Diabetes prediction

A diabetes dataset is given to me which has only pregnant women's data. I am required to build a Machine Learning model which will predict for future pregnant ladies about whether they have diabetes or not.

The following are the features present in the dataset:

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)

In [1]:
```
#First the required libraries are imported
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
from sklearn.feature_selection import chi2
from sklearn.feature_selection import SelectKBest
```

In [2]:
```
diabetes = pd.read_csv(r"E:\Data Analyst Journey\Projects\Meriskill\Project 2 - Diabetes I
```

In [3]:
```
diabetes.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

1.Data Cleaning

Checking for Null values

In [4]:
```
diabetes.isnull().sum()
```

Out[4]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [5]:
```
diabetes.duplicated().sum()
```

Out[5]:
```
0
```

As shown above no null values or duplicate values are present.

In [6]:
```
diabetes.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
```

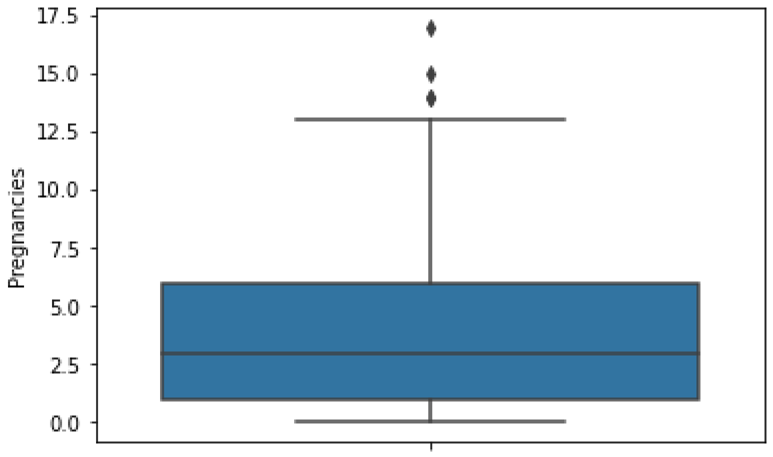
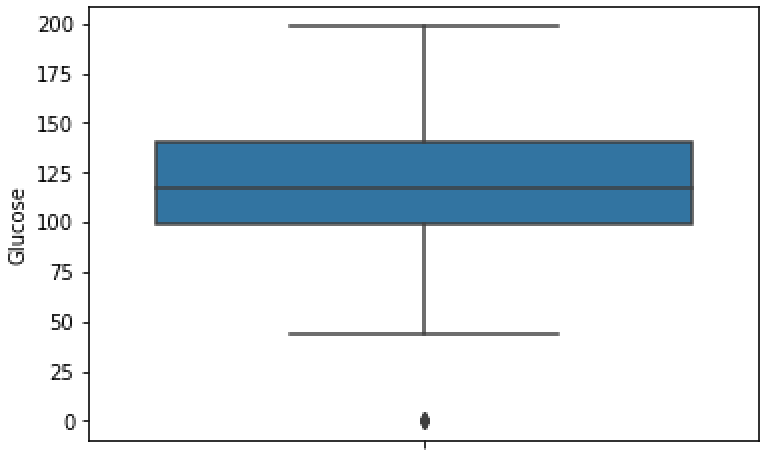
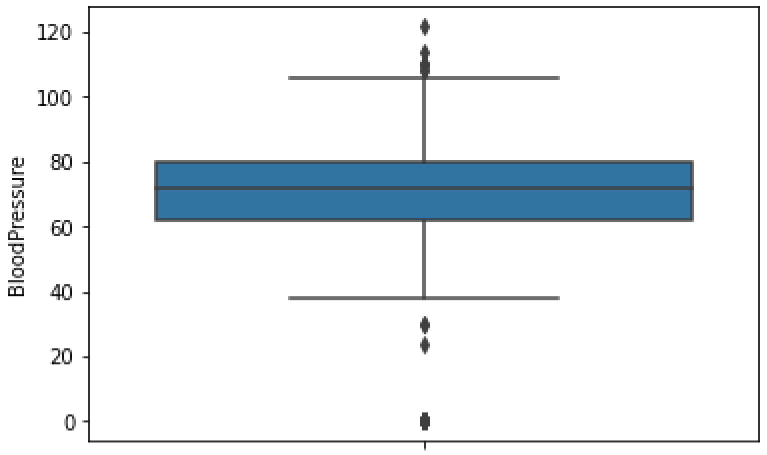
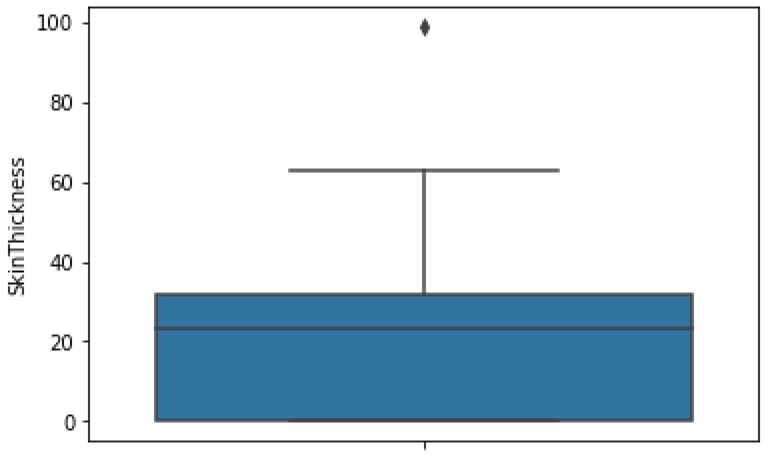
In [7]:
```
diabetes.describe()
```

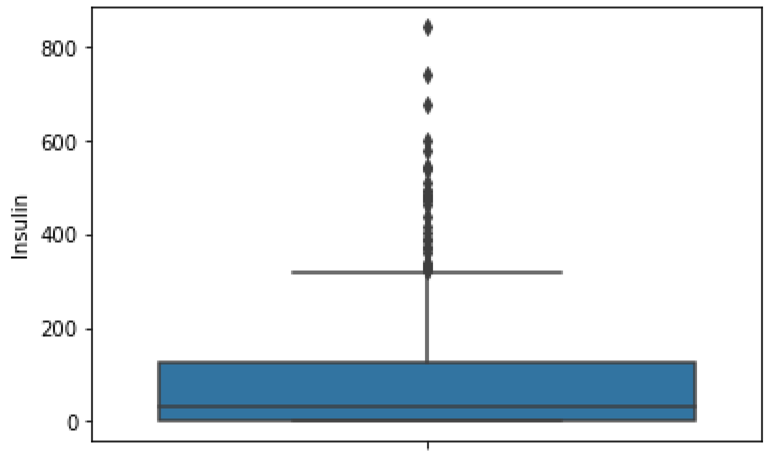
Out[7]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81

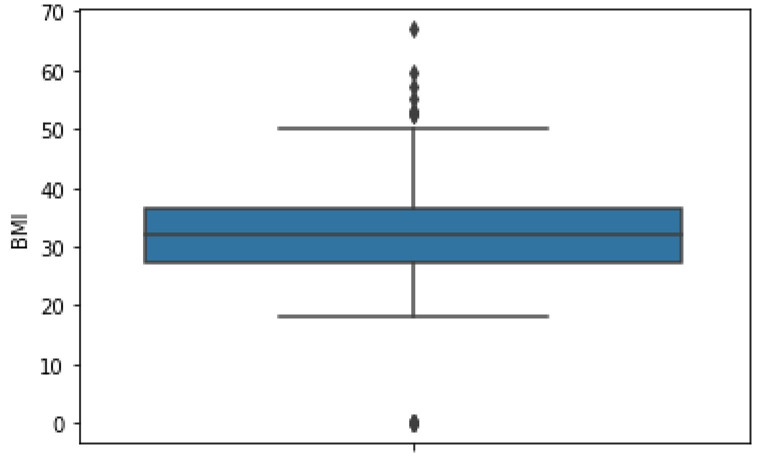
Outlier Detection

In [8]:
```
for i in diabetes.select_dtypes(np.number).columns:
    plt.figure()
    sns.boxplot( y = i,data = diabetes)
```

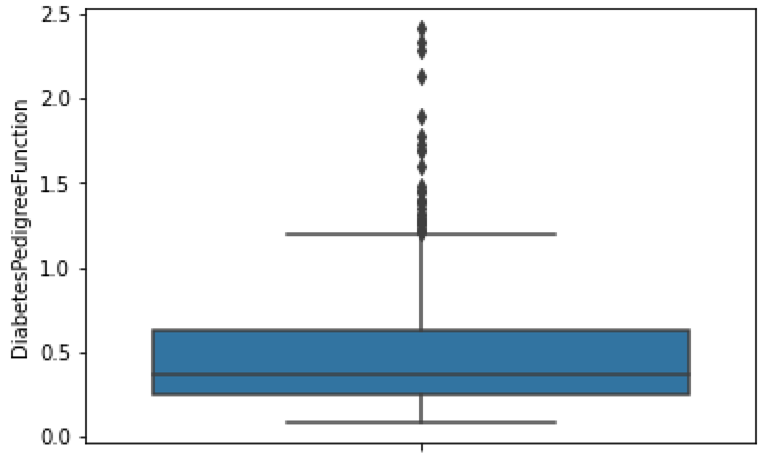

17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0
Pregnancies

200
175
150
125
100
75
50
25
0
Glucose

120
100
80
60
40
20
0
BloodPressure

100
80
60
40
20
0
SkinThickness



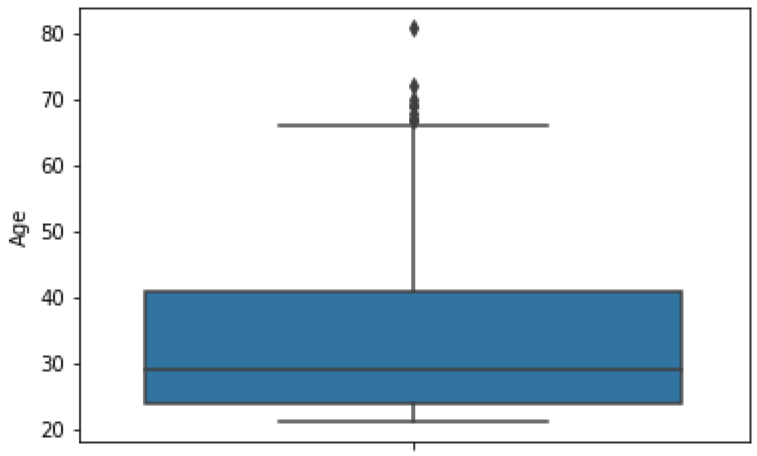
Insulin
0
200
400
600
800



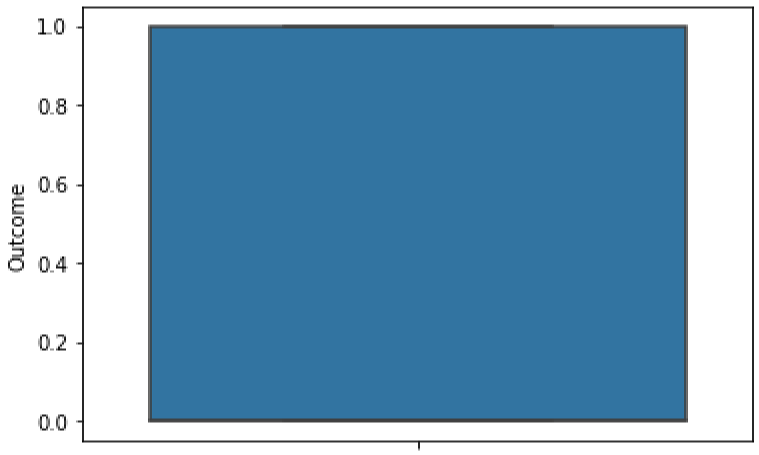
BMI
0
10
20
30
40
50
60
70



DiabetesPedigreeFunction
0.0
0.5
1.0
1.5
2.0
2.5



Age
20
30
40
50
60
70
80



defining a function to remove outliers from the dataset.

In [9]:
```
def outlier_removal(column):
    Q1=diabetes[column].quantile(0.25)
    Q3=diabetes[column].quantile(0.75)
    IQR = Q3-Q1
    global UB,LB
    UB = Q3+1.5*IQR
    LB = Q1-1.5*IQR
    print(f"For {column} column the IQR value is:{IQR} ")
    print(f"For {column} column the UB  value is:{UB} ")
    print(f"For {column} column the LB  value is:{LB} ")
    diabetes[column]=np.where(diabetes[column]>UB,UB,np.where(diabetes[column]<LB,LB,diabe
```

In [10]:
```
diabetes.columns
```

Out[10]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

In [11]:
```
outlier_removal('Pregnancies')
```

```
For Pregnancies column the IQR value is:5.0
For Pregnancies column the UB  value is:13.5
For Pregnancies column the LB  value is:-6.5
```

In [12]:
```
diabetes.loc[diabetes['Glucose']==0 ]
```

Out[12]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
75	1.0	0	48	20	0	24.7	0.140	22	0
182	1.0	0	74	20	23	27.7	0.299	21	0
342	1.0	0	68	35	0	32.0	0.389	22	0
349	5.0	0	80	32	0	41.0	0.346	37	1
502	6.0	0	68	41	0	39.0	0.727	41	1

In [13]:
```
## Dropping the rows where Glucose value is 0
diabetes.drop(diabetes.loc[diabetes['Glucose']==0].index,inplace = True)
```

In [14]:

```
#Dropping rows where Bloodpresuure value is below 60
diabetes.drop(diabetes.loc[diabetes['BloodPressure']==0].index,inplace = True)
```

Skinthickness cant be 100 show the outlier must be removed

In [15]:
```
diabetes.loc[diabetes['SkinThickness']>90]
```

Out[15]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
579	2.0	197	70	99	0	34.7	0.575	62	1

In [16]:
```
diabetes.drop(diabetes.loc[diabetes['SkinThickness']>90].index,inplace = True)
```

In [17]:
```
diabetes.loc[diabetes['SkinThickness']==0]
```

Out[17]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
2	8.0	183	64	0	0	23.3	0.672	32	1
5	5.0	116	74	0	0	25.6	0.201	30	0
9	8.0	125	96	0	0	0.0	0.232	54	1
10	4.0	110	92	0	0	37.6	0.191	30	0
11	10.0	168	74	0	0	38.0	0.537	34	1
...	...	...	...	...	...	...	...	...	...
757	0.0	123	72	0	0	36.3	0.258	52	1
758	1.0	106	76	0	0	37.5	0.197	26	0
759	6.0	190	92	0	0	35.5	0.278	66	1
762	9.0	89	62	0	0	22.5	0.142	33	0
766	1.0	126	60	0	0	30.1	0.349	47	1

194 rows × 9 columns

Also Skinthickness can't be Zero so is is replaced by the median value

In [18]:
```
diabetes['SkinThickness']=np.where(diabetes['SkinThickness']==0,diabetes['SkinThickness']
```

In [ ]:
```

```

Replacing the insulin values with median values

Defining a function that will found out the outliers and replace them with median values

In [19]:
```
def outier_replace(column, replace = False):
    q1=diabetes[column].quantile(0.25)
    q3=diabetes[column].quantile(0.75)
    iqr = q3-q1
    global ub,lb
    ub = q3+1.5*iqr
    lb = q1-1.5*iqr
    print(f"For {column} column the IQR value is:{iqr} ")
    print(f"For {column} column the UB  value is:{ub} ")
    print(f"For {column} column the LB  value is:{lb} ")
    median=diabetes[column].median()
    print(f"For {column} column the median value is:{median} ")
    diabetes[column]=np.where(diabetes[column]>ub,median,np.where(diabetes[column]<lb,medi
```

In [20]:

```
outier_replace('Insulin')
```

```
For Insulin column the IQR value is:130.0
For Insulin column the UB  value is:325.0
For Insulin column the LB  value is:-195.0
For Insulin column the median value is:48.0
```

In [21]:

```
outier_replace('BMI')
```

```
For BMI column the IQR value is:9.200000000000003
For BMI column the UB  value is:50.400000000000006
For BMI column the LB  value is:13.599999999999994
For BMI column the median value is:32.3
```

In [22]:

```
outier_replace('DiabetesPedigreeFunction')
```

```
For DiabetesPedigreeFunction column the IQR value is:0.385
For DiabetesPedigreeFunction column the UB  value is:1.2075
For DiabetesPedigreeFunction column the LB  value is:-0.3325
For DiabetesPedigreeFunction column the median value is:0.38
```

In [23]:

```
outlier_removal('Age')
```

```
For Age column the IQR value is:17.0
For Age column the UB  value is:66.5
For Age column the LB  value is:-1.5
```

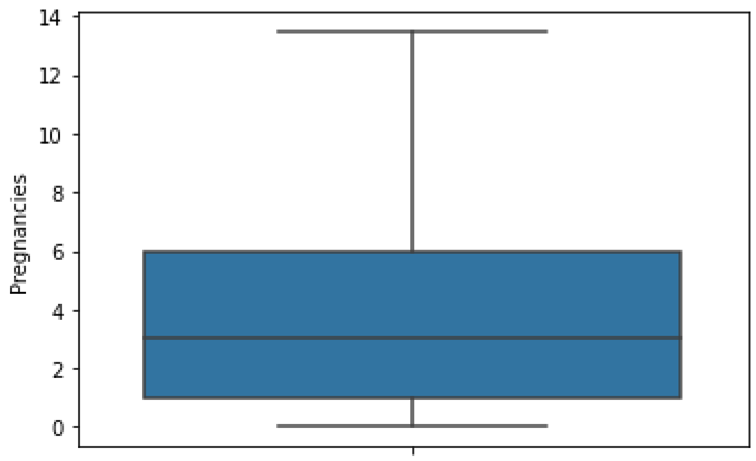
In [24]:

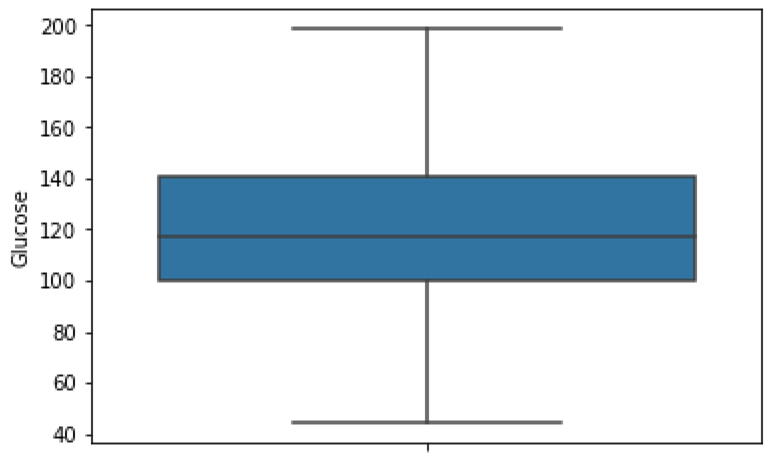
```
outlier_removal('BloodPressure')
```

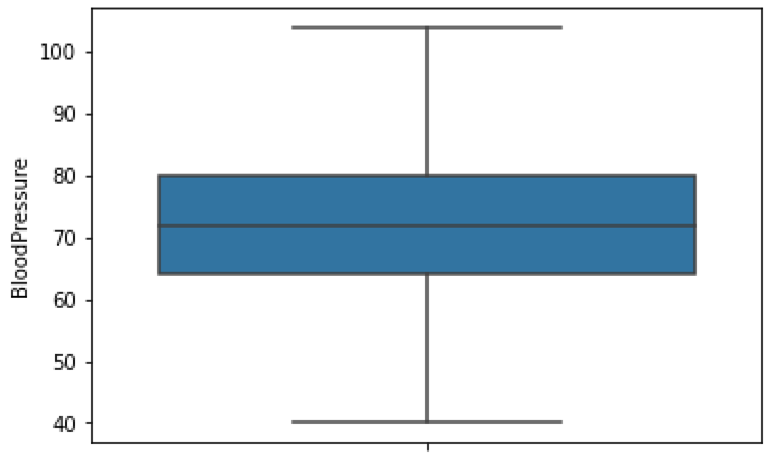
```
For BloodPressure column the IQR value is:16.0
For BloodPressure column the UB  value is:104.0
For BloodPressure column the LB  value is:40.0
```

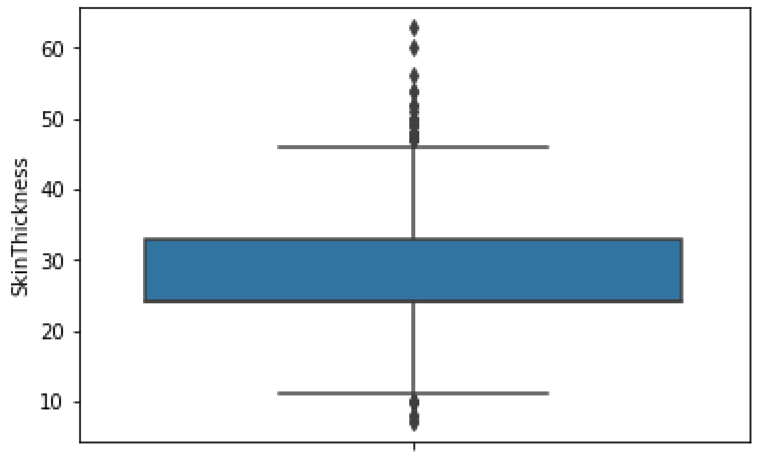
In [25]:

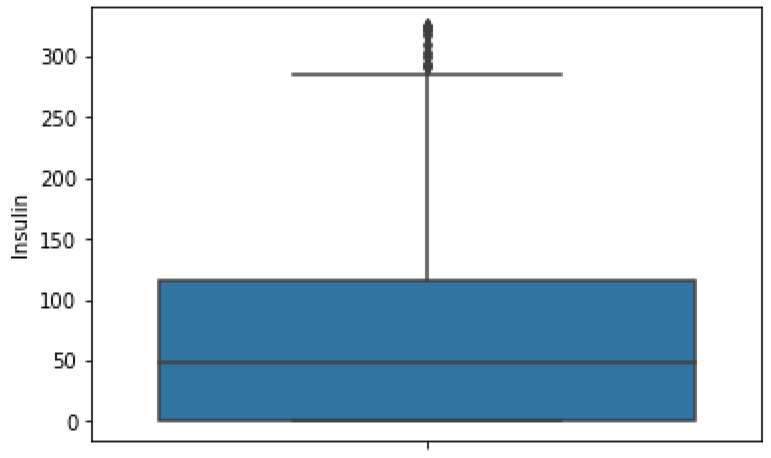
```
for i in diabetes.select_dtypes(np.number).columns:
    plt.figure()
    sns.boxplot( y = i,data = diabetes)
```

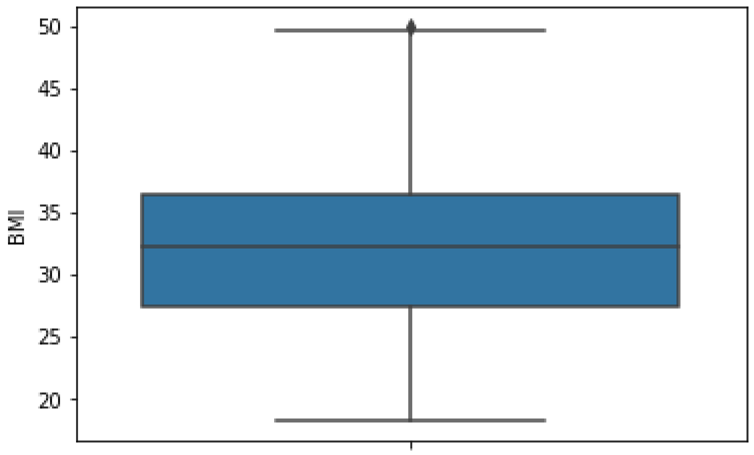


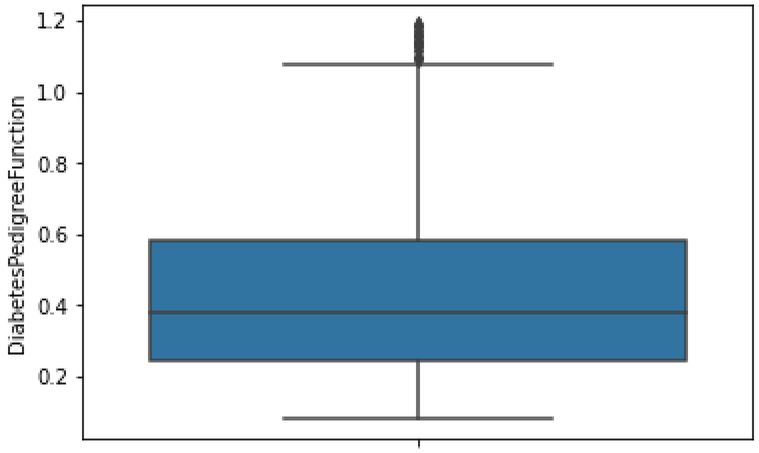

Glucose
200
180
160
140
120
100
80
60
40

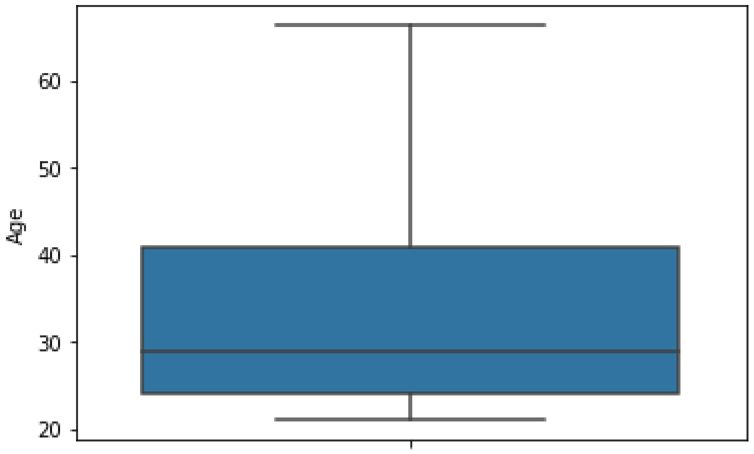

BloodPressure
100
90
80
70
60
50
40

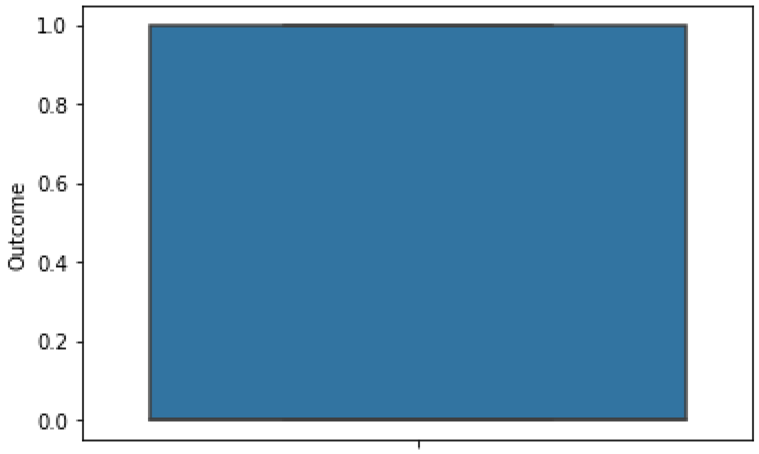

SkinThickness
60
50
40
30
20
10


Insulin
300
250
200
150
100
50
0


50
45
40
35
30
25
20
BMI


1.2
1.0
0.8
0.6
0.4
0.2
DiabetesPedigreeFunction


60
50
40
30
20
Age


1.0
0.8
0.6
0.4
0.2
0.0
Outcome

```
In [ ]:
```

```
In [ ]:
```

In [ ]:

In [ ]:

In [ ]:

In [26]:
```
diabetes_cleaned=diabetes.copy()
```

In [27]:
```
diabetes_cleaned.describe()
```

Out[27]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	
count	727.000000	727.000000	727.000000	727.000000	727.000000	727.000000	727.000000	727
mean	3.856946	121.770289	72.411279	27.686382	66.660248	32.227785	0.429979	33
std	3.338176	30.573279	11.982427	8.906810	80.455787	6.425622	0.245070	1
min	0.000000	44.000000	40.000000	7.000000	0.000000	18.200000	0.078000	2
25%	1.000000	100.000000	64.000000	24.000000	0.000000	27.500000	0.245000	2
50%	3.000000	117.000000	72.000000	24.000000	48.000000	32.300000	0.380000	2
75%	6.000000	141.000000	80.000000	33.000000	116.000000	36.400000	0.583000	4
max	13.500000	199.000000	104.000000	63.000000	325.000000	50.000000	1.191000	6

Exploratory Data Analysis

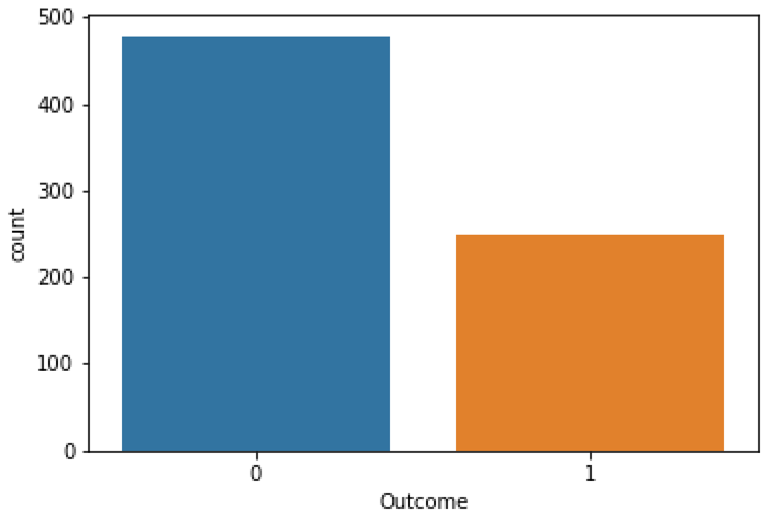
Here we will understand the relations that input columns have with the output columns.

Univariate Analysis

In [28]:
```
sns.countplot(diabetes['Outcome'])
```

```
C:\Users\ASUS\anaconda3\lib\site-packages\seaborn\_decorators.py:36: FutureWarning: Pass t
he following variable as a keyword arg: x. From version 0.12, the only valid positional ar
gument will be `data`, and passing other arguments without an explicit keyword will result
in an error or misinterpretation.
  warnings.warn(
```

Out[28]:
```
<AxesSubplot:xlabel='Outcome', ylabel='count'>
```



```
In [ ]:
```

Checking for Skewness

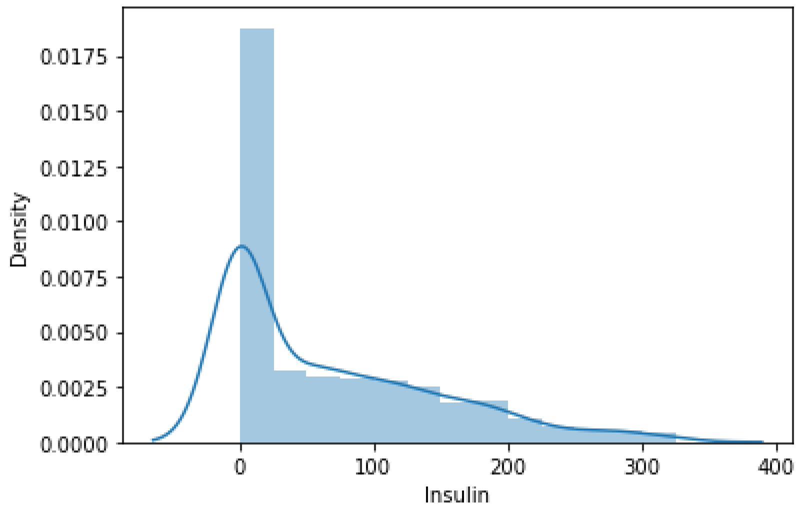
```
In [29]: diabetes_cleaned.skew()
```

```
Out[29]:
Pregnancies                 0.848345
Glucose                     0.524409
BloodPressure               0.101889
SkinThickness               0.617028
Insulin                     1.103980
BMI                         0.257447
DiabetesPedigreeFunction    0.960786
Age                         1.037838
Outcome                     0.665150
dtype: float64
```

As a general rule of thumb: If skewness is less than -1 or greater than 1, the distribution is highly skewed. If skewness is between -1 and -0.5 or between ***0.5 and 1, the distribution is moderately skewed.*** If skewness is between -0.5 and 0.5, the distribution is approximately symmetric.

```
In [30]: sns.distplot(diabetes_cleaned['Insulin'])
```

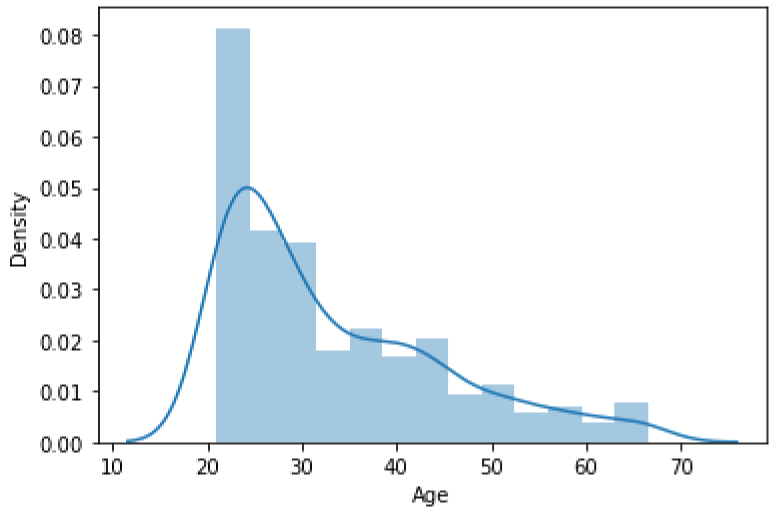
```
C:\Users\ASUS\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `d
istplot` is a deprecated function and will be removed in a future version. Please adapt yo
ur code to use either `displot` (a figure-level function with similar flexibility) or `his
tplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
Out[30]: <AxesSubplot:xlabel='Insulin', ylabel='Density'>
```



In [31]:
```
sns.distplot(diabetes_cleaned['Age'])
```

```
C:\Users\ASUS\anaconda3\lib\site-packages\seaborn\distributions.py:2619: FutureWarning: `d
istplot` is a deprecated function and will be removed in a future version. Please adapt yo
ur code to use either `displot` (a figure-level function with similar flexibility) or `his
tplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

Out[31]:
```
<AxesSubplot:xlabel='Age', ylabel='Density'>
```



Multivariate Analysis

Bivariate analysis is a statistical method used to examine the relationship between two different variables or sets of data. It focuses on understanding how changes in one variable are associated with changes in another.

In [32]:
```
diabetes_cleaned.corr(method ='pearson')
```

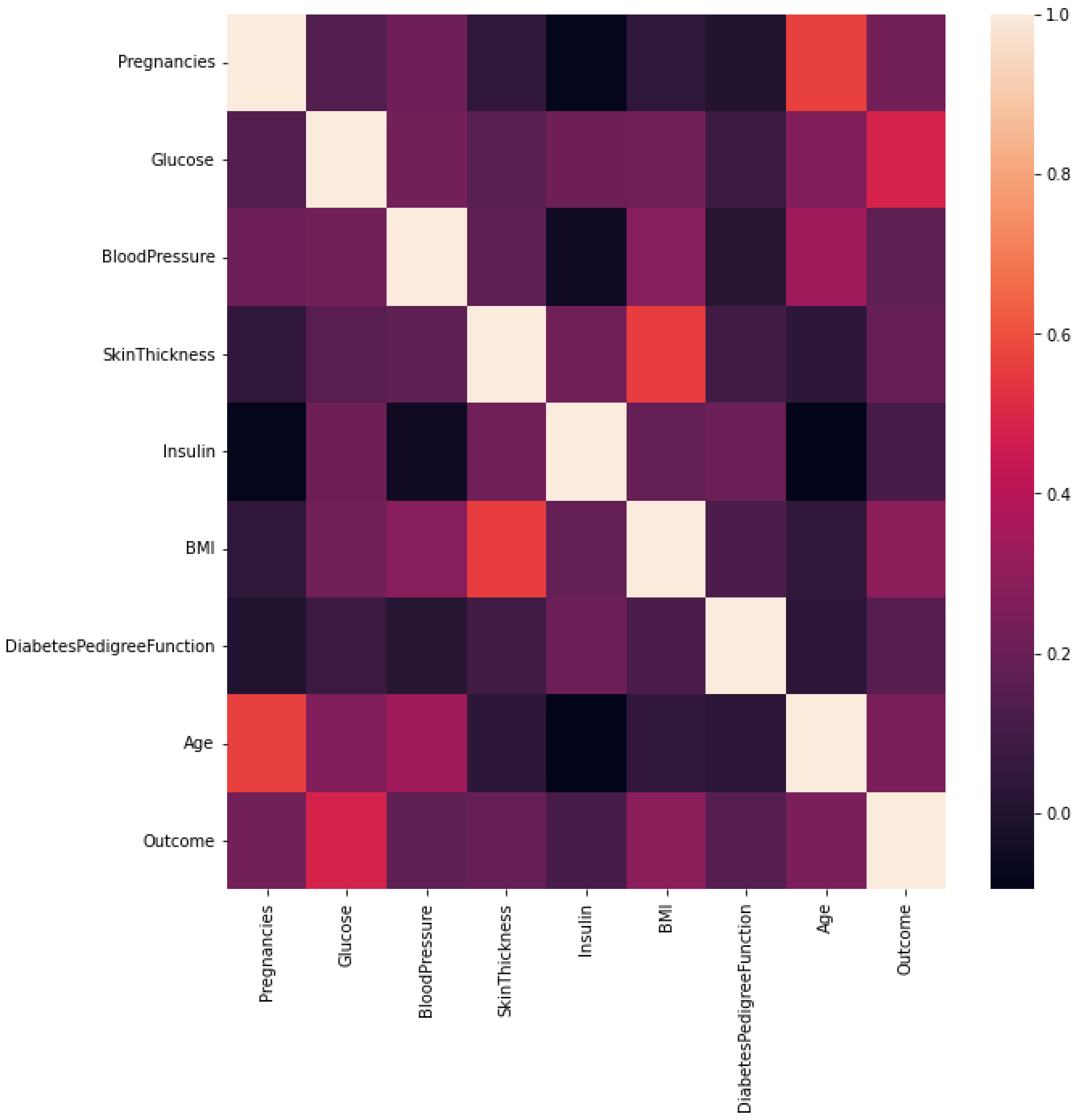
Out[32]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigre
Pregnancies	1.000000	0.137204	0.215009	0.041434	-0.084505	0.040545	
Glucose	0.137204	1.000000	0.226146	0.159803	0.209066	0.219946	
BloodPressure	0.215009	0.226146	1.000000	0.170384	-0.050046	0.277353	
SkinThickness	0.041434	0.159803	0.170384	1.000000	0.222459	0.557906	
Insulin	-0.084505	0.209066	-0.050046	0.222459	1.000000	0.187287	
BMI	0.040545	0.219946	0.277353	0.557906	0.187287	1.000000	

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigree
DiabetesPedigreeFunction	0.006664	0.075086	0.016696	0.092681	0.204444	0.123072	
Age	0.566329	0.259487	0.338745	0.036592	-0.095857	0.049145	
Outcome	0.227325	0.485485	0.172981	0.194122	0.111927	0.288848	

In [33]:
```
fig, ax = plt.subplots(figsize=(10,10))
sns.heatmap(diabetes_cleaned.corr(method ='pearson'))
```

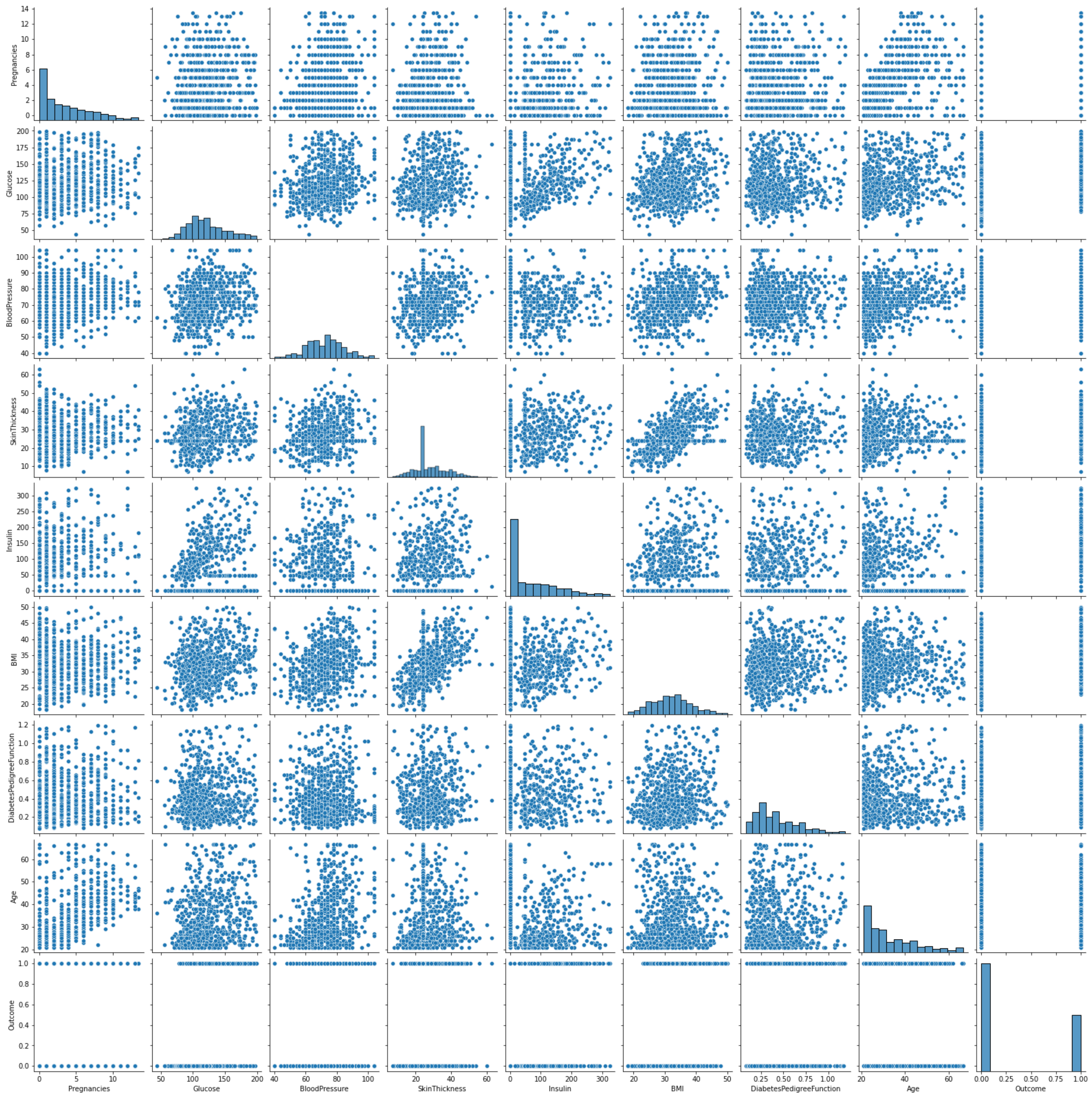
Out[33]:
```
<AxesSubplot:>
```



From above it is to be understood that Glucose,BMI and Age are having high correlation values compared to others.

In [34]:
```
sns.pairplot(diabetes_cleaned)
```

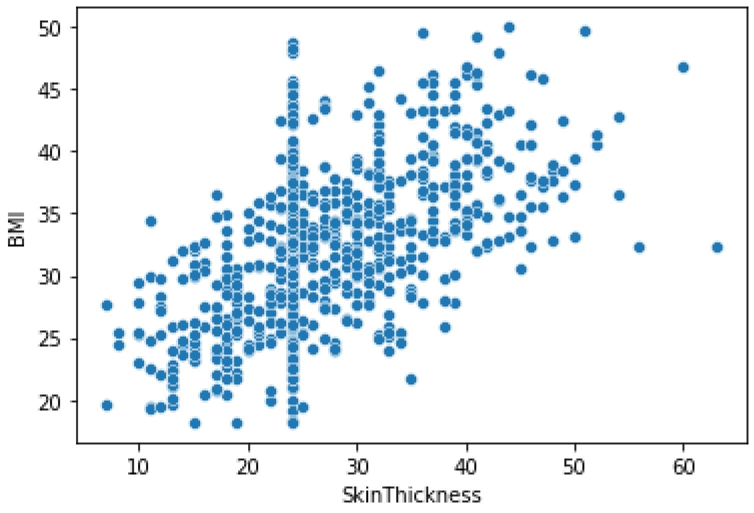
```
Out[34]: <seaborn.axisgrid.PairGrid at 0x216ee69aeb0>
```



Bivariate Analysis

```
In [35]: sns.scatterplot(x="SkinThickness",y="BMI",data=diabetes_cleaned)
```

```
Out[35]: <AxesSubplot:xlabel='SkinThickness', ylabel='BMI'>
```



In [36]:
```
crosstb = pd.crosstab(diabetes_cleaned.Age, diabetes_cleaned.Outcome)
```

In [37]:
```
crosstb
```

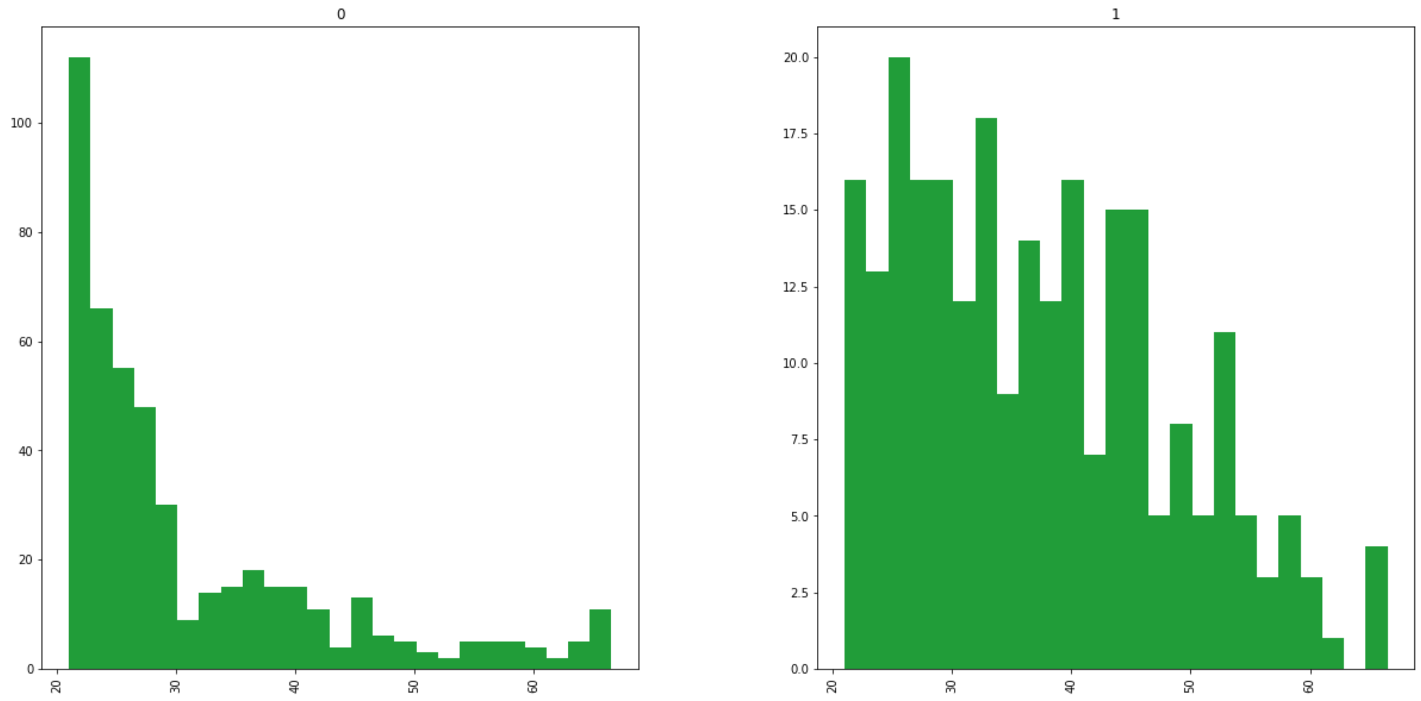
Out[37]:

Outcome	0	1
Age		
21.0	56	5
22.0	56	11
23.0	29	6
24.0	37	7
25.0	31	13
26.0	24	7
27.0	24	7
28.0	24	9
29.0	15	12
30.0	15	4
31.0	9	12
32.0	7	8
33.0	7	10
34.0	10	4
35.0	5	5
36.0	6	9
37.0	12	5
38.0	6	9
39.0	9	3
40.0	7	5
41.0	8	11
42.0	11	7

Outcome	0	1
Age		
43.0	2	11
44.0	2	4
45.0	7	8
46.0	6	7
47.0	2	4
48.0	4	1
49.0	2	3
50.0	3	5
51.0	3	5
52.0	1	7
53.0	1	4
54.0	2	4
55.0	3	1
56.0	1	2
57.0	4	1
58.0	4	3
59.0	1	2
60.0	3	2
61.0	1	1
62.0	2	1
63.0	4	0
64.0	1	0
65.0	3	0
66.0	2	2
66.5	6	2

```
In [38]: diabetes_cleaned.hist(column='Age',bins=25,by='Outcome',figsize=(20,10),color='#219D39')
```

```
Out[38]: array([<AxesSubplot:title={'center':'0'}>,
                <AxesSubplot:title={'center':'1'}>], dtype=object)
```



```
In [ ]:
```

Feature Selection and Feature Encoding

The preceding research shows that particular features, such as ***glucose, BMI, and age*** have a greater impact on the output feature.

As the features have numerical in nature so no need for feature encoding.

Modeling

Now we have our dataset ready for building a machine learning-based classifier. There are several classification models that can be used for this task. In this analysis, we will build five different types of classification models namely ***Random Forest, Decision Tree, XGBoost and, K-Nearest Neighbors (KNN).*** These are the most popular models used for solving classification problems.

Train-test Split

In [39]:
```
X=diabetes_cleaned[['Glucose','BMI','Age']]
Y=diabetes_cleaned['Outcome']
print('X shape',format(X.shape))
print('Y shape',format(Y.shape))
```

```
X shape (727, 3)
Y shape (727,)
```

In [40]:
```
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test = train_test_split(X,Y,test_size=0.3,random_state=42)
```

Perform Feature Scaling

After we've split the dataset into training and testing sets, we'll perform feature scaling. Feature scaling is the process of standardizing the range of features. It's an important step because it ensures that all features are given equal importance during training.

In [41]:
```
from sklearn.preprocessing import StandardScaler
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)
```

In [ ]:

Random Forest

In [42]:
```
from sklearn.ensemble import RandomForestClassifier
```

In [43]:
```
rfc = RandomForestClassifier(n_estimators=200)
rfc.fit(X_train, y_train)
##n_estimators represents the number of trees in the forest. Usually the higher the numbe
```

Out[43]:
```
▾       RandomForestClassifier
RandomForestClassifier(n_estimators=200)
```

In [44]:
```
#Checkiing the Accuracy
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.

In [97]:
```
predictions = rfc.predict(X_test)
RF=metrics.accuracy_score(y_test, predictions)
print(f"Accuracy_Score_RF is {RF}")
```

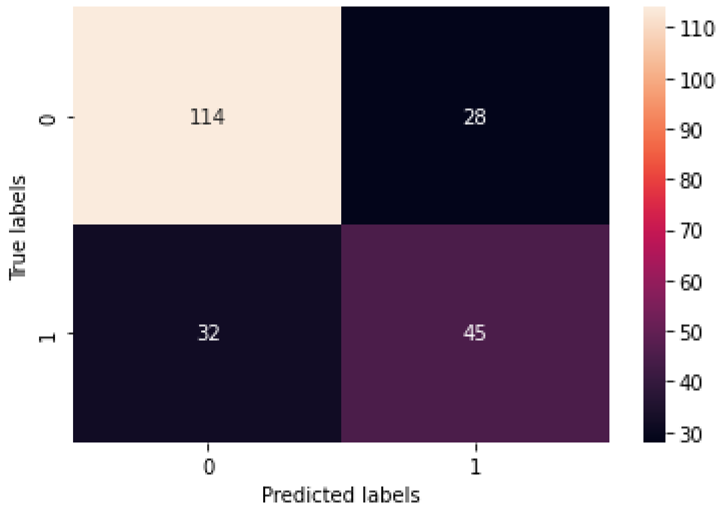
```
Accuracy_Score_RF is 0.726027397260274
```

In [ ]:

In [48]:
```
from sklearn.metrics import confusion_matrix
cm=confusion_matrix(y_test, predictions)
```

In [47]:
```
## complete all other models with feature importance check
## See analytics vidya
#perform chi square test
```

In [51]:
```
ax= plt.subplot()
sns.heatmap(cm, annot=True, fmt='g', ax=ax);
ax.set_xlabel('Predicted labels');ax.set_ylabel('True labels');
```



```
In [53]: X_test.shape
```

```
Out[53]: (219, 3)
```

Decision Tree

```
In [68]: from sklearn.tree import DecisionTreeClassifier
dtree = DecisionTreeClassifier()
dtree.fit(X_train,y_train)
```

```
Out[68]: ▾ DecisionTreeClassifier

DecisionTreeClassifier()
```

```
In [69]: from sklearn import metrics
predictionsd = dtree.predict(X_test)
```

```
In [99]: DT=metrics.accuracy_score(y_test,predictionsd)
print(f"Accuracy_Score_RF is {DT}")
```

```
Accuracy_Score_RF is 0.634703196347032
```

XgBoost classifier

Building model using XGBoost

```
In [77]: from xgboost import XGBClassifier
xgb_model = XGBClassifier(gamma=0)
xgb_model.fit(X_train,y_train)
```

```
Out[77]:
```

```
▾                               XGBClassifier
XGBClassifier(base_score=None, booster=None, callbacks=None,
              colsample_bylevel=None, colsample_bynode=None,
              colsample_bytree=None, early_stopping_rounds=None,
              enable_categorical=False, eval_metric=None, feature_types=None,
              gamma=0, gpu_id=None, 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,
              n_estimators=100, n_jobs=None, num_parallel_tree=None,
              predictor=None, random_state=None, ...)
```

In [101…
```
xgb_pred = xgb_model.predict(X_test)
```

In [102…
```
xgb=metrics.accuracy_score(y_test, xgb_pred)
print(f"Accuracy_Score_RF is {xgb}")
```

```
Accuracy_Score_RF is 0.6986301369863014
```

In [ ]:

Conclusion

In [110…
```
model={'Model_Name': ['Random Forest','Decision tree','XGBoost'],
       'Accuracies':[RF*100,DT*100,xgb*100]}
```

In [114…
```
Final_Result=pd.DataFrame(model)
```

In [115…
```
Final_Result
```

Out[115…

	Model_Name	Accuracies
0	Random Forest	72.602740
1	Decision tree	63.470320
2	XGBoost	69.863014

We can consider Random Forest for Prediction as this model is showing promising accuracy in testing.

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