diabetes-prediction-system

December 28, 2023

[1]:

```
#Import
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
%pip install xgboost
```

```
Requirement already satisfied: xgboost in d:\users\mathi\anaconda3\lib\site-
packages (2.0.3)
Requirement already satisfied: numpy in d:\users\mathi\anaconda3\lib\site-
packages (from xgboost) (1.24.3)
Requirement already satisfied: scipy in d:\users\mathi\anaconda3\lib\site-
packages (from xgboost) (1.11.1)
Note: you may need to restart the kernel to use updated packages.
```

[8]:

```
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import␣
 ↪accuracy_score,classification_report,confusion_matrix
from sklearn.preprocessing import StandardScaler
from sklearn.ensemble import RandomForestClassifier,AdaBoostClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from xgboost import XGBClassifier
```

[3]:

```
data=pd.read_csv("D:\power bi\Meriskill\diabetes.csv")
data
```

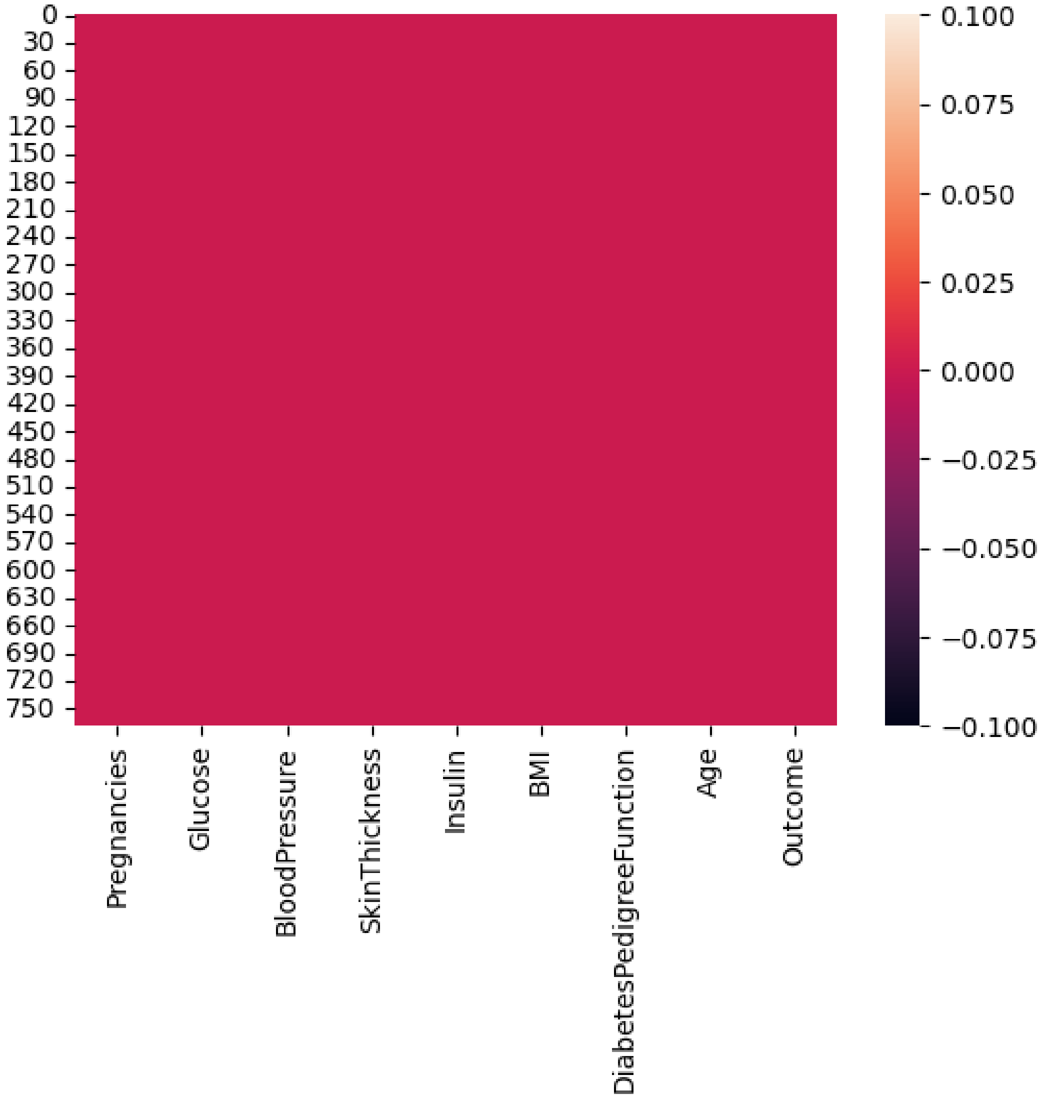
[3]:

```
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0              6      148             72             35        0  33.6
1              1       85             66             29        0  26.6
2              8      183             64              0        0  23.3
3              1       89             66             23       94  28.1
4              0      137             40             35      168  43.1
..           …        …              …              …        …     …
763           10      101             76             48      180  32.9
764            2      122             70             27        0  36.8
765            5      121             72             23      112  26.2
```

```
766            1      126             60              0        0  30.1
767            1       93             70             31        0  30.4

     DiabetesPedigreeFunction  Age  Outcome
0                       0.627   50        1
1                       0.351   31        0
2                       0.672   32        1
3                       0.167   21        0
4                       2.288   33        1
..                        …  …      …
763                     0.171   63        0
764                     0.340   27        0
765                     0.245   30        0
766                     0.349   47        1
767                     0.315   23        0

[768 rows x 9 columns]
```

```
[5]: sns.heatmap(data.isnull())
```

```
[5]: <Axes: >
```



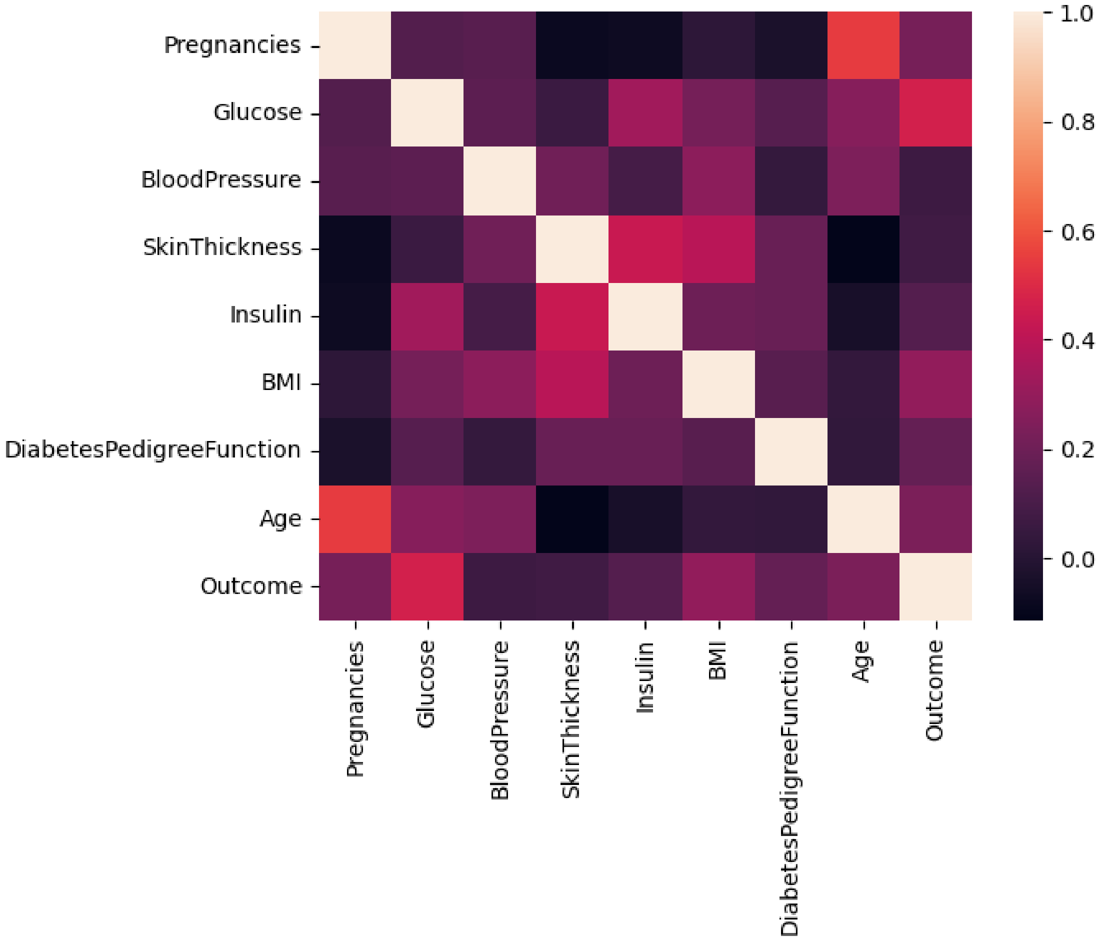
[11]:
```
correlation =data.corr()
print(correlation)
```

```
                          Pregnancies   Glucose  BloodPressure  SkinThickness  \
Pregnancies                  1.000000  0.129459       0.141282      -0.081672
Glucose                      0.129459  1.000000       0.152590       0.057328
BloodPressure                0.141282  0.152590       1.000000       0.207371
SkinThickness               -0.081672  0.057328       0.207371       1.000000
Insulin                     -0.073535  0.331357       0.088933       0.436783
BMI                          0.017683  0.221071       0.281805       0.392573
DiabetesPedigreeFunction    -0.033523  0.137337       0.041265       0.183928
Age                          0.544341  0.263514       0.239528      -0.113970
Outcome                      0.221898  0.466581       0.065068       0.074752
```

```
                           Insulin       BMI  DiabetesPedigreeFunction  \
Pregnancies              -0.073535  0.017683                 -0.033523
Glucose                   0.331357  0.221071                  0.137337
BloodPressure             0.088933  0.281805                  0.041265
SkinThickness             0.436783  0.392573                  0.183928
Insulin                   1.000000  0.197859                  0.185071
BMI                       0.197859  1.000000                  0.140647
DiabetesPedigreeFunction  0.185071  0.140647                  1.000000
Age                      -0.042163  0.036242                  0.033561
Outcome                   0.130548  0.292695                  0.173844

                               Age   Outcome
Pregnancies               0.544341  0.221898
Glucose                   0.263514  0.466581
BloodPressure             0.239528  0.065068
SkinThickness            -0.113970  0.074752
Insulin                  -0.042163  0.130548
BMI                       0.036242  0.292695
DiabetesPedigreeFunction  0.033561  0.173844
Age                       1.000000  0.238356
Outcome                   0.238356  1.000000
```

[10]:
```
sns.heatmap(data.corr())
```

[10]:
```
<Axes: >
```



[14]:
```
#preparing the data
X=data.drop("Outcome",axis=1)
Y=data['Outcome']
X_train,X_test,Y_train,Y_test=train_test_split(X,Y,test_size=0.2,random_state=42)
```

[16]:
```
#standardize the feature
scaler=StandardScaler()
X_train_scaled=scaler.fit_transform(X_train)
X_test_scaled=scaler.transform(X_test)
```

[20]:
```
#train a random classifier
model=RandomForestClassifier(random_state=42)
model.fit(X_train_scaled,Y_train)
```

[20]:
```
RandomForestClassifier(random_state=42)
```

[17]:

```python
#evaluation
Accuracy=accuracy_score(Prediction,Y_test)
print(Accuracy)
```

```
0.7272727272727273
```

[8]:

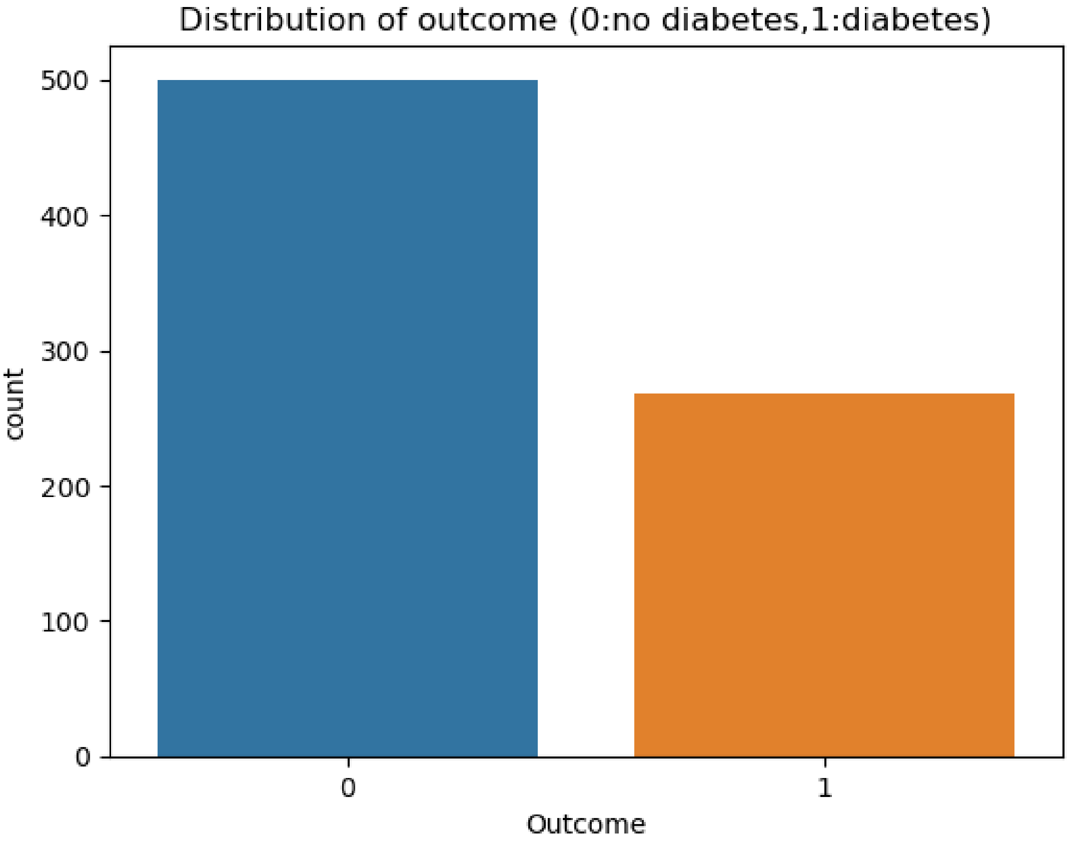
```python
#display the first few rows
print(data.head())
#checking for missing values
print(data.isnull().sum())
#statistical summary
print(data.describe())
```

```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35        0  33.6
1            1       85             66             29        0  26.6
2            8      183             64              0        0  23.3
3            1       89             66             23       94  28.1
4            0      137             40             35      168  43.1

   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
1                     0.351   31        0
2                     0.672   32        1
3                     0.167   21        0
4                     2.288   33        1
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
       Pregnancies     Glucose  BloodPressure  SkinThickness     Insulin  \
count   768.000000  768.000000     768.000000     768.000000  768.000000
mean      3.845052  120.894531      69.105469      20.536458   79.799479
std       3.369578   31.972618      19.355807      15.952218  115.244002
min       0.000000    0.000000       0.000000       0.000000    0.000000
25%       1.000000   99.000000      62.000000       0.000000    0.000000
50%       3.000000  117.000000      72.000000      23.000000   30.500000
75%       6.000000  140.250000      80.000000      32.000000  127.250000
max      17.000000  199.000000     122.000000      99.000000  846.000000

              BMI  DiabetesPedigreeFunction         Age     Outcome
count  768.000000                768.000000  768.000000  768.000000
```

```
mean    31.992578                   0.471876   33.240885    0.348958
std      7.884160                   0.331329   11.760232    0.476951
min      0.000000                   0.078000   21.000000    0.000000
25%     27.300000                   0.243750   24.000000    0.000000
50%     32.000000                   0.372500   29.000000    0.000000
75%     36.600000                   0.626250   41.000000    1.000000
max     67.100000                   2.420000   81.000000    1.000000
```

[13]:

```
#distribution of target variable
sns.countplot(x='Outcome',data=data)
plt.title('Distribution of outcome (0:no diabetes,1:diabetes)')
plt.show()
```



[23]:

```
#additional evaluation metrics
print('\n classification report:')
print(classification_report(Y_test,predictions))
```

```
 classification report:
              precision    recall  f1-score   support
```

```
           0       0.79      0.78      0.78        99
           1       0.61      0.62      0.61        55

    accuracy                           0.72       154
   macro avg       0.70      0.70      0.70       154
weighted avg       0.72      0.72      0.72       154
```

[24]:

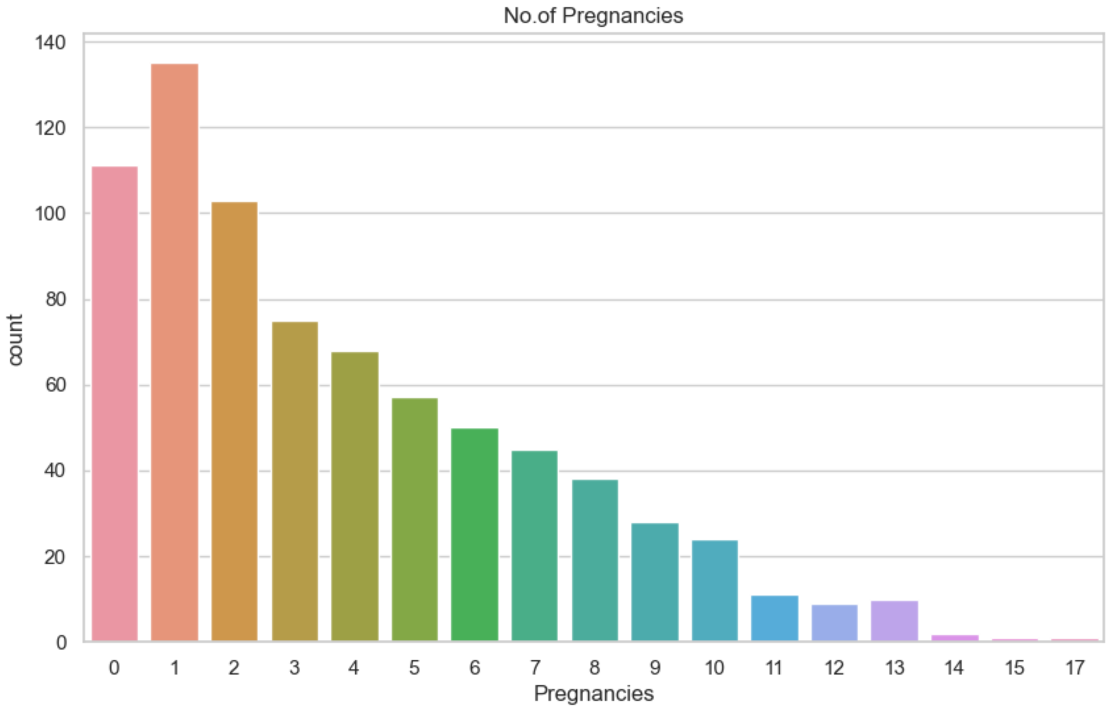
```python
print('\nConfusion matrix:')
print(confusion_matrix(Y_test,predictions))
```

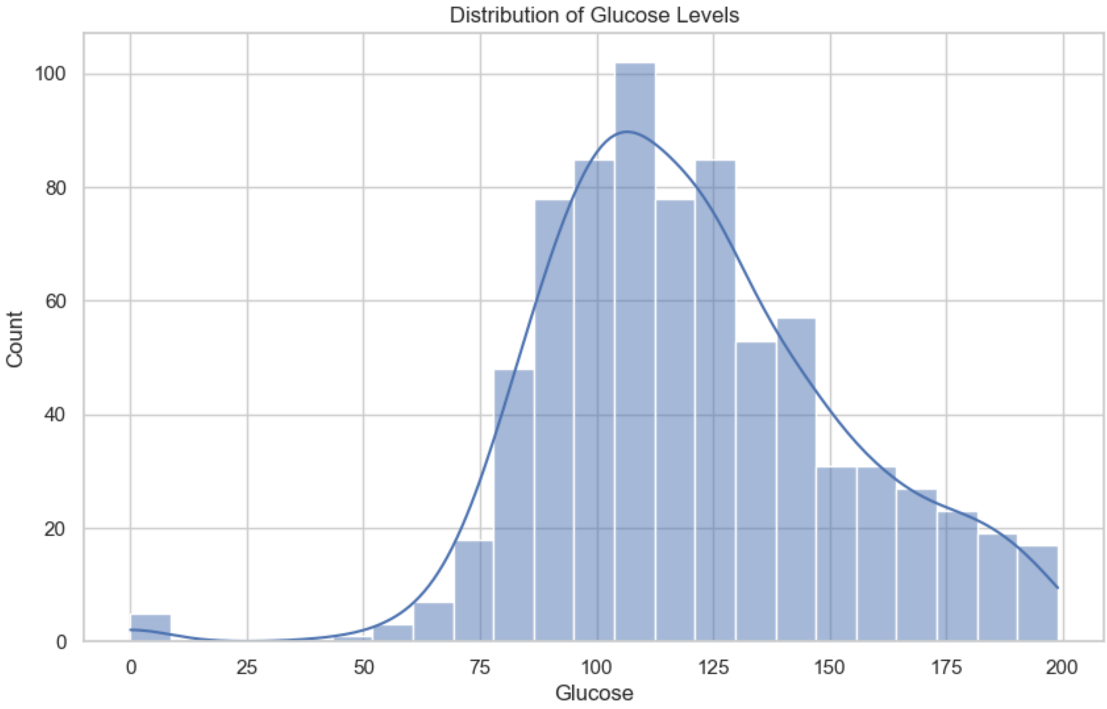
```
Confusion matrix:
[[77 22]
 [21 34]]
```

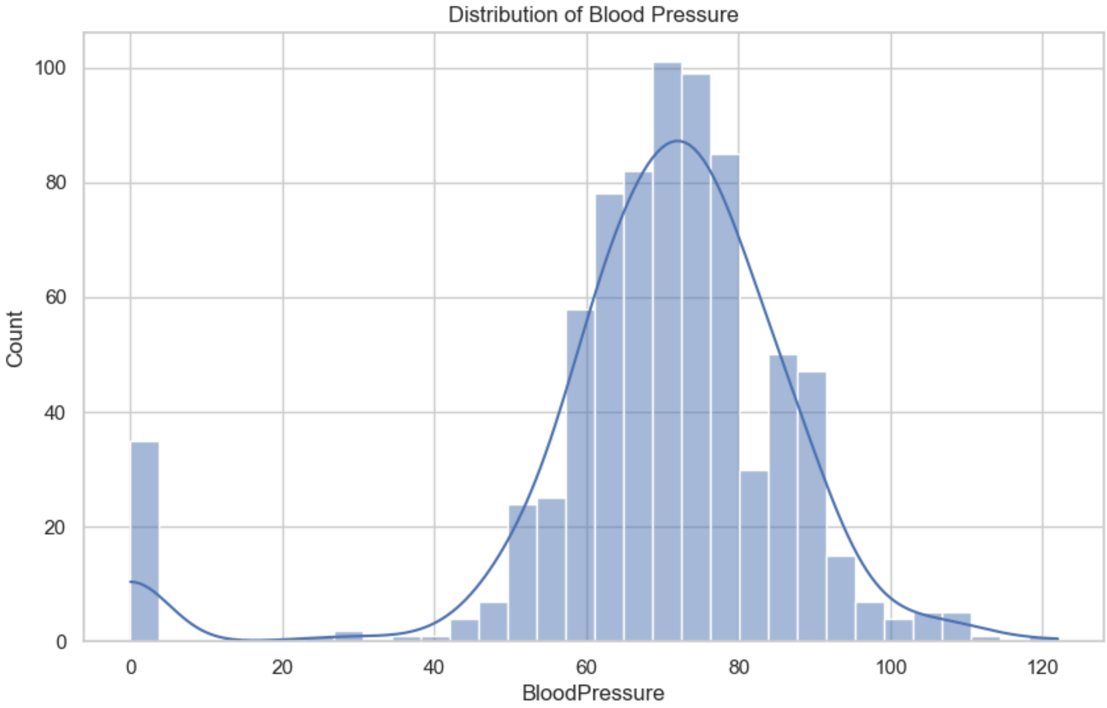
[29]:

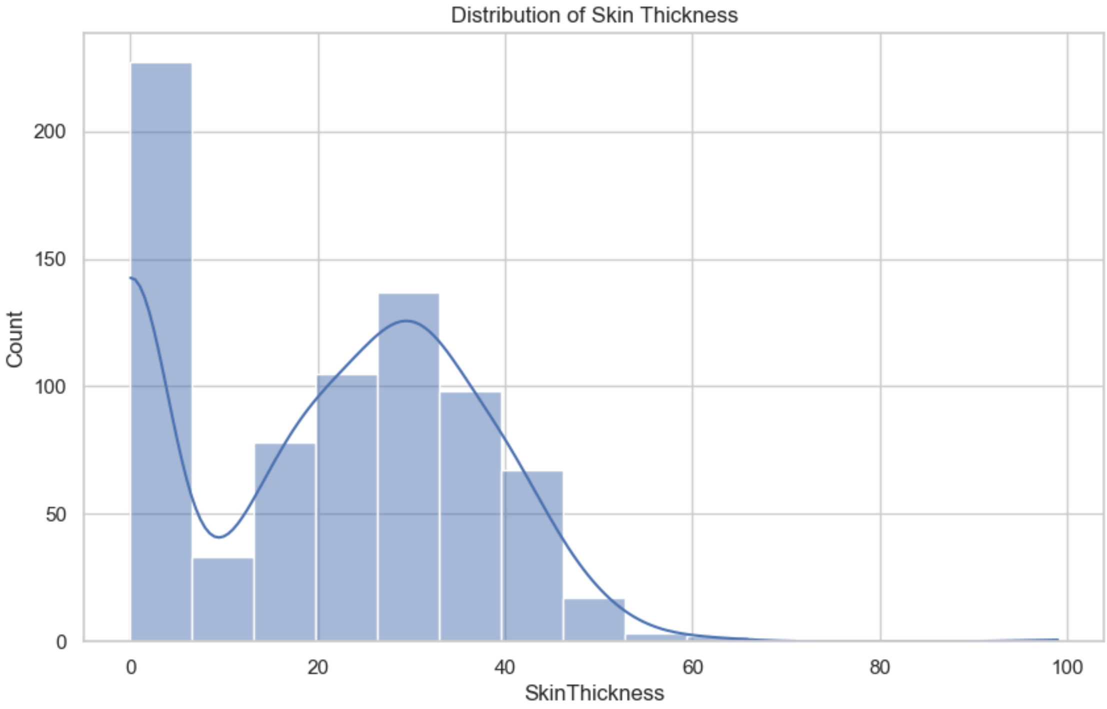
```python
sns.set(style="whitegrid")
#1.Pregnancies
plt.figure(figsize=(10,6))
sns.countplot(x='Pregnancies',data=data)
plt.title('No.of Pregnancies')
plt.show()
#2.Glucose
plt.figure(figsize=(10,6))
sns.histplot(x='Glucose',data=data,kde=True)
plt.title('Distribution of Glucose Levels')
plt.show()
#3.Blood Pressure
plt.figure(figsize=(10,6))
sns.histplot(x='BloodPressure',data=data,kde=True)
plt.title('Distribution of Blood Pressure')
plt.show()
#4.Skin THickness
plt.figure(figsize=(10,6))
sns.histplot(x='SkinThickness',data=data,kde=True)
plt.title('Distribution of Skin Thickness')
plt.show()
#5.Insulin
plt.figure(figsize=(10,6))
sns.histplot(x='Insulin',data=data,kde=True)
plt.title('Distribution of Insulin Levels')
plt.show()
#6.BMI
plt.figure(figsize=(10,6))
sns.histplot(x='BMI',data=data,kde=True)
plt.title('Distribution of BMI')
plt.show()
```

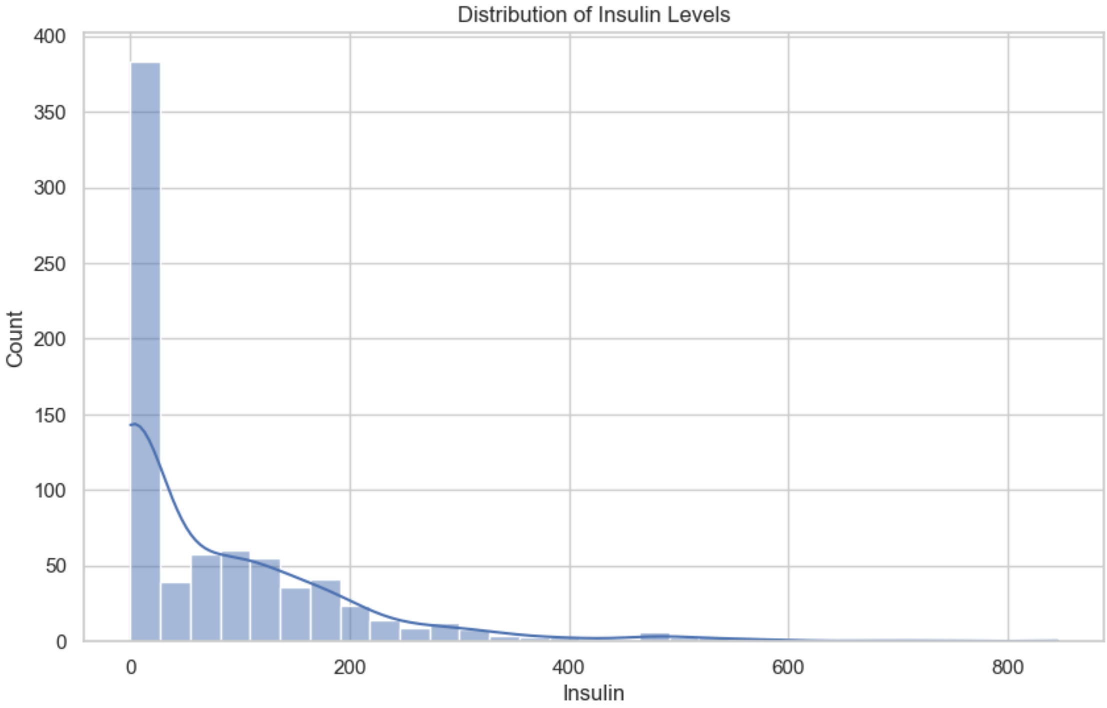
```python
#7.Diabetes Pedigree Function
plt.figure(figsize=(10,6))
sns.histplot(x='DiabetesPedigreeFunction',data=data,kde=True)
plt.title('Distribution of Diabetes Pedigree Function Scores')
plt.show()
#8.Age
plt.figure(figsize=(10,6))
sns.histplot(x='Age',data=data,kde=True)
plt.title('Distribution of Age')
plt.show()
#9.Outcome
plt.figure(figsize=(10,6))
sns.countplot(x='Outcome',data=data)
plt.title('Distribution of Outcome 1: Diabetes (0: No Diabetes)')
plt.show()
```

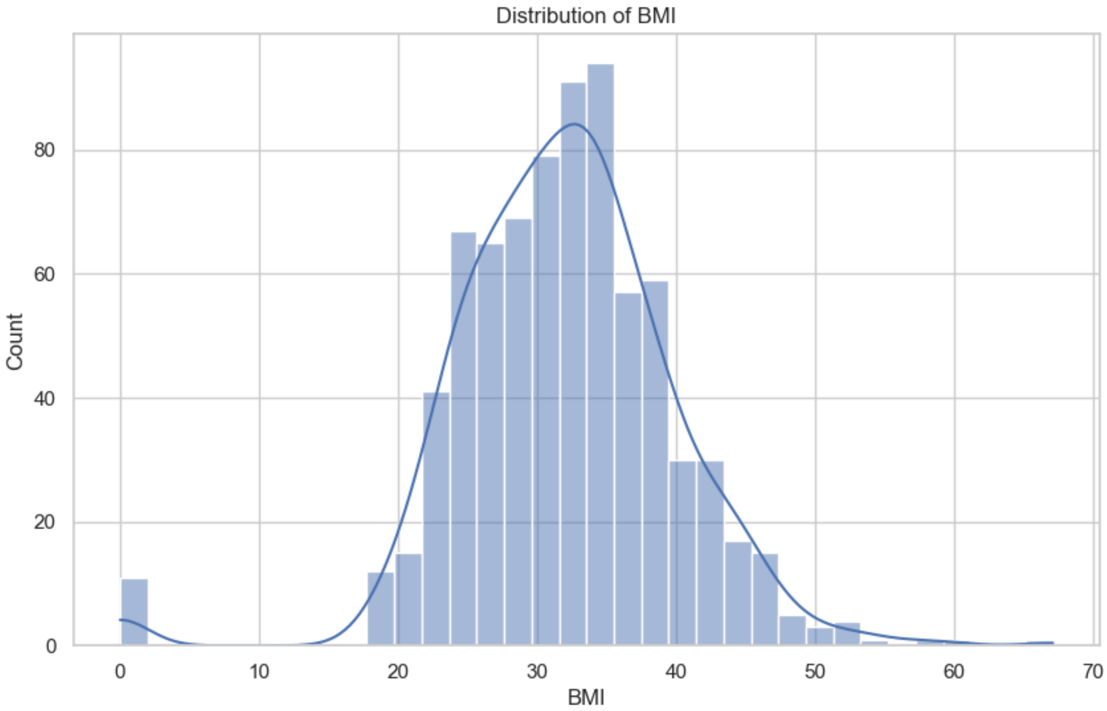


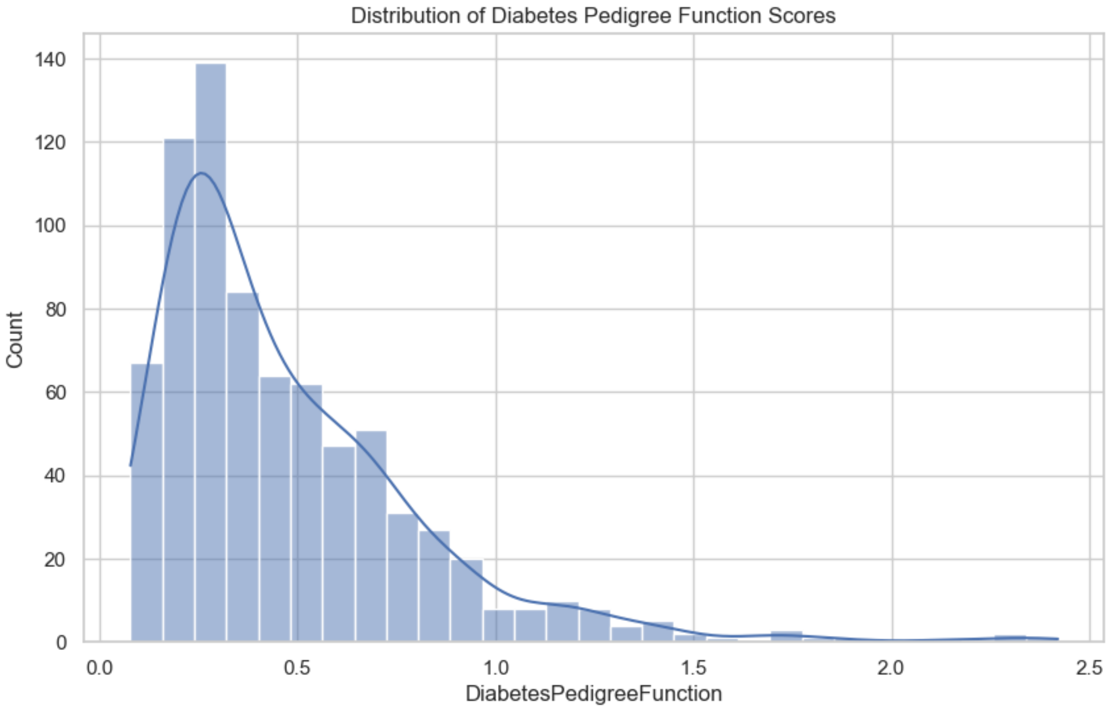

Distribution of Glucose Levels
Count
0
20
40
60
80
100
0
25
50
75
100
125
150
175
200
Glucose

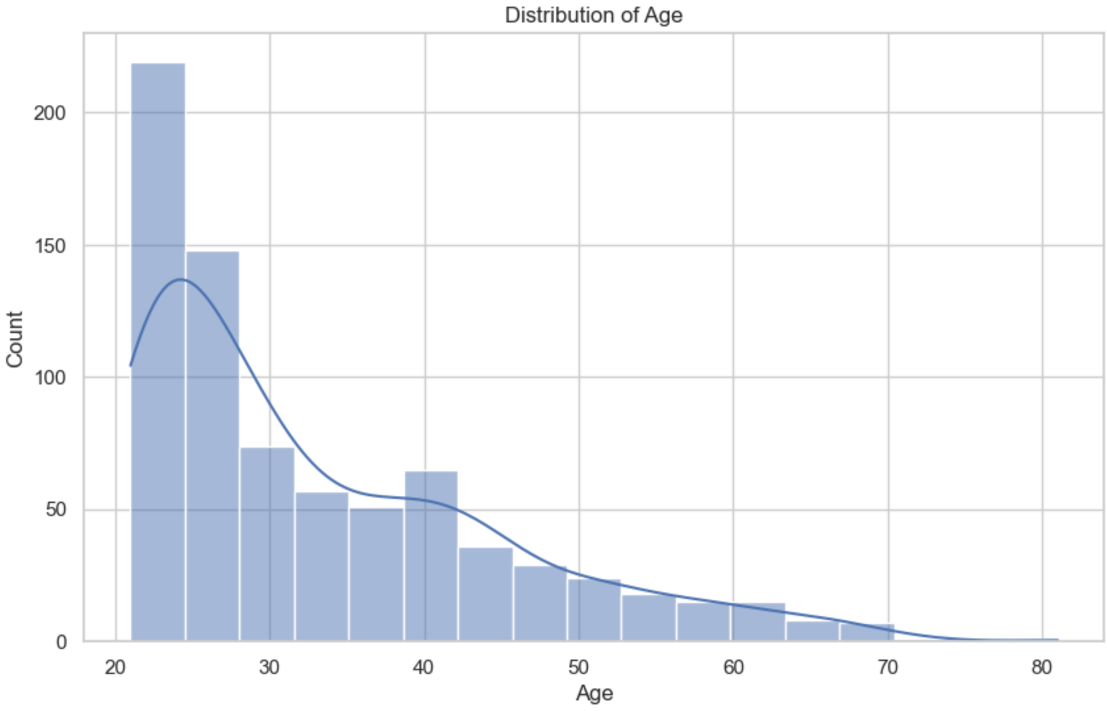

Distribution of Blood Pressure
Count
0
20
40
60
80
100
0
20
40
60
80
100
120
BloodPressure

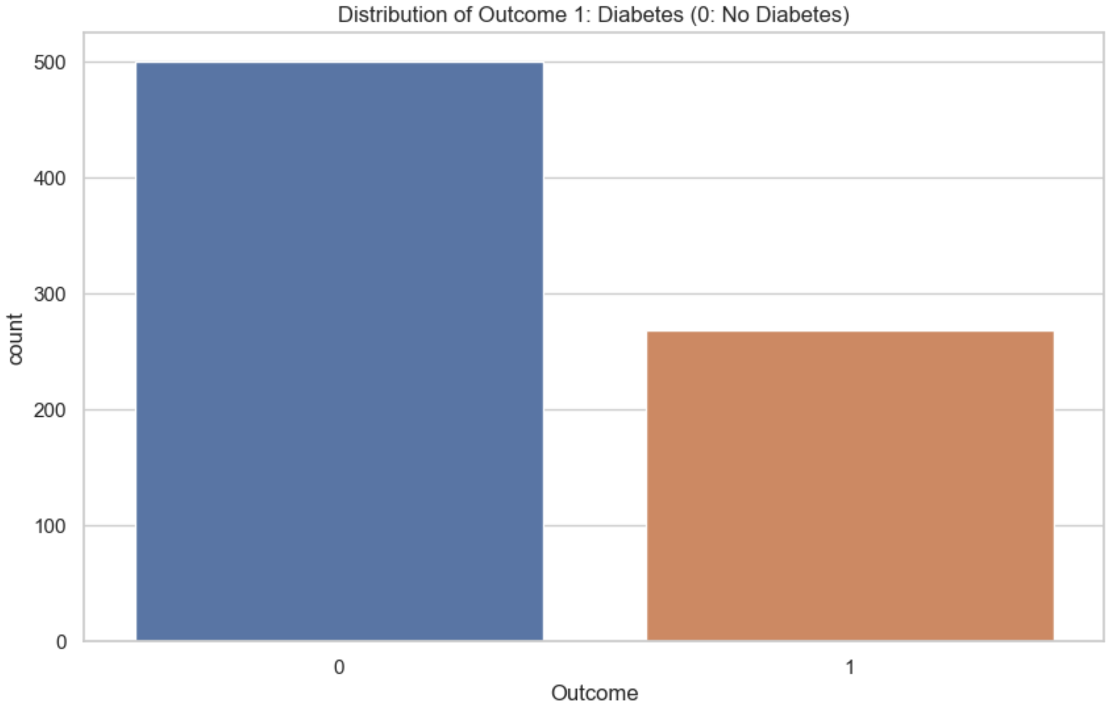

Distribution of Skin Thickness
Count
0
50
100
150
200
0
20
40
60
80
100
SkinThickness


Distribution of Insulin Levels
Count
0
50
100
150
200
250
300
350
400
0
200
400
600
800
Insulin


Distribution of BMI
Count
0
20
40
60
80
0
10
20
30
40
50
60
70
BMI

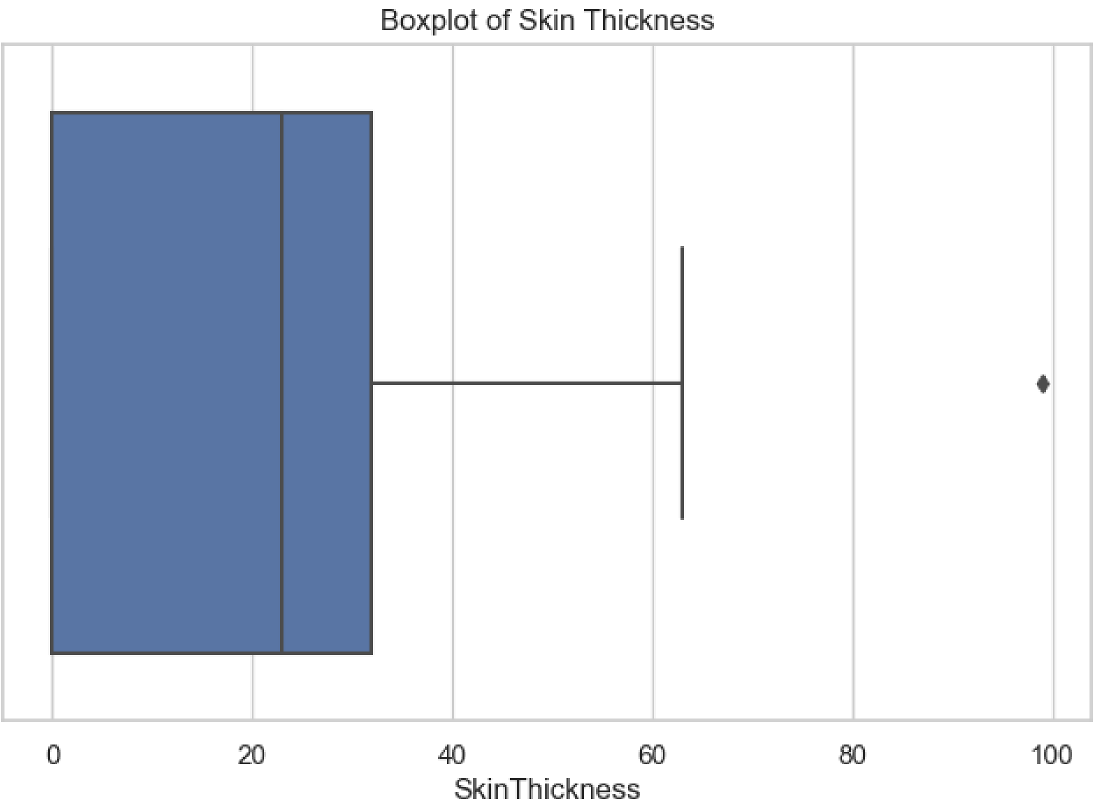

Distribution of Diabetes Pedigree Function Scores
Count
0
20
40
60
80
100
120
140
0.0
0.5
1.0
1.5
2.0
2.5
DiabetesPedigreeFunction


Distribution of Age
Count
0
50
100
150
200
20
30
40
50
60
70
80
Age


Distribution of Outcome 1: Diabetes (0: No Diabetes)
count
0
100
200
300
400
500
0
1
Outcome

[31]:

```
#Boxplot of skin thickness
plt.figure(figsize=(8,5))
sns.boxplot(x='SkinThickness',data=data)
plt.title('Boxplot of Skin Thickness')
plt.show()
```



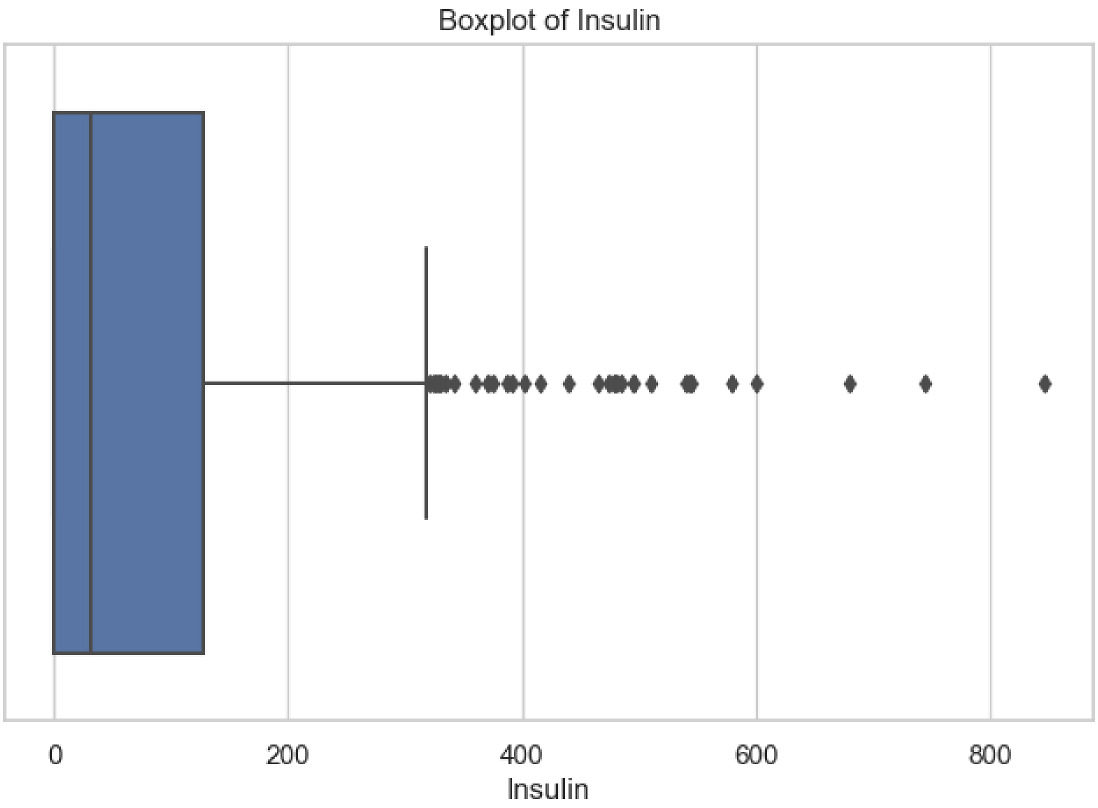
[32]:

```
#outliners in skin thickness
Q1_skin_thickness = data['SkinThickness'].quantile(0.25)
Q3_skin_thickness = data['SkinThickness'].quantile(0.75)
IQR_skin_thickness = Q3_skin_thickness - Q1_skin_thickness
lower_bound_skin_thickness = Q1_skin_thickness - 1.5 * IQR_skin_thickness
upper_bound_skin_thickness = Q3_skin_thickness + 1.5 * IQR_skin_thickness
outliers_skin_thickness = data[(data['SkinThickness'] <␣
 ↪lower_bound_skin_thickness) | (data['SkinThickness'] >␣
 ↪upper_bound_skin_thickness)]

print(f'Number of outliers in SkinThickness: {len(outliers_skin_thickness)}')
```

```
Number of outliers in SkinThickness: 1
```

[33]:

```
#Boxplot of insulin
plt.figure(figsize=(8,5))
sns.boxplot(x='Insulin',data=data)
plt.title('Boxplot of Insulin')
plt.show()
```



[35]:

```
#outliners in insulin
Q1_insulin = data['Insulin'].quantile(0.25)
Q3_insulin = data['Insulin'].quantile(0.75)
IQR_insulin = Q3_insulin - Q1_insulin
lower_bound_insulin = Q1_insulin - 1.5 * IQR_insulin
upper_bound_insulin = Q3_insulin + 1.5 * IQR_insulin
outliers_insulin = data[(data['Insulin'] < lower_bound_insulin) |␣
 ↪(data['Insulin'] > upper_bound_insulin)]

print(f'Number of outliers in Insulin: {len(outliers_insulin)}')
```

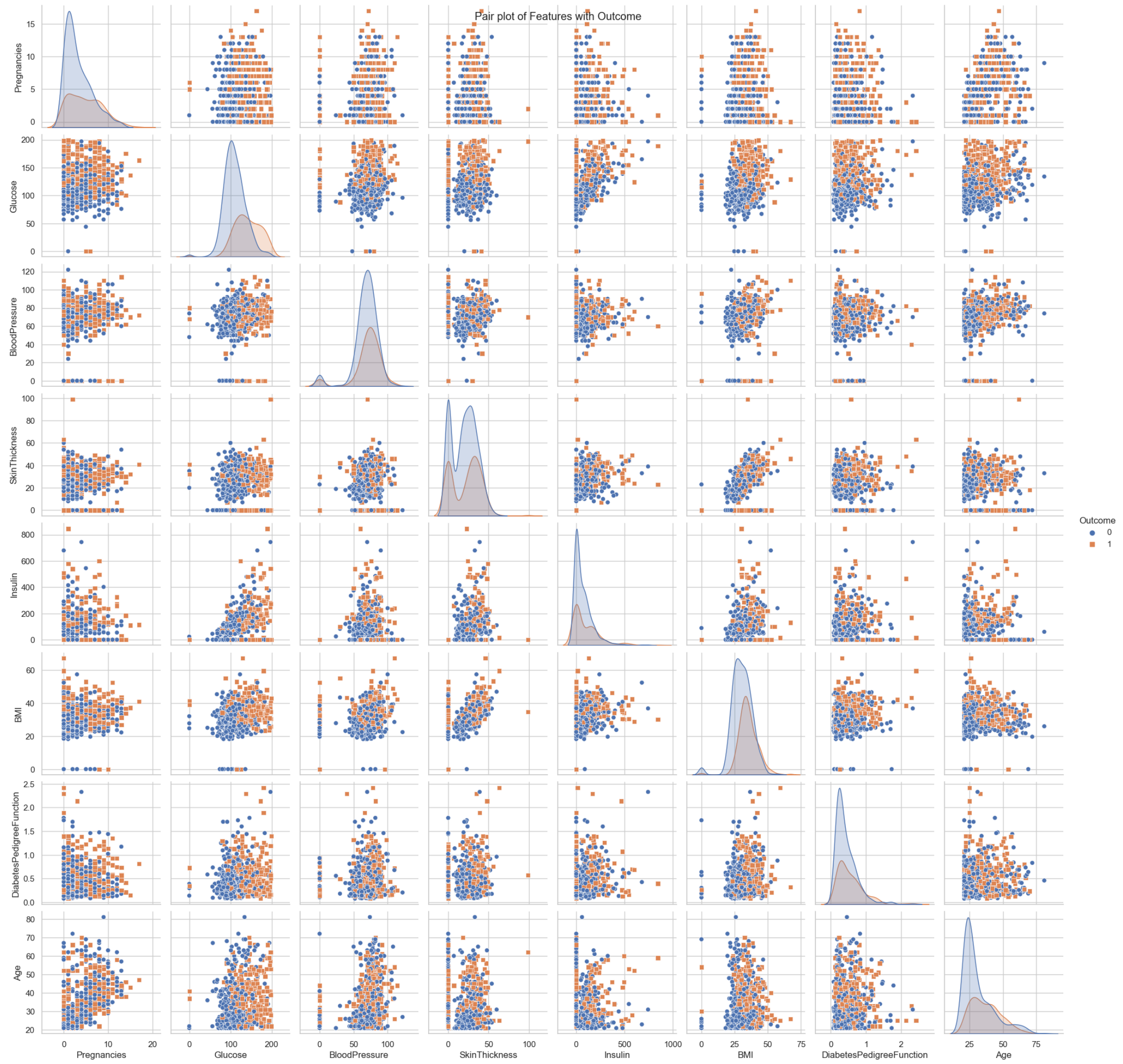
```
Number of outliers in Insulin: 34
```

[36]:

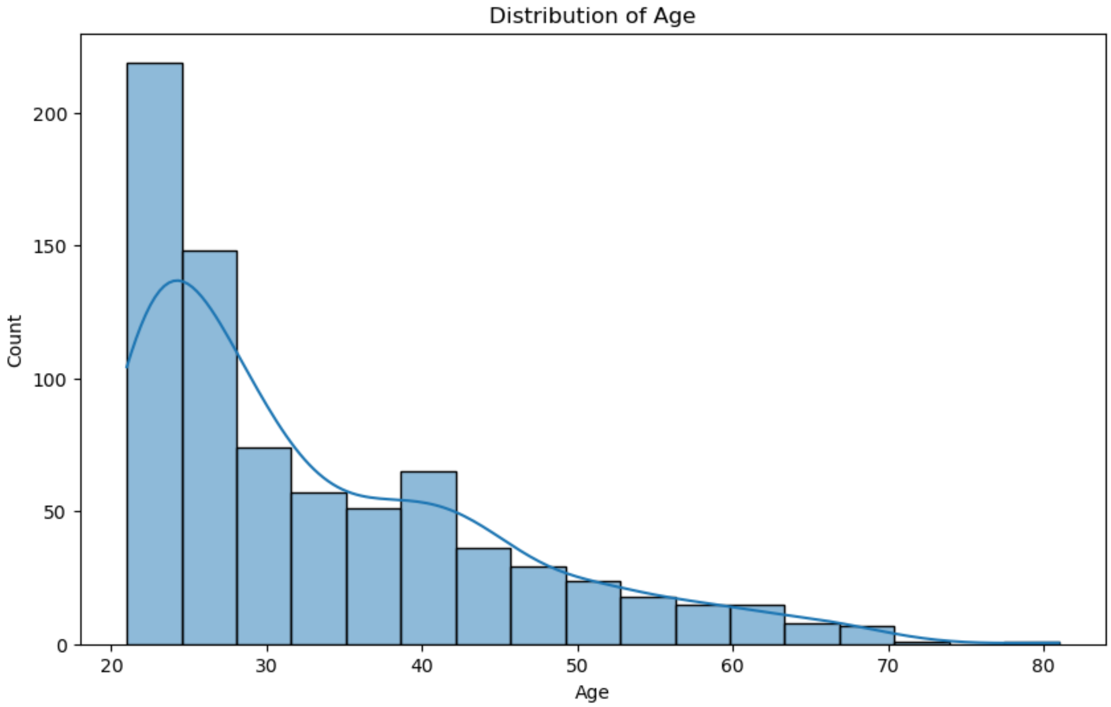
```
#visualization between features and pair plot
sns.pairplot(data,hue='Outcome',diag_kind='kde',markers=["o","s"])
```

```
plt.suptitle('Pair plot of Features with Outcome')
plt.show()
```

```
D:\Users\mathi\anaconda3\Lib\site-packages\seaborn\axisgrid.py:118: UserWarning:
The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```

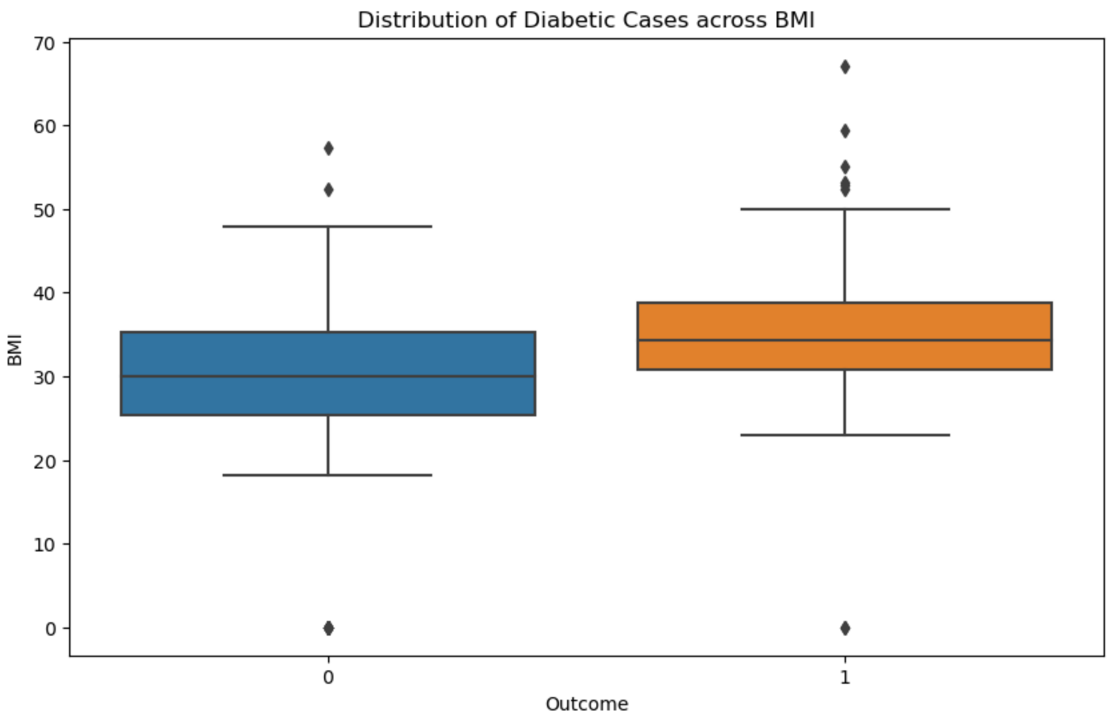


```
[12]: #Distribution of Age
plt.figure(figsize=(10, 6))plt.figure(figsize=(10, 6))
sns.histplot(x='Age', data=data, kde=True)
plt.title('Distribution of Age')
plt.show()
```

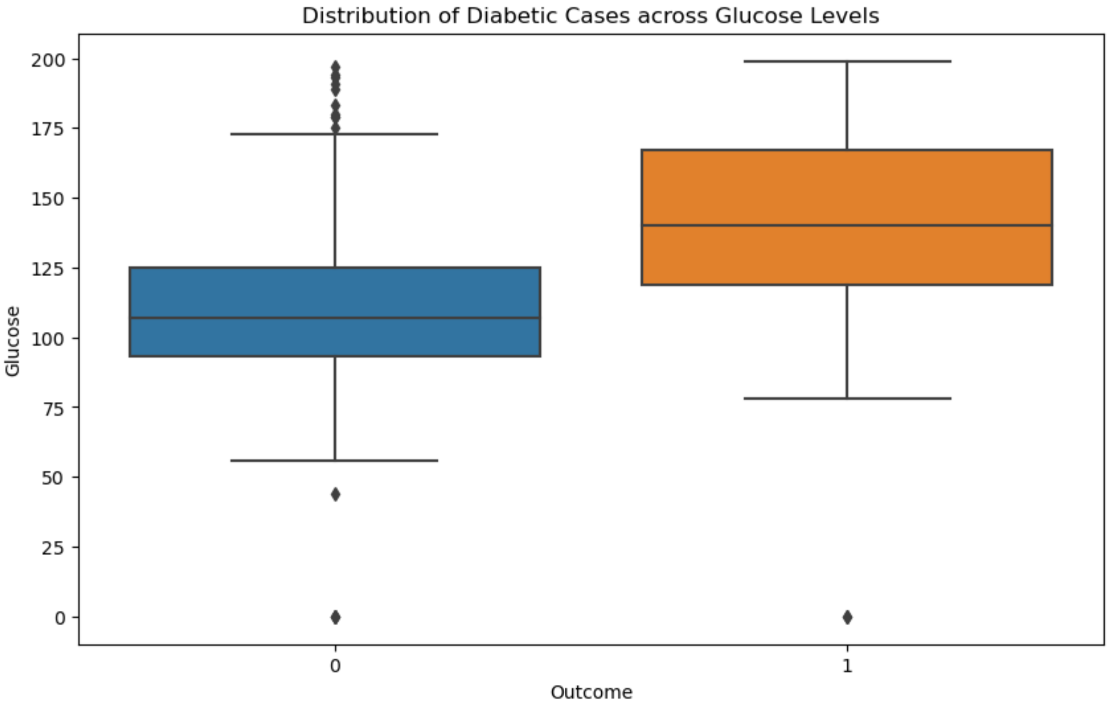


[13]:

```
#Distribution of cases accross BMI
plt.figure(figsize=(10, 6))plt.figure(figsize=(10, 6))
sns.boxplot(x='Outcome', y='BMI', data=data)
plt.title('Distribution of Diabetic Cases across BMI')
plt.show()
```



```
[14]: #Distribution of cases accross glucose level
plt.figure(figsize=(10, 6))
sns.boxplot(x='Outcome', y='Glucose', data=data)
plt.title('Distribution of Diabetic Cases across Glucose Levels')
plt.show()
```


Distribution of Diabetic Cases across Glucose Levels
Glucose
200
175
150
125
100
75
50
25
0
Outcome
0
1

```
[ ]:
```