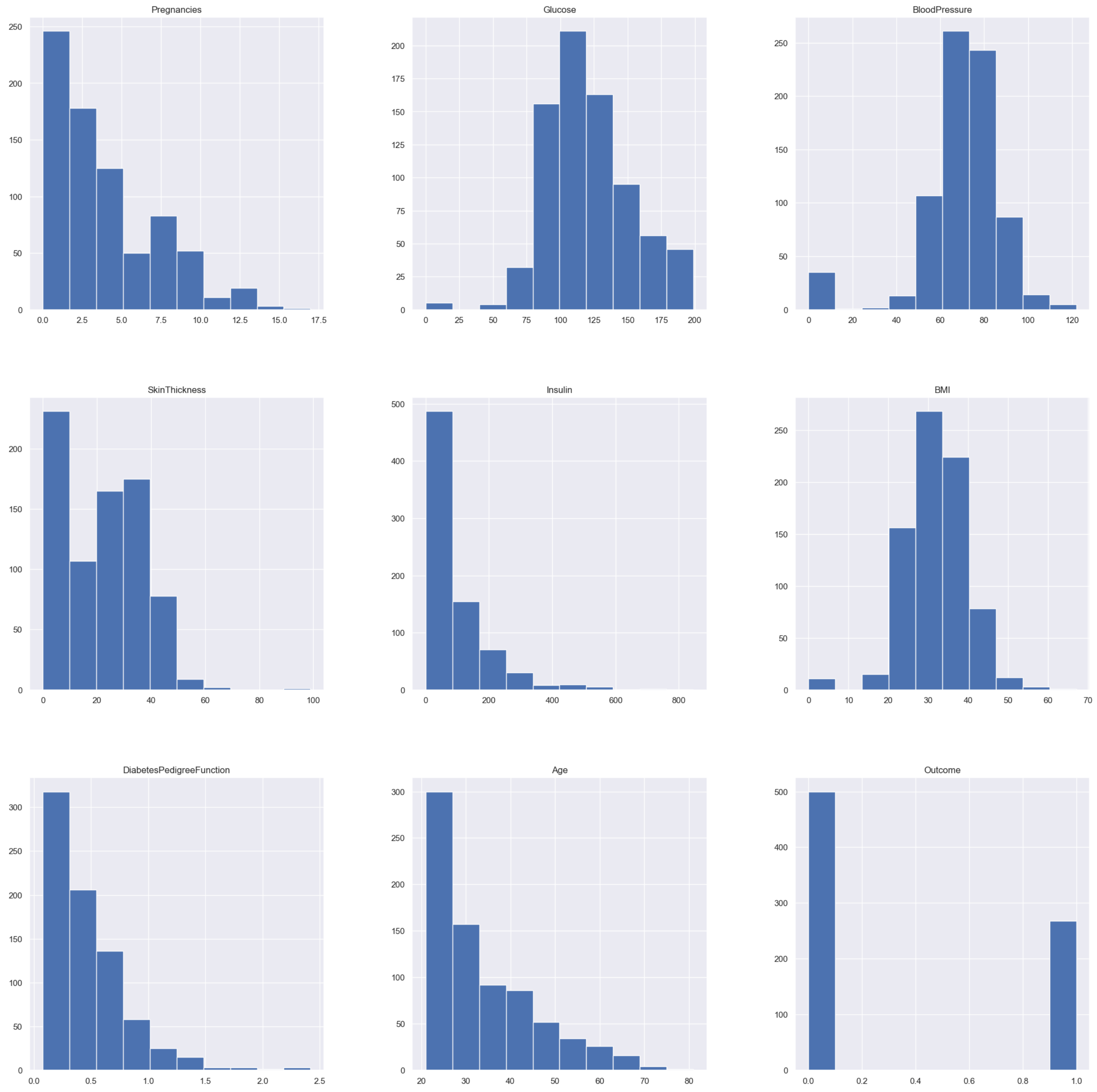
In [31]:
```
diabetes_df_copy = diabetes_df.copy(deep = True)
diabetes_df_copy[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']] = diabetes_df_copy
print(diabetes_df_copy.isnull().sum())
```

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

4, Data Visualization

4.1, Data distribution plots before removing null values

In [38]:
```
p = diabetes_df.hist(figsize = (25,25))
```

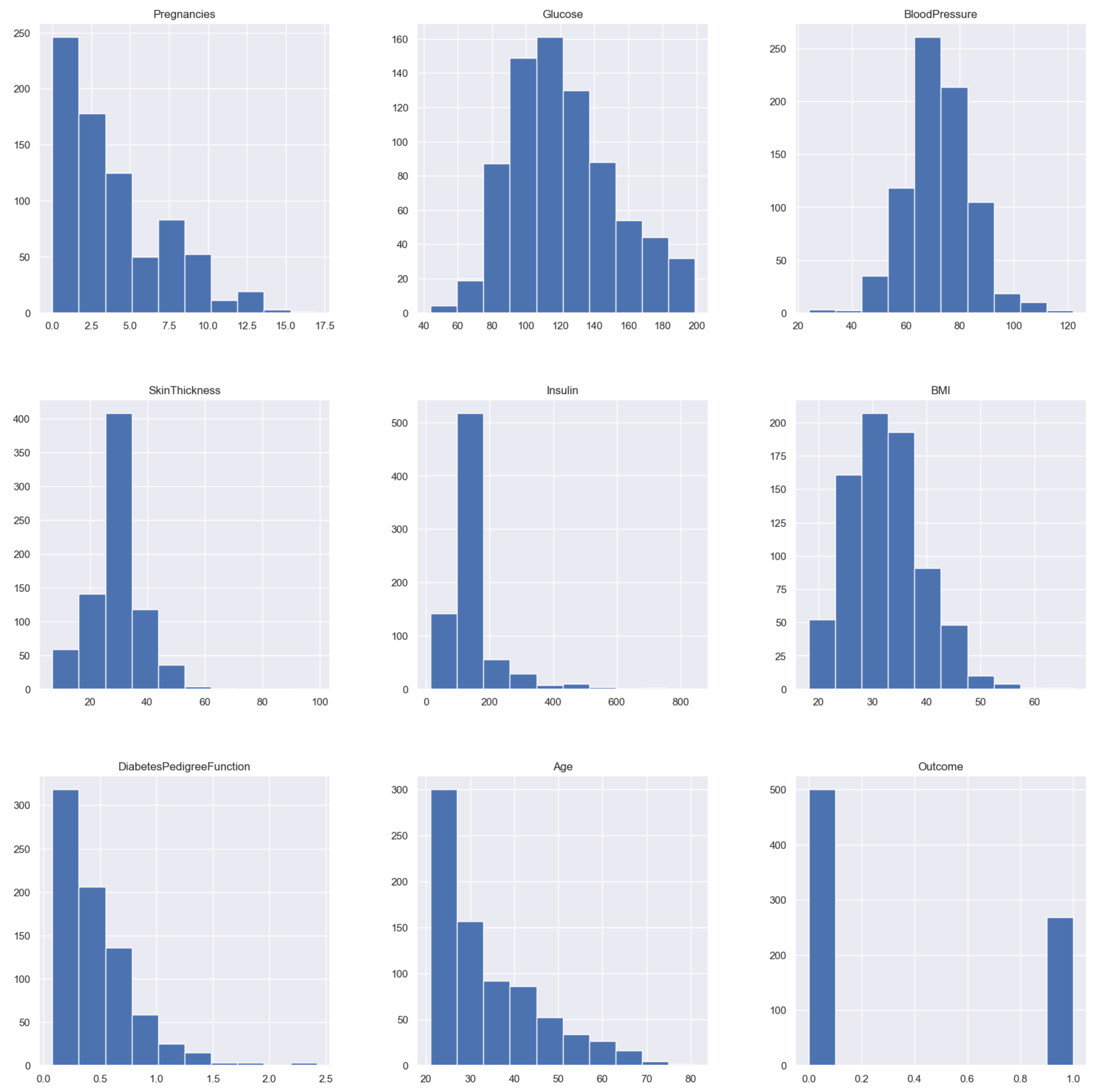


Inference: So here I have seen the distribution of each feature whether it is dependent data or independent data and one thing which could always strike that why do I need to see the distribution of data? So the answer is simple it is the best way to start the analysis of the dataset as it shows the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

4.2, Now I will be imputing the mean value of the column to each missing value of that particular column and Plotting the distributions after removing the NAN values.

In [41]:
```
diabetes_df_copy['Glucose'].fillna(diabetes_df_copy['Glucose'].mean(), inplace = True)
diabetes_df_copy['BloodPressure'].fillna(diabetes_df_copy['BloodPressure'].mean(), inplace = Tru
```

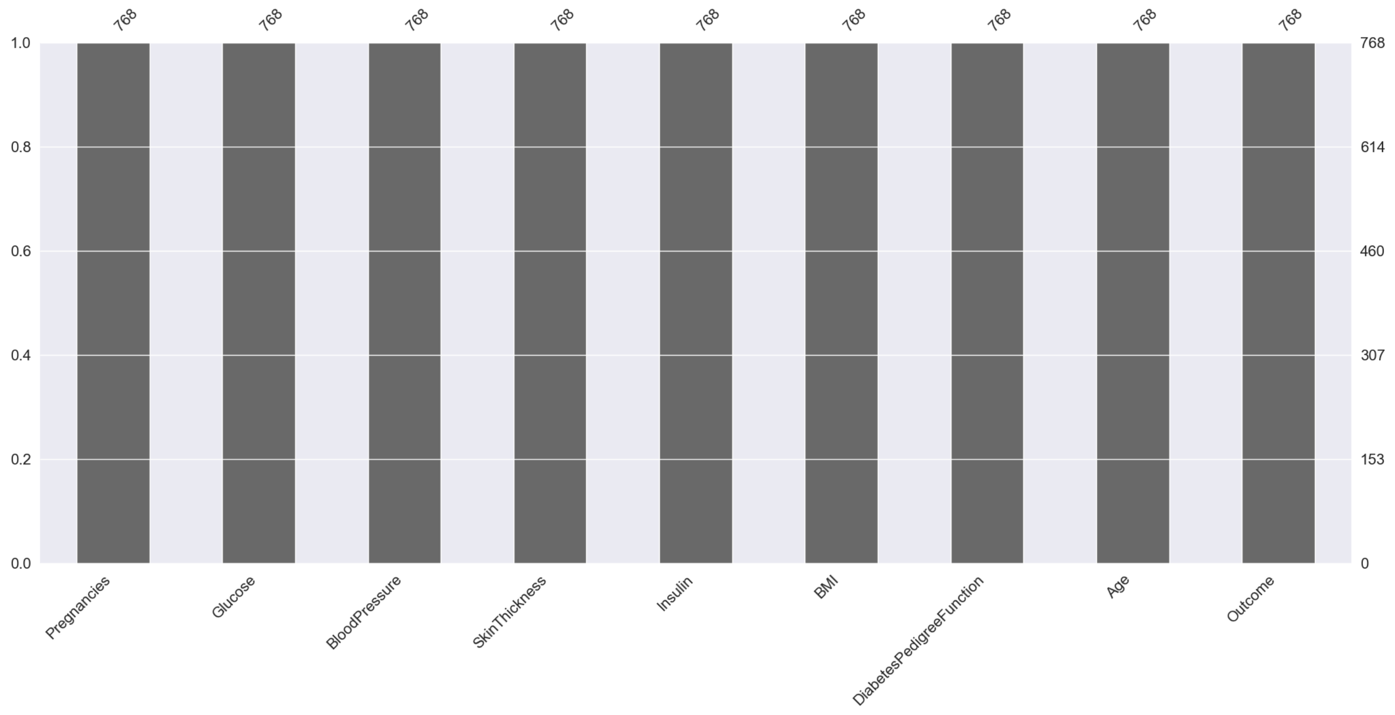
```python
diabetes_df_copy['SkinThickness'].fillna(diabetes_df_copy['SkinThickness'].median(), inplace = Tr
diabetes_df_copy['Insulin'].fillna(diabetes_df_copy['Insulin'].median(), inplace = True)
diabetes_df_copy['BMI'].fillna(diabetes_df_copy['BMI'].median(), inplace = True)

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



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

4.3, Plotting Null Count Analysis Plot

In [44]:
```python
p = msno.bar(diabetes_df)
```

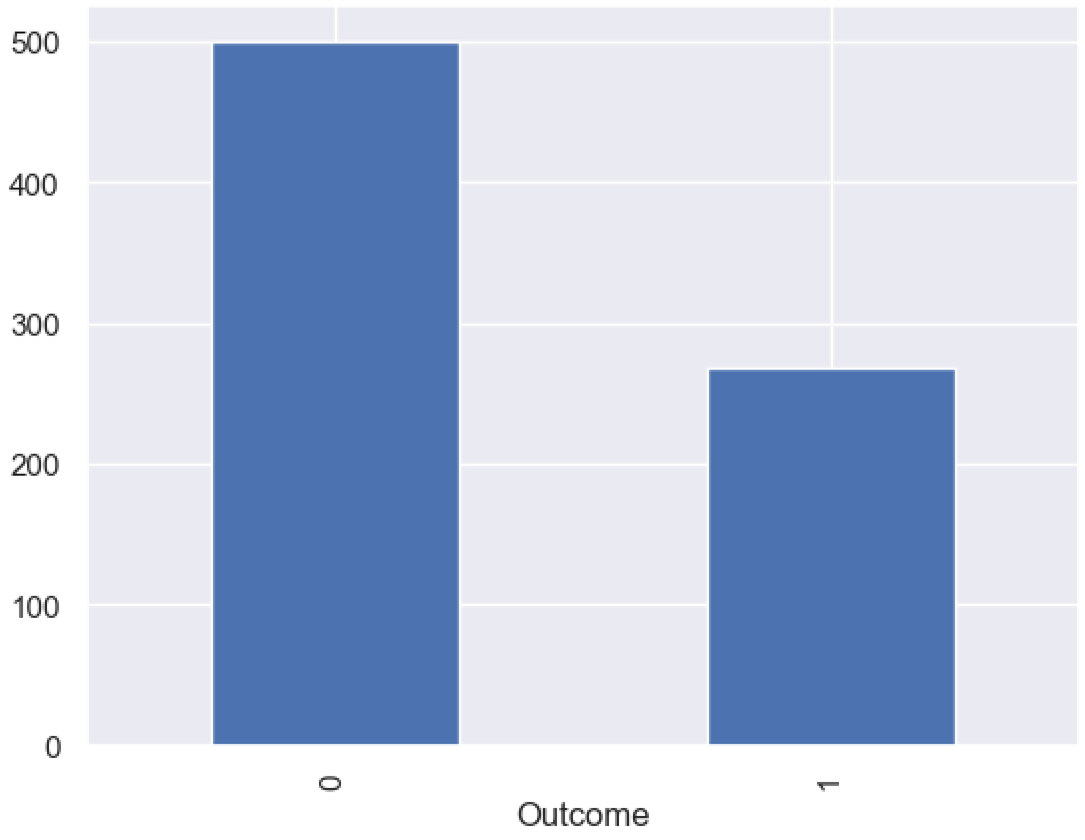


Inference: Now in the above graph, see that there are no null values in the dataset.

4.4 check how well the outcome column is balanced

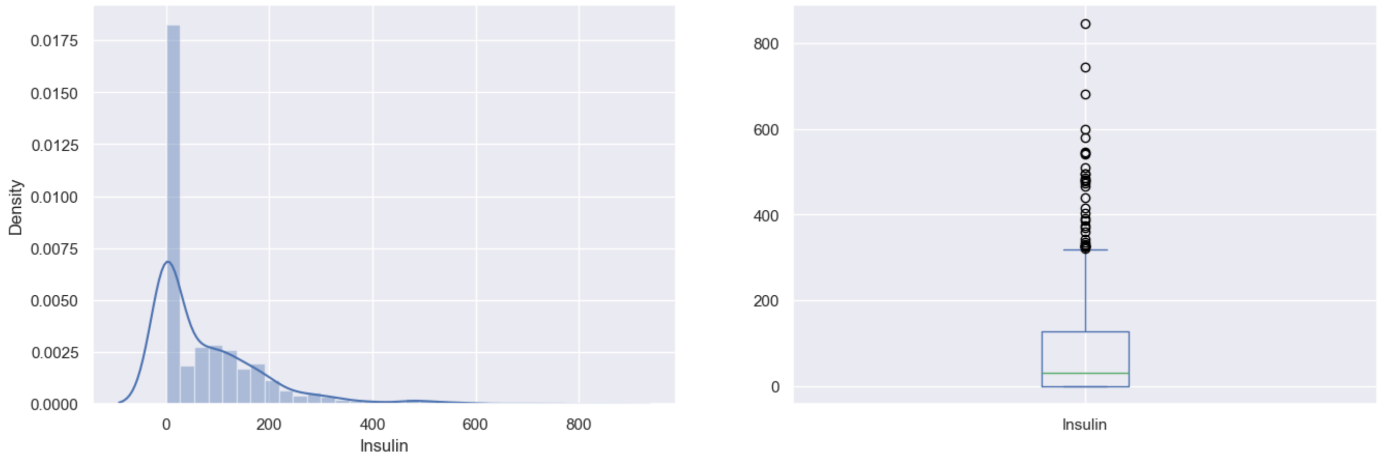
In [45]:
```
color_wheel = {1: "#0392cf", 2: "#7bc043"}
colors = diabetes_df["Outcome"].map(lambda x: color_wheel.get(x + 1))
print(diabetes_df.Outcome.value_counts())
p=diabetes_df.Outcome.value_counts().plot(kind="bar")
```

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



Inference: Here from the above visualization it is clearly visible that the dataset is completely imbalanced the number of ***patients who are diabetic is half of the patients who are non-diabetic***.

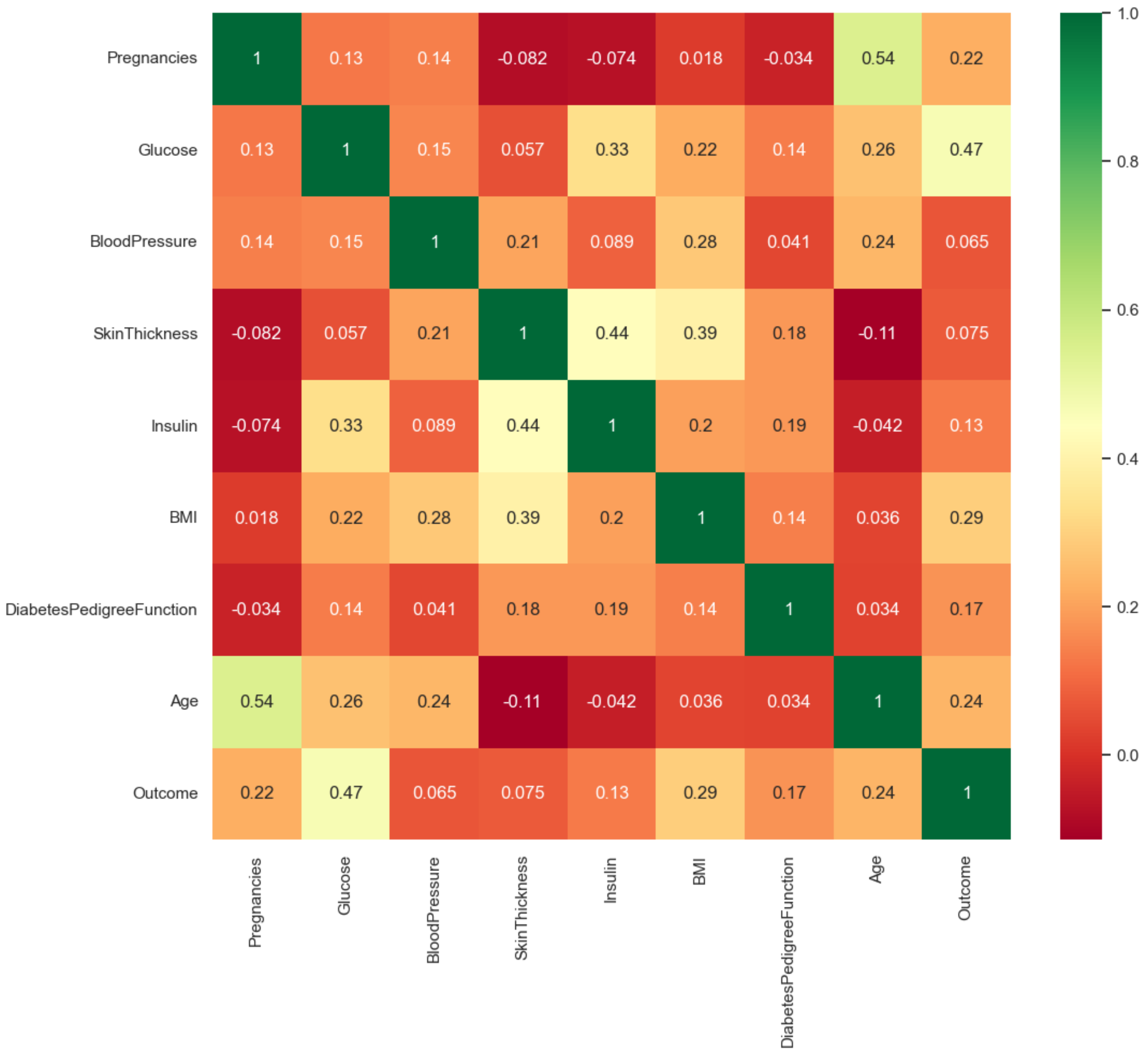
In [46]:
```
plt.subplot(121), sns.distplot(diabetes_df['Insulin'])
plt.subplot(122), diabetes_df['Insulin'].plot.box(figsize=(16,5))
plt.show()
```



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

4.5, Correlation between all the features before cleaning

In [47]:
```
plt.figure(figsize=(12,10))
# seaborn has an easy method to showcase heatmap
p = sns.heatmap(diabetes_df.corr(), annot=True,cmap ='RdYlGn')
```



5, Scaling the Data

5.1, Before scaling down the data, have a look into it

```
In [48]: diabetes_df_copy.head()
```

Out[48]:

	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

5.1, After scaling down the data

```
In [50]: sc_X = StandardScaler()
         X =  pd.DataFrame(sc_X.fit_transform(diabetes_df_copy.drop(["Outcome"],axis = 1),), columns=['Pr
         'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI', 'DiabetesPedigreeFunction', 'Age'
         X.head()
```

Out[50]:

	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 the dataset will look like when it is scaled down or can see every value now is on the same scale which will help the ***ML model to give a better result***.

6, Model Building

6.1, Splitting the dataset

```
In [52]: X = diabetes_df.drop('Outcome', axis=1)
         y = diabetes_df['Outcome']
```

Now split the data into training and testing data using the train_test_split function

```
In [53]: 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)
```

6.2, Using Random Forest

```
In [55]: from sklearn.ensemble import RandomForestClassifier

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

```
Out[55]: ▾          RandomForestClassifier
         RandomForestClassifier(n_estimators=200)
```

Now after building the model, check the accuracy of the model on the training dataset.

```
In [56]: 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, The training dataset of the model is overfitted.

Getting the accuracy score for Random Forest

In [57]:
```
from sklearn import metrics

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

```
Accuracy_Score = 0.7677165354330708
```

6.3, Using Decision Tree

In [58]:
```
from sklearn.tree import DecisionTreeClassifier

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

Out[58]:
```
▾ DecisionTreeClassifier
DecisionTreeClassifier()
```

Getting the accuracy score for Decision Tree

In [59]:
```
from sklearn import metrics

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

```
Accuracy Score = 0.7047244094488189
```

Classification report and confusion matrix of the decision tree model

In [60]:
```
from sklearn.metrics import classification_report, confusion_matrix

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

```
[[127  35]
 [ 40  52]]
              precision    recall  f1-score   support

           0       0.76      0.78      0.77       162
           1       0.60      0.57      0.58        92

    accuracy                           0.70       254
   macro avg       0.68      0.67      0.68       254
weighted avg       0.70      0.70      0.70       254
```

6.4, Using XgBoost classifier

In [62]:
```
from xgboost import XGBClassifier

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

```
Out[62]: ▾ XGBClassifier

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,
```

Getting the accuracy score for the XgBoost classifier

```
In [68]: 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
```

classification report and confusion matrix of the XgBoost classifier

```
In [69]: from sklearn.metrics import classification_report, confusion_matrix

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

```
[[128  34]
 [ 35  57]]
              precision    recall  f1-score   support

           0       0.79      0.79      0.79       162
           1       0.63      0.62      0.62        92

    accuracy                           0.73       254
   macro avg       0.71      0.70      0.71       254
weighted avg       0.73      0.73      0.73       254
```

6.5, Using Support Vector Machine (SVM)

```
In [67]: from sklearn.svm import SVC

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

```
Out[67]: ▾ SVC

SVC()
```

Prediction from support vector machine model on the testing data

```
In [70]: svc_pred = svc_model.predict(X_test)
```

Accuracy score for SVM

```
In [71]: from sklearn import metrics

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

```
Accuracy Score = 0.7480314960629921
```

Classification report and confusion matrix of the SVM classifier

```
In [73]: 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
```

7, Conclusion from Model Building

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

8, Feature Importance

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

7.1,

Getting feature importanes

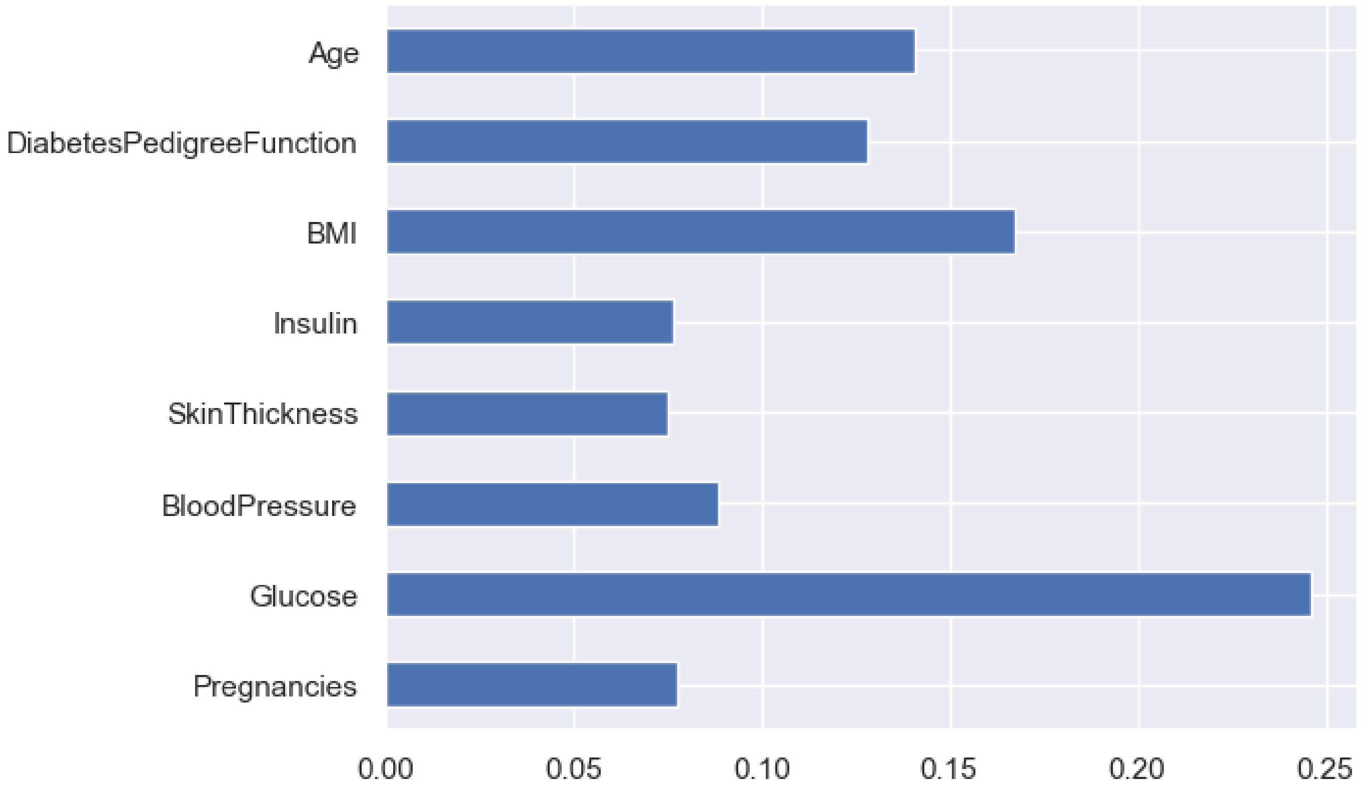
```
In [74]: rfc.feature_importances_
```

```
Out[74]: array([0.07750562, 0.24623499, 0.08878221, 0.07488274, 0.07641025,
                0.16712498, 0.12838834, 0.14067087])
```

7.2, Plotting feature importances

```
In [75]: (pd.Series(rfc.feature_importances_, index=X.columns).plot(kind='barh'))
```

```
Out[75]: <Axes: >
```



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

8, Saving Model – Random Forest

In [76]:
```
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[76]:
```
array([0, 1, 1, 0, 1, 1, 0, 0, 1, 0, 1, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0,
       1, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 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, 0, 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, 1, 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, 1, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 1, 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, 1, 1, 0,
       0, 0, 0, 0, 1, 1, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 1, 0, 0,
       0, 1, 1, 0, 1, 1, 0, 0, 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 [77]:
```
diabetes_df.head()
```

Out[77]:

	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 [78]:
```
diabetes_df.tail()
```

Out[78]:

	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

Putting data points in the model will either return 0 or 1 i.e. person suffering from diabetes or not.

In [88]:
```
rfc.predict([[0,137,40,35,168,43.1,2.228,33]]) #4th patient
```
Out[88]:
```
array([1], dtype=int64)
```

In [84]:
```
rfc.predict([[10,101,76,48,180,32.9,0.171,63]])  # 763 th patient
```
Out[84]:
```
array([0], dtype=int64)
```

In [90]:
```
rfc.predict([[4, 150, 85, 30, 200, 35, 0.8, 50]])  # Random generated data, expected the patient
```
Out[90]:
```
array([1], dtype=int64)
```

In [91]:
```
rfc.predict([[1, 85, 115, 18, 85, 22, 0.3, 30]])  # Random generated data, expected the patient
```
Out[91]:
```
array([0], dtype=int64)
```

9, Conclusion

After using all these patient records, built 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.