Exploratory Data analysis and Predictive Modelling Algorithm For Diabetes

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 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.2 From the data set in the (.csv) File We can find several variables, some of them are independent (several medical predictor variables) and only one target dependent variable (Outcome).

Aim: To use the knowledge of EDA and machine learning to derive insight from the data and make good predictive algorithm based on the Diagnotic measurement given from the data.

The Data would be thoroughly cleaned and analysed and will use different machine learning algorithm and considering the one that works best.

Importing Neccesary Libraries

In [1]:

```
#Libraries for Data cleaning and analysis
import pandas as pd
import numpy as np


#Libraries for Data Visualizations
import matplotlib.pyplot as plt
%matplotlib inline
import seaborn as sns

# Data for machine learning algorithm modelling and predicting and scoring
from sklearn.metrics import mean_squared_error, r2_score
from sklearn.neighbors import KNeighborsRegressor
from sklearn.tree import DecisionTreeRegressor
from sklearn.ensemble import RandomForestRegressor,AdaBoostRegressor
from sklearn.svm import SVR
from sklearn.linear_model import LinearRegression, Ridge,Lasso
from sklearn.metrics import r2_score, mean_absolute_error, mean_squared_error
from sklearn.model_selection import RandomizedSearchCV
#from catboost import CatBoostRegressor
#from xgboost import XGBRegressor




#Libraries to avoid errors
import warnings
warnings.filterwarnings('ignore')
```

In [2]:

```
#Loading the data from csv into our project as a Dataframe format.
data = pd.read_csv("diabetes.csv")
data.head(20)   #Viewing the first 20 rows
```

Out[2]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
0	6	148	72	35	0	33.6	0.62
1	1	85	66	29	0	26.6	0.35
2	8	183	64	0	0	23.3	0.67
3	1	89	66	23	94	28.1	0.16
4	0	137	40	35	168	43.1	2.28
5	5	116	74	0	0	25.6	0.20
6	3	78	50	32	88	31.0	0.24
7	10	115	0	0	0	35.3	0.13
8	2	197	70	45	543	30.5	0.15
9	8	125	96	0	0	0.0	0.23
10	4	110	92	0	0	37.6	0.19
11	10	168	74	0	0	38.0	0.53
12	10	139	80	0	0	27.1	1.44
13	1	189	60	23	846	30.1	0.39
14	5	166	72	19	175	25.8	0.58
15	7	100	0	0	0	30.0	0.48
16	0	118	84	47	230	45.8	0.55
17	7	107	74	0	0	29.6	0.25
18	1	103	30	38	83	43.3	0.18
19	1	115	70	30	96	34.6	0.52

In [3]:

```
#getting the Number of columns in the data set

data.columns
```

Out[3]:

```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insuli
n',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

In [4]:

```
data.shape
print(f'The shape of the data is {data.shape}')
```

```
The shape of the data is (768, 9)
```

In [5]:
```
data.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]:
```
#Checking for null values int the data
data.isnull().sum()
```

Out[6]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [7]:
```
#Checking for duplicates in the data
data.duplicated().sum()
```

Out[7]:
```
0
```

In [8]:
```
#Getting the number of unique values for all the columns

data.nunique()
```

Out[8]:
```
Pregnancies                  17
Glucose                     136
BloodPressure                47
SkinThickness                51
Insulin                     186
BMI                         248
DiabetesPedigreeFunction    517
Age                          52
Outcome                       2
dtype: int64
```

In [9]:
```
# Looking into the statistical summary of the data
data.describe()
```

Out[9]:

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

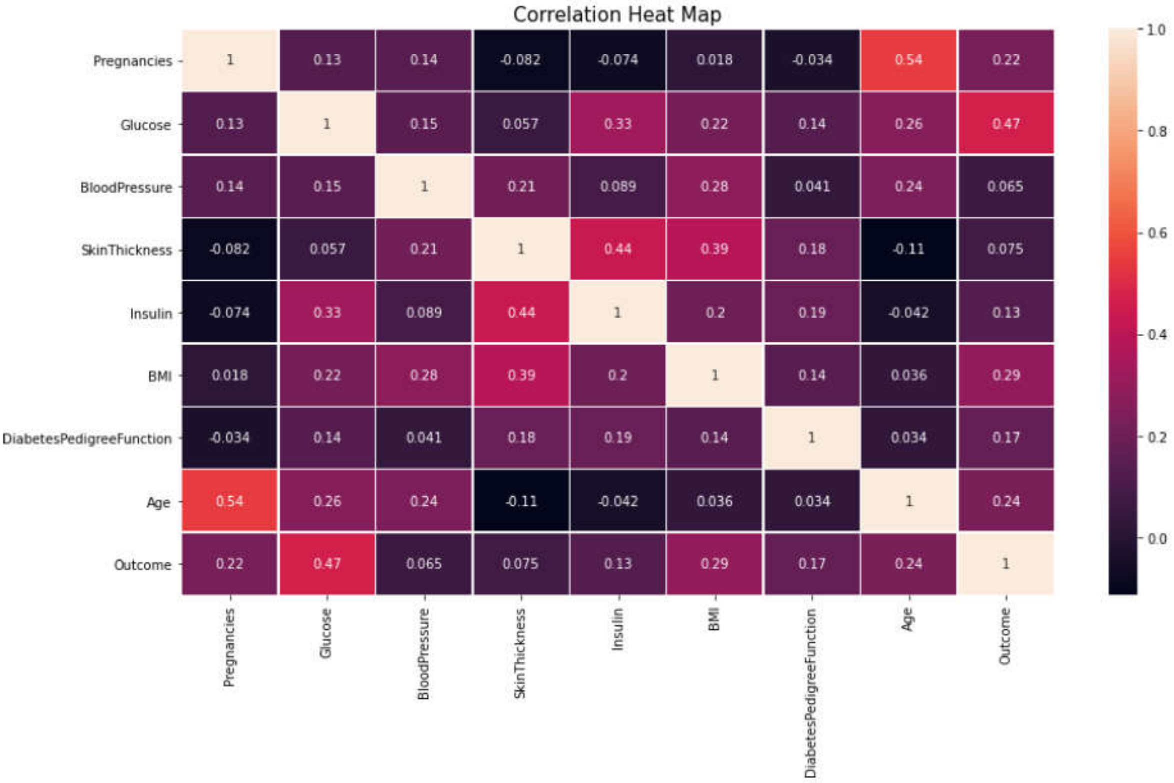
In [10]:
```
#Checking for the correlation of the data

data.corr()
```

Out[10]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.01
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.22
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.28
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.39
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.19
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.00
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.14
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.03
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.29

In [11]:

```
# multivariate analysis
# lets check the Heat Map for the Data with respect to correlation.

plt.rcParams['figure.figsize'] = (15, 8)
sns.heatmap(data.corr(), annot = True, linewidth = 0.5, linewidths=.5)
plt.title('Correlation Heat Map', fontsize = 15)
plt.xticks(rotation = 90)
plt.show()
```

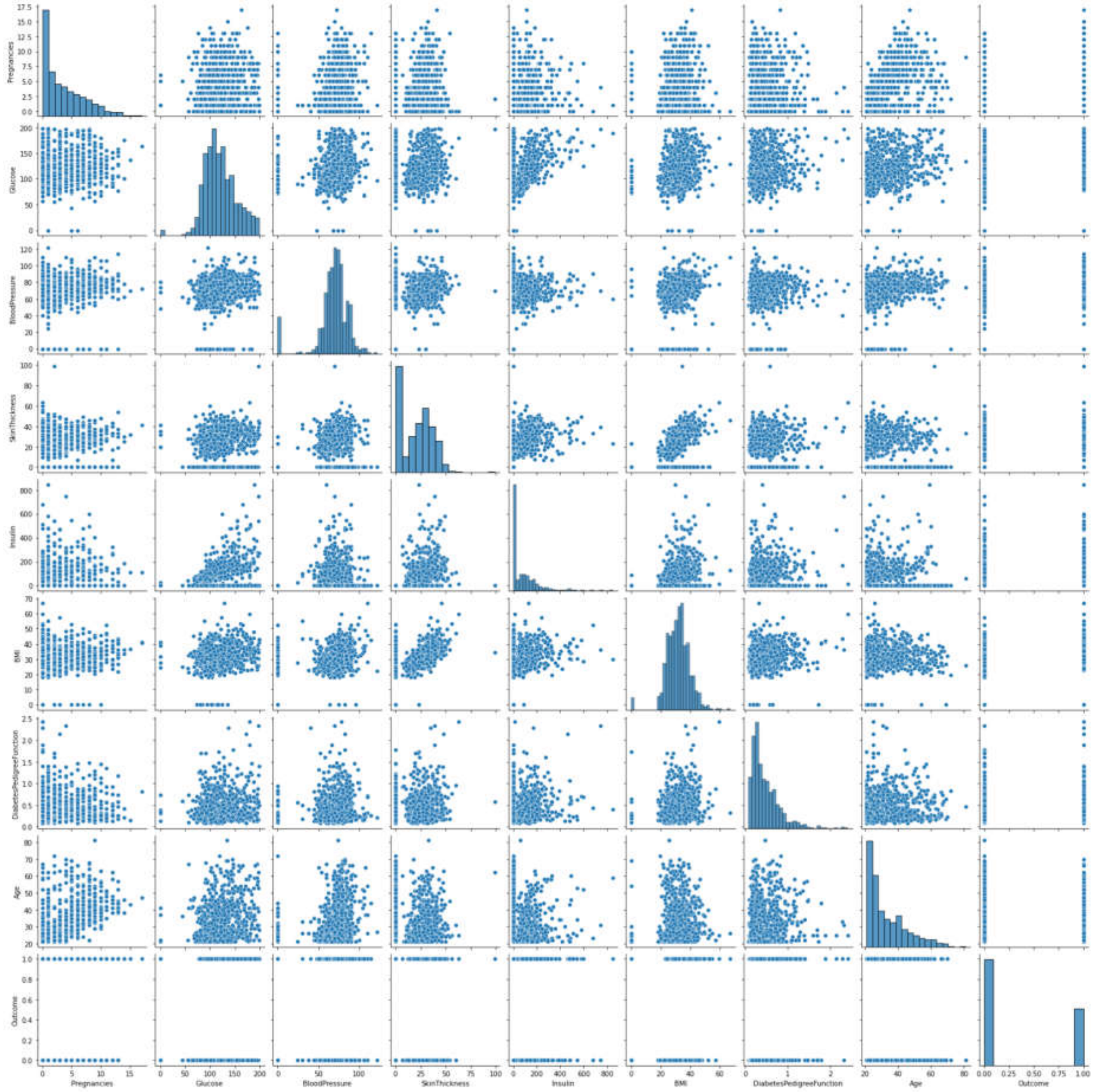


In [12]:

```
# Visualizing our correlation
import seaborn as sns
sns.pairplot(data)
```

Out[12]:

```
<seaborn.axisgrid.PairGrid at 0x1e1401b5940>
```

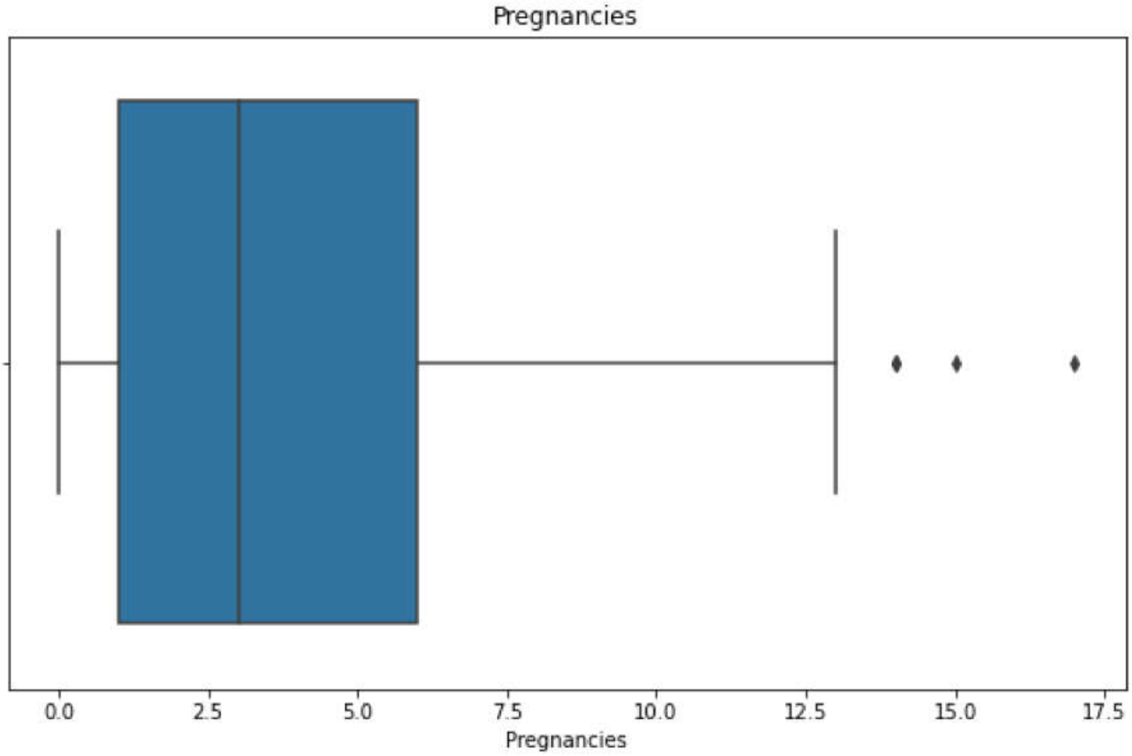


In [13]:

```
#Checking the Outliers present in the data
```

In [14]:

```
plt.figure(figsize=(10,6))
sns.boxplot(data['Pregnancies'])
plt.title('Pregnancies')
plt.show()
```

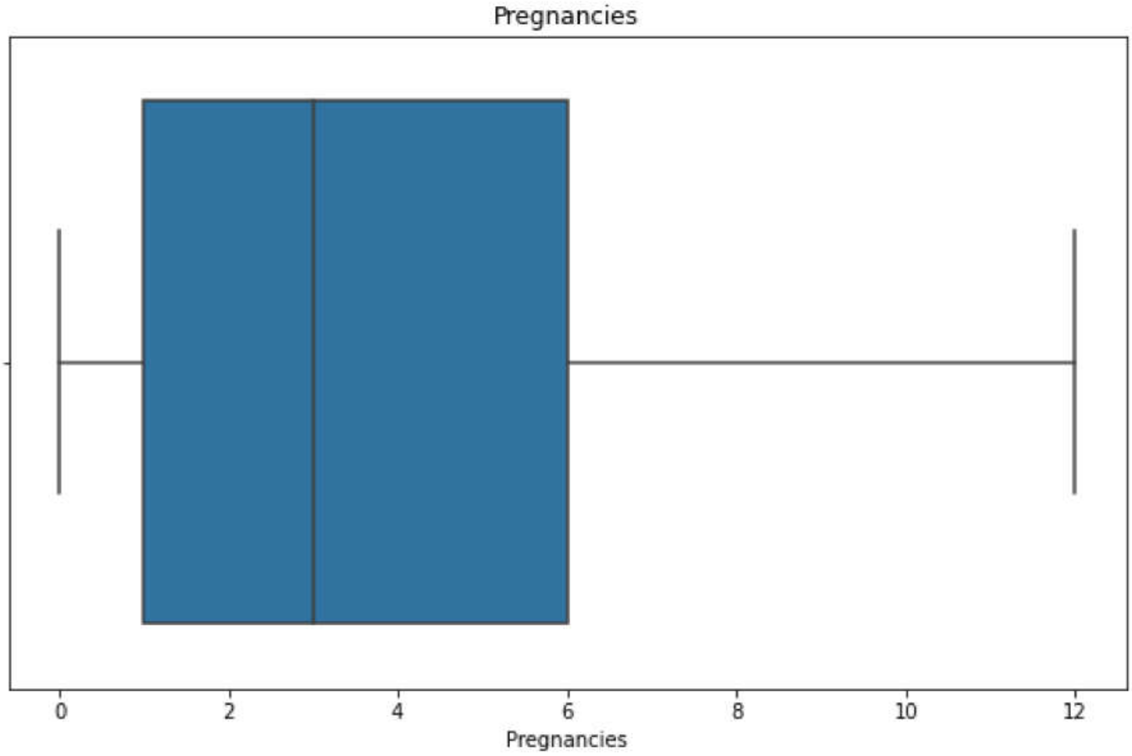


In [15]:

```
data = data[data['Pregnancies']<13]
# Getting rid of the outliers
```

In [16]:

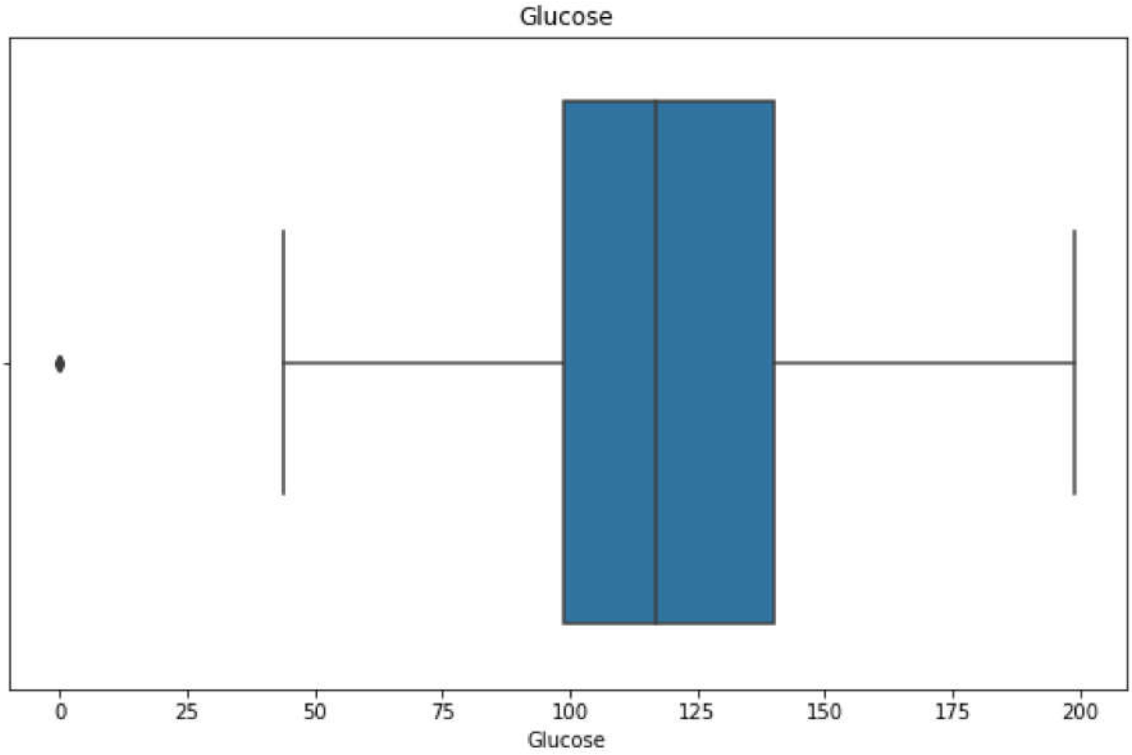
```
plt.figure(figsize=(10,6))
sns.boxplot(data['Pregnancies'])
plt.title('Pregnancies')
plt.show()
```



So we no longer have Outliers in the pregnancies column

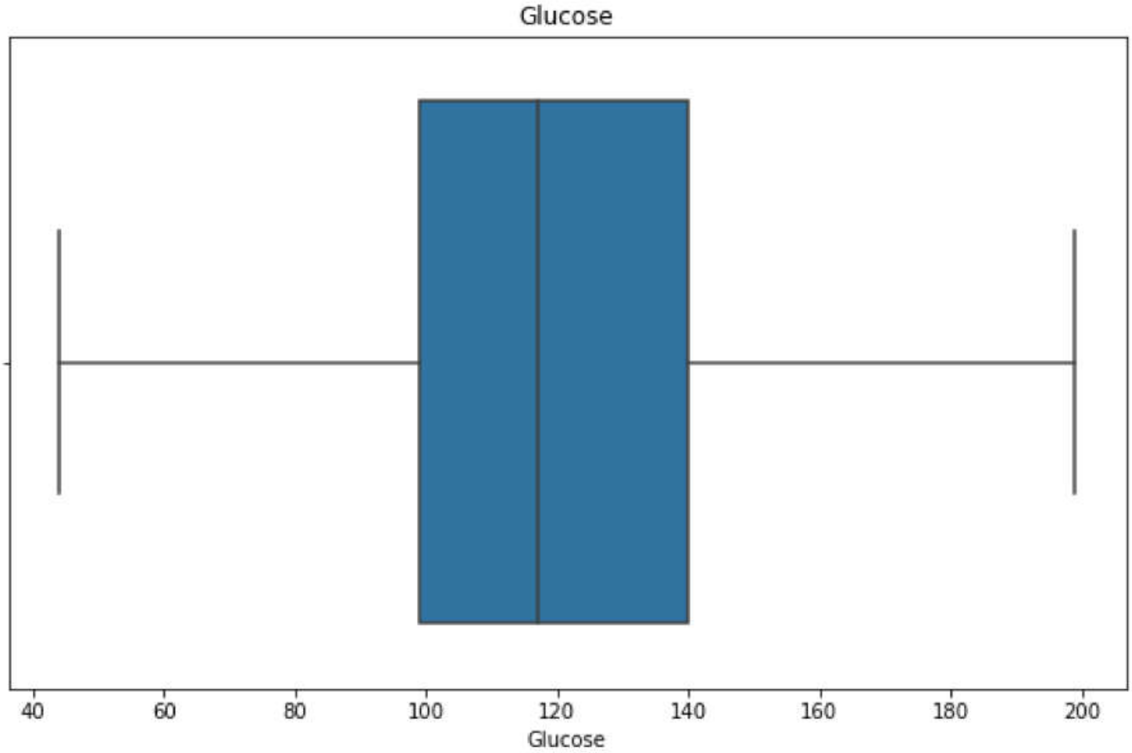
```
In [ ]:
```

```
In [17]: plt.figure(figsize=(10,6))

         sns.boxplot(data['Glucose'])
         plt.title('Glucose')
         plt.show()
```



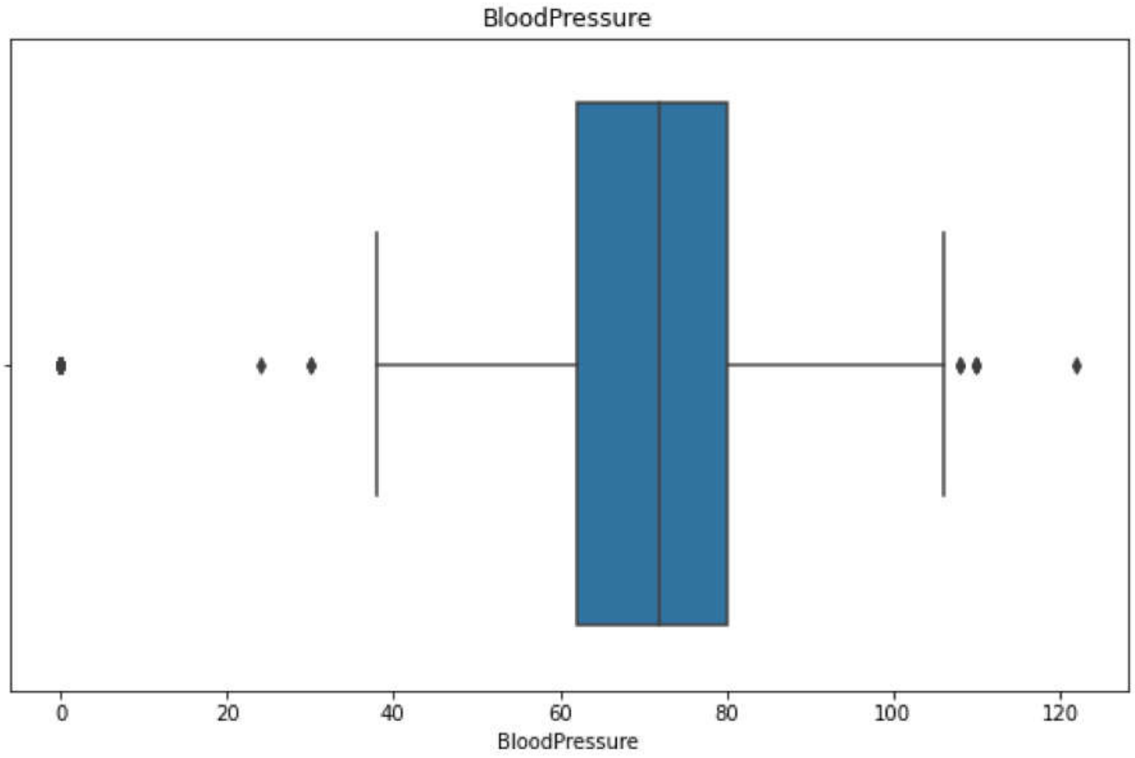
```
In [18]: data = data[data['Glucose']>1]
```

In [19]:
```
plt.figure(figsize=(10,6))

sns.boxplot(data['Glucose'])
plt.title('Glucose')
plt.show()
```



So we no longer have Outliers on the Glucose Column

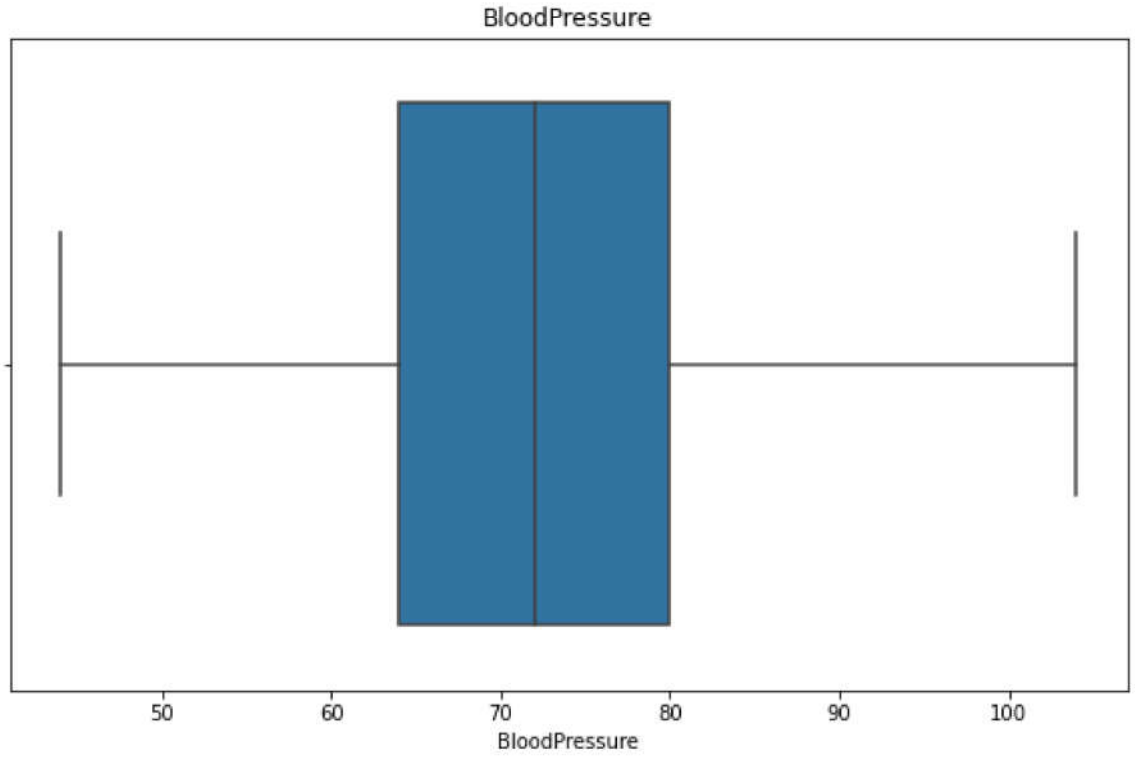
In [20]:
```
plt.figure(figsize=(10,6))

sns.boxplot(data['BloodPressure'])
plt.title('BloodPressure')
plt.show()
```



In [21]:
```
data = data[data['BloodPressure']<105]
data = data[data['BloodPressure']>40]
```

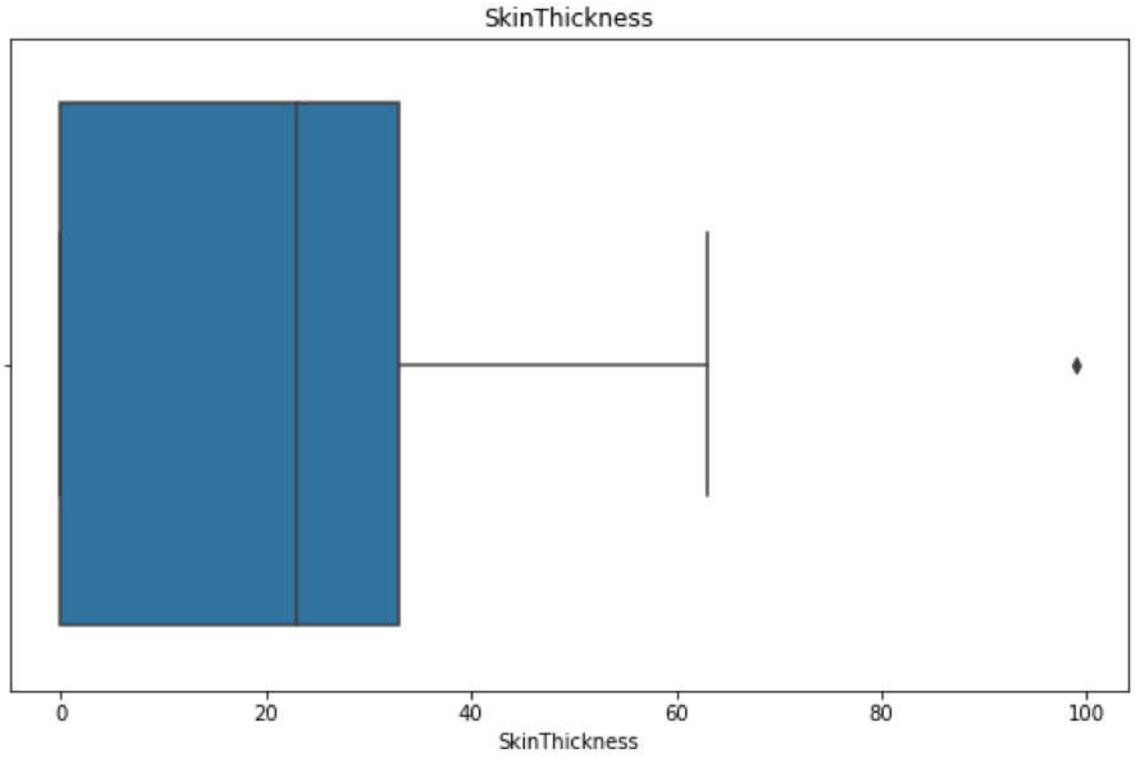
In [22]:

```
plt.figure(figsize=(10,6))

sns.boxplot(data['BloodPressure'])
plt.title('BloodPressure')
plt.show()
```



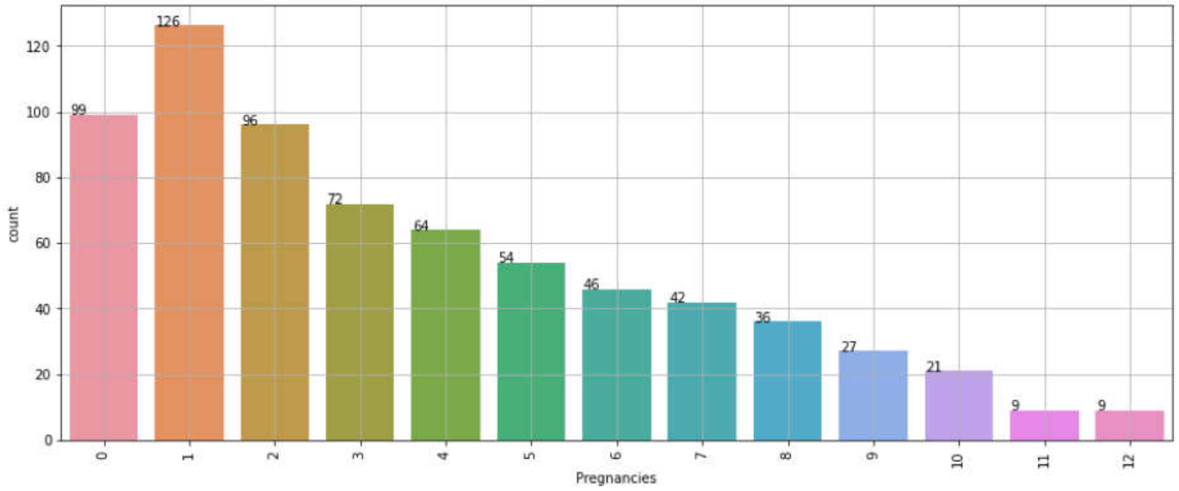
So we no longer have outliers in the Blood

In [23]:
```
plt.figure(figsize=(10,6))

sns.boxplot(data['SkinThickness'])
plt.title('SkinThickness')
plt.show()
```



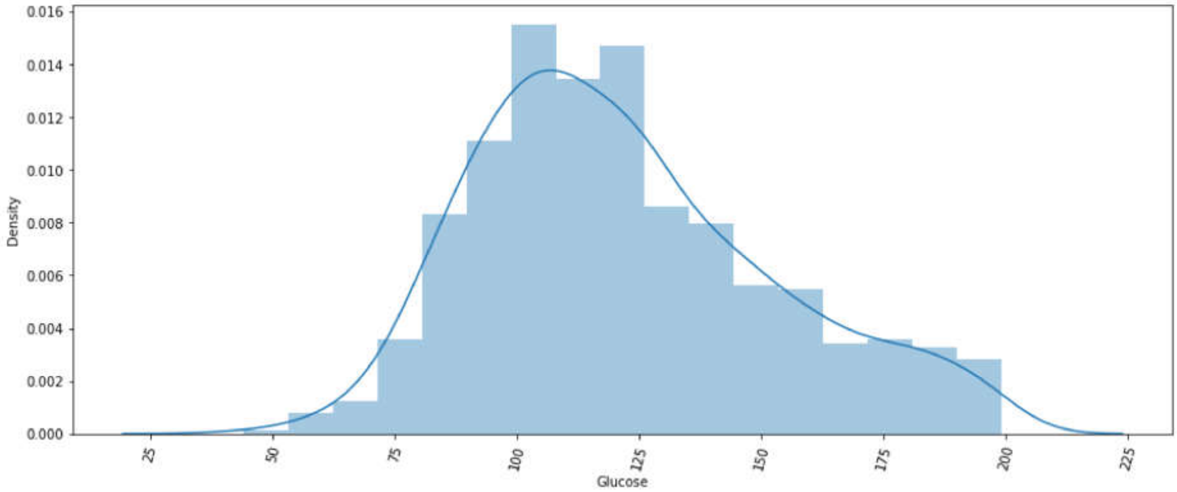
Univariate Analysis

In [24]:
```
plt.figure(figsize=(15,6))
a=sns.countplot(data['Pregnancies'])
for p in a.patches:
    a.annotate('{:}'.format(p.get_height()),
                  (p.get_x()+0.01, p.get_height()+0.01))
plt.grid()
plt.xticks(rotation = 90)
plt.show()
```



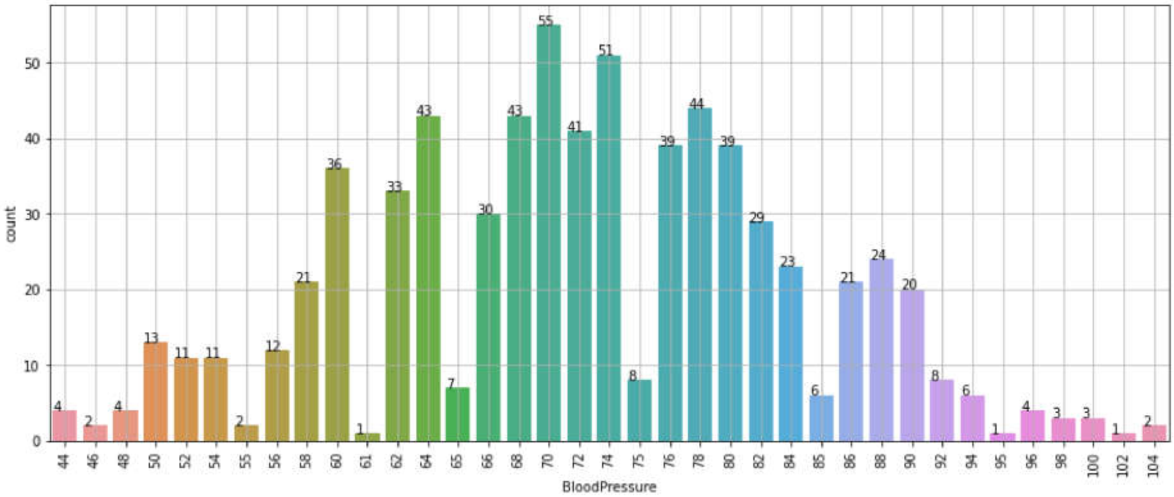
In [25]:

```
plt.figure(figsize=(15,6))
sns.distplot(data['Glucose'])
plt.xticks(rotation = 75)
plt.show()
```

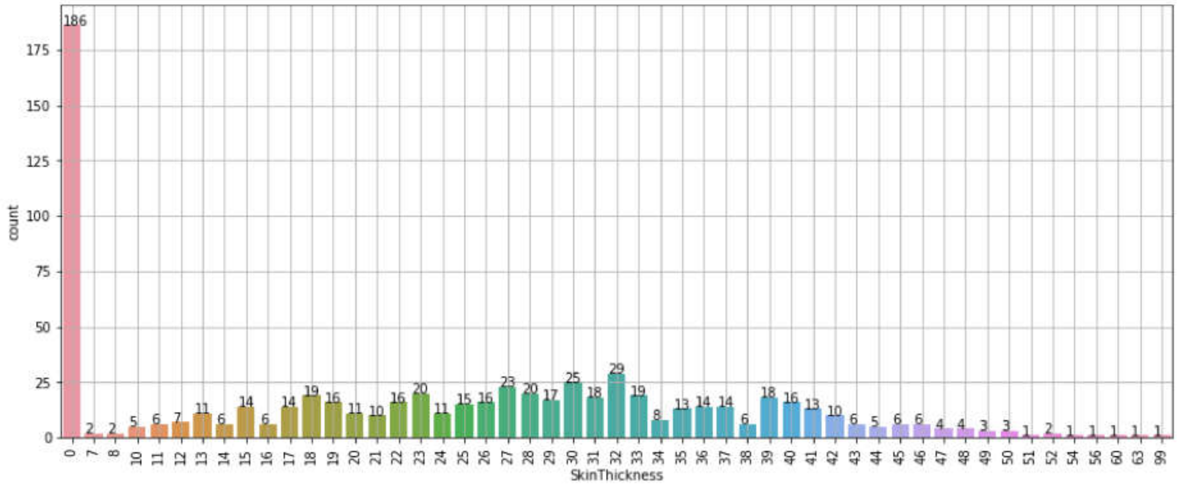


In [26]:

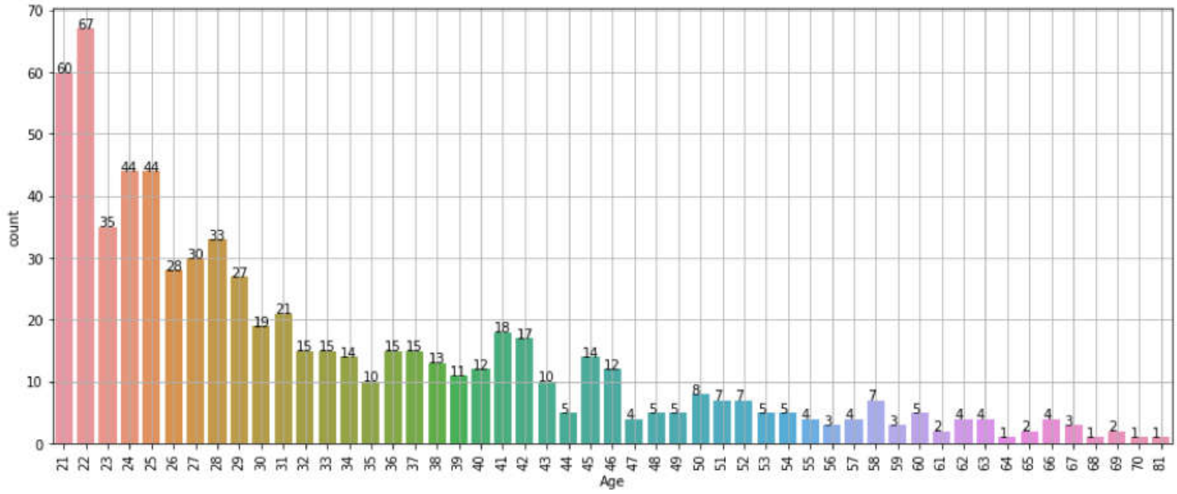
```
plt.figure(figsize=(15,6))
a=sns.countplot(data['BloodPressure'])
for p in a.patches:
    a.annotate('{:}'.format(p.get_height()),
                (p.get_x()+0.01, p.get_height()+0.01))
plt.grid()
plt.xticks(rotation = 90)
plt.show()
```



In [27]:
```
plt.figure(figsize=(15,6))
a=sns.countplot(data['SkinThickness'])
for p in a.patches:
    a.annotate('{:}'.format(p.get_height()),
               (p.get_x()+0.01, p.get_height()+0.01))
plt.grid()
plt.xticks(rotation = 90)
plt.show()
```



In [28]:
```
plt.figure(figsize=(15,6))
a=sns.countplot(data['Age'])
for p in a.patches:
    a.annotate('{:}'.format(p.get_height()),
               (p.get_x()+0.01, p.get_height()+0.01))
plt.grid()
plt.xticks(rotation = 90)
plt.show()
```



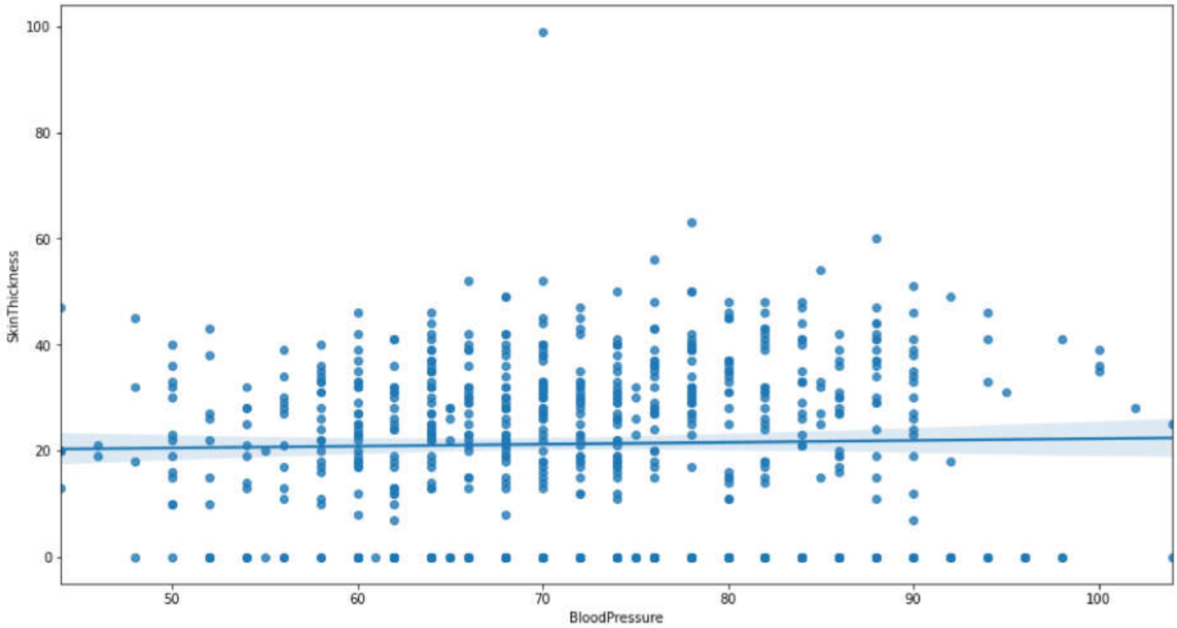
Bivariate Analysis

In [29]:

```
sns.regplot( x='BloodPressure',y='SkinThickness', data=data)
```

Out[29]:

```
<AxesSubplot:xlabel='BloodPressure', ylabel='SkinThickness'>
```

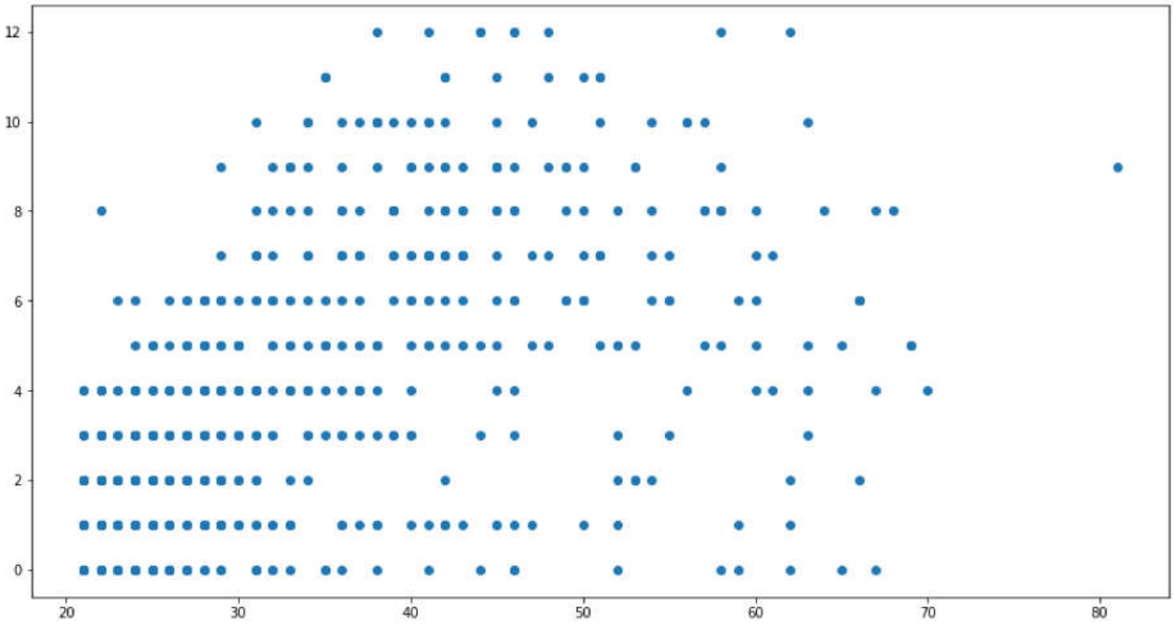


In [30]:

```
# A Plot showing the correlation of CRIM and PRICES
plt.scatter(data['Age'],data['Pregnancies'])
```

Out[30]:

```
<matplotlib.collections.PathCollection at 0x1e145ed6940>
```



Splitting Data

In [31]:

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

In [32]:
```
X.head()
```

Out[32]:

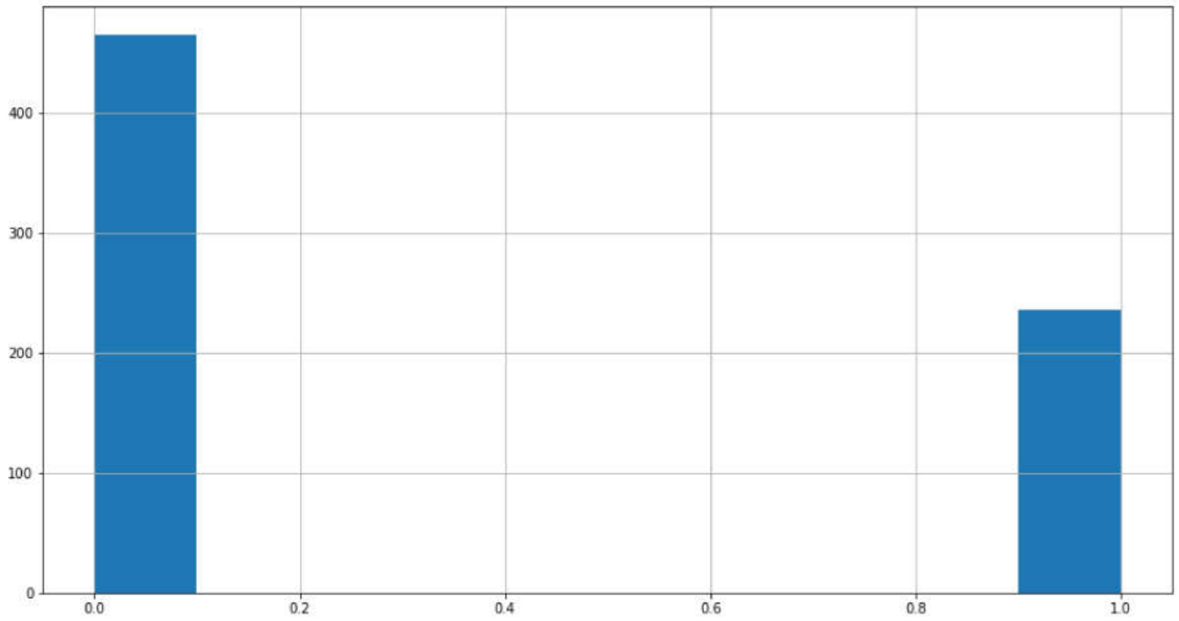
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction
0	6	148	72	35	0	33.6	0.627
1	1	85	66	29	0	26.6	0.351
2	8	183	64	0	0	23.3	0.672
3	1	89	66	23	94	28.1	0.167
5	5	116	74	0	0	25.6	0.201

In [33]:
```
y.head()
```

Out[33]:
```
0    1
1    0
2    1
3    0
5    0
Name: Outcome, dtype: int64
```

In [34]:
```
data.Outcome.hist()
```

Out[34]:
```
<AxesSubplot:>
```



In [35]:
```
## Train Test Split
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_
```

In [36]:

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import confusion_matrix
from sklearn.metrics import f1_score
from sklearn.metrics import accuracy_score
```

In [37]:

```
sc_x=StandardScaler()
X_train= sc_x.fit_transform(X_train)
X_test = sc_x.transform(X_test)
```

In [ ]:

In [38]:

```
from sklearn.linear_model import LogisticRegression   # Importing our linear m
from sklearn.model_selection import GridSearchCV    # Importing our hyperparam


param_lrg = {
    'penalty' : ['l1', 'l2', 'elasticnet', 'none'],
    'dual':[True, False] ,
    'fit_intercept':[True, False] ,
    'solver' :['newton-cg', 'lbfgs', 'liblinear', 'sag', 'saga'] ,
    'max_iter' :[1,10,20,30,40,50,60,70,80,90,100] ,
    'multi_class' :['auto', 'ovr', 'multinomial'] ,
    'warm_start':[True, False]
}


lrg=LogisticRegression()


grid_lrg = GridSearchCV(estimator=lrg, param_grid=param_lrg, cv=5, scoring='ac
grid_lrg.fit(X_train, y_train)  # Fitting our training data to our model


print(f"Best hyperparameters: {grid_lrg.best_params_}")  # determining our bes
print(f"Best score: {grid_lrg.best_score_}")   # Our Best score


best_lrg = LogisticRegression(**grid_lrg.best_params_)    # Using our best par
best_lrg.fit(X_train, y_train)     # Fit our training dataset to our new model

test_score = best_lrg.score(X_test, y_test)   # Getting our accuracy score
print(f"Test score: {test_score}")
```

```
Best hyperparameters: {'dual': False, 'fit_intercept': True, 'max_iter': 1,
'multi_class': 'multinomial', 'penalty': 'l1', 'solver': 'saga', 'warm_star
t': False}
Best score: 0.7877551020408164
Test score: 0.7677725118483413
```

So using Logistic Regression, we could see we got accuracy score of 76.77%