In [1]:
```python
# importing all the necessary packages
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:
```python
# Loading the data set

data=pd.read_csv(r'C:\Users\parak\Downloads\diabetes.csv')
```

In [3]:
```python
data.head(10)
```

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
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

In [4]:
```python
data.tail()
```

Out[4]:

	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 [5]:
```python
# Lets check the dimension of the data set
data.shape
```

Out[5]:
```
(768, 9)
```

In [6]:
```python
# Printing the first 5 records of the data set
data.head()
```

Out[6]:

	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 [7]:
```python
# Lets start by checking the count of records in each column of the data set.
# If the count of records is lesser than the total number of records i.e. 768, we can conclude that there
# are blank records.

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 [8]:
```python
# Since all the predictor columns are continuous in nature, there might be a chance that 0's
#in these columns indicate missing data.

# Lets check the above claim.

data.describe()
```

Out[8]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	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	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

In [9]:
```python
# Replacing the 0's with NaN.
# The records that have 0's in columns Glucose, Blood Preassure, Skin Thickness, Insulin and BMI will be replaced with NaN
from numpy import nan
data['Glucose']=data['Glucose'].replace(0,np.nan)
data['BloodPressure']=data['BloodPressure'].replace(0,np.nan)
data['SkinThickness']=data['SkinThickness'].replace(0,np.nan)
data['Insulin']=data['Insulin'].replace(0,np.nan)
data['BMI']=data['BMI'].replace(0,np.nan)
```

In [10]:
```python
#Lets check if the above code has worked
data.head()
# All the 0's have been replaced by NaN
```

Out[10]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.0	35.0	NaN	33.6	0.627	50	1
1	1	85.0	66.0	29.0	NaN	26.6	0.351	31	0
2	8	183.0	64.0	NaN	NaN	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 [11]:
```python
data.isnull().any()
```

Out[11]:
```
Pregnancies                 False
Glucose                      True
BloodPressure                True
SkinThickness                True
Insulin                      True
BMI                          True
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

In [12]:
```python
# Count of NaN values in the dataset
print(data.isnull().sum())
```

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

In [13]:
```python
data.median()
```

Out[13]:
```
Pregnancies                   3.0000
Glucose                     117.0000
BloodPressure                72.0000
SkinThickness                29.0000
Insulin                     125.0000
BMI                          32.3000
DiabetesPedigreeFunction      0.3725
Age                          29.0000
Outcome                       0.0000
dtype: float64
```

In [14]:
```python
# Imputing missing values with their respective columns median
data.fillna(data.median(), inplace=True)
```

In [15]:
```python
# Checking if the missing values have been imputed
print(data.isnull().sum())
```

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [16]:
```python
# Outlier detection using boxplots
plt.figure(figsize= (20,15))
plt.subplot(4,4,1)
sns.boxplot(data['Pregnancies'])

plt.subplot(4,4,2)
sns.boxplot(data['Glucose'])

plt.subplot(4,4,3)
sns.boxplot(data['BloodPressure'])

plt.subplot(4,4,4)
sns.boxplot(data['SkinThickness'])

plt.subplot(4,4,5)
sns.boxplot(data['Insulin'])

plt.subplot(4,4,6)
sns.boxplot(data['BMI'])

plt.subplot(4,4,7)
sns.boxplot(data['DiabetesPedigreeFunction'])

plt.subplot(4,4,8)
sns.boxplot(data['Age'])
```

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

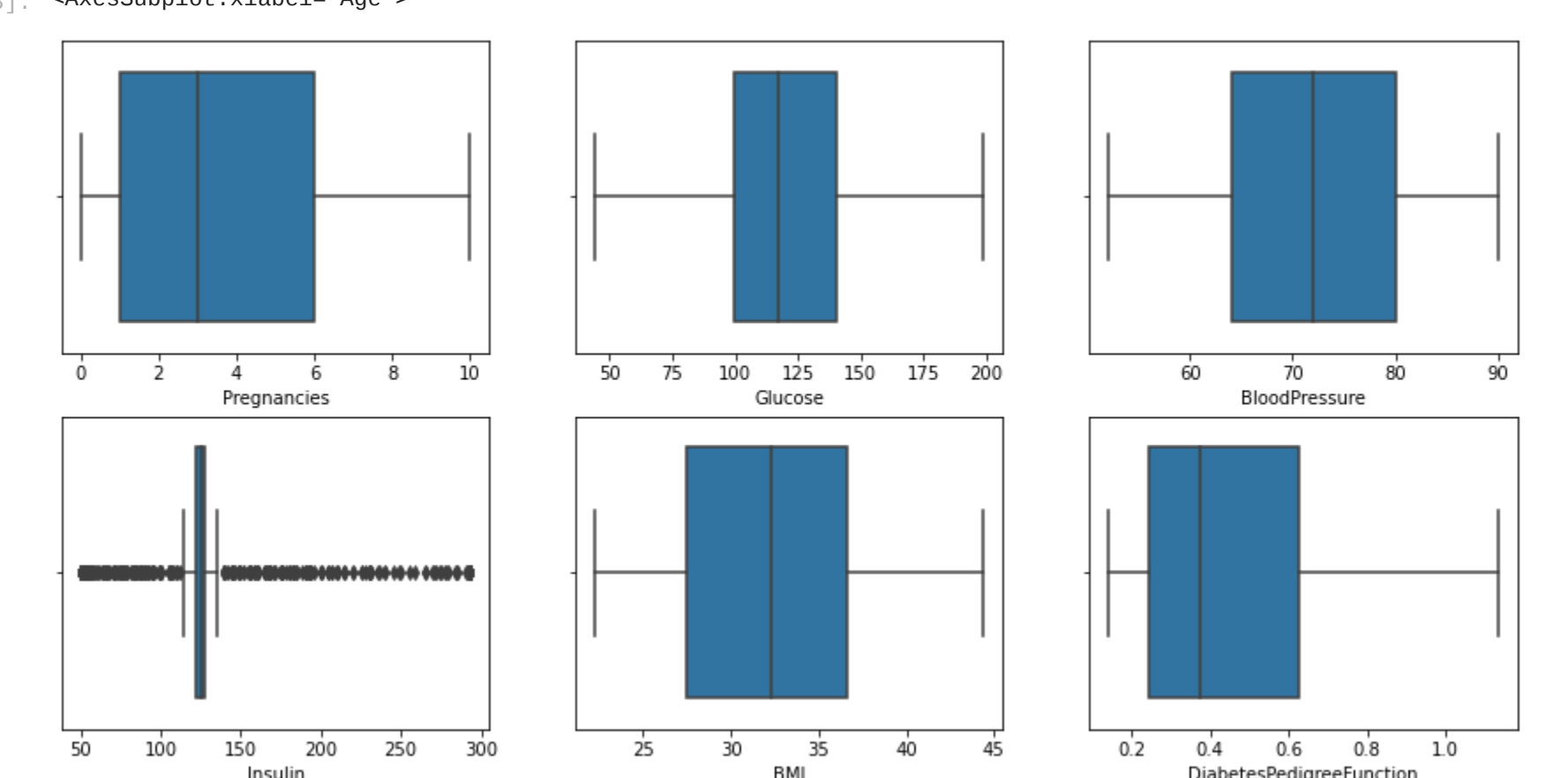
Out[16]:
```
<AxesSubplot:xlabel='Age'>
```

In [17]:
```python
data['Pregnancies']=data['Pregnancies'].clip(lower=data['Pregnancies'].quantile(0.05), upper=data['Pregnancies'].quantile(0.95))
data['BloodPressure']=data['BloodPressure'].clip(lower=data['BloodPressure'].quantile(0.05), upper=data['BloodPressure'].quantile(0.95))
data['SkinThickness']=data['SkinThickness'].clip(lower=data['SkinThickness'].quantile(0.05), upper=data['SkinThickness'].quantile(0.95))
data['Insulin']=data['Insulin'].clip(lower=data['Insulin'].quantile(0.05), upper=data['Insulin'].quantile(0.95))
data['BMI']=data['BMI'].clip(lower=data['BMI'].quantile(0.05), upper=data['BMI'].quantile(0.95))
data['DiabetesPedigreeFunction']=data['DiabetesPedigreeFunction'].clip(lower=data['DiabetesPedigreeFunction'].quantile(0.05), upper=data['DiabetesPedigreeFunction'].quantile(0.95))
data['Age']=data['Age'].clip(lower=data['Age'].quantile(0.05), upper=data['Age'].quantile(0.95))
```

In [18]:
```python
# Lets visualise the boxplots after imputing the outliers
plt.figure(figsize= (20,15))
plt.subplot(4,4,1)
sns.boxplot(data['Pregnancies'])

plt.subplot(4,4,2)
sns.boxplot(data['Glucose'])

plt.subplot(4,4,3)
sns.boxplot(data['BloodPressure'])

plt.subplot(4,4,4)
sns.boxplot(data['SkinThickness'])

plt.subplot(4,4,5)
sns.boxplot(data['Insulin'])

plt.subplot(4,4,6)
sns.boxplot(data['BMI'])

plt.subplot(4,4,7)
sns.boxplot(data['DiabetesPedigreeFunction'])

plt.subplot(4,4,8)
sns.boxplot(data['Age'])
```

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

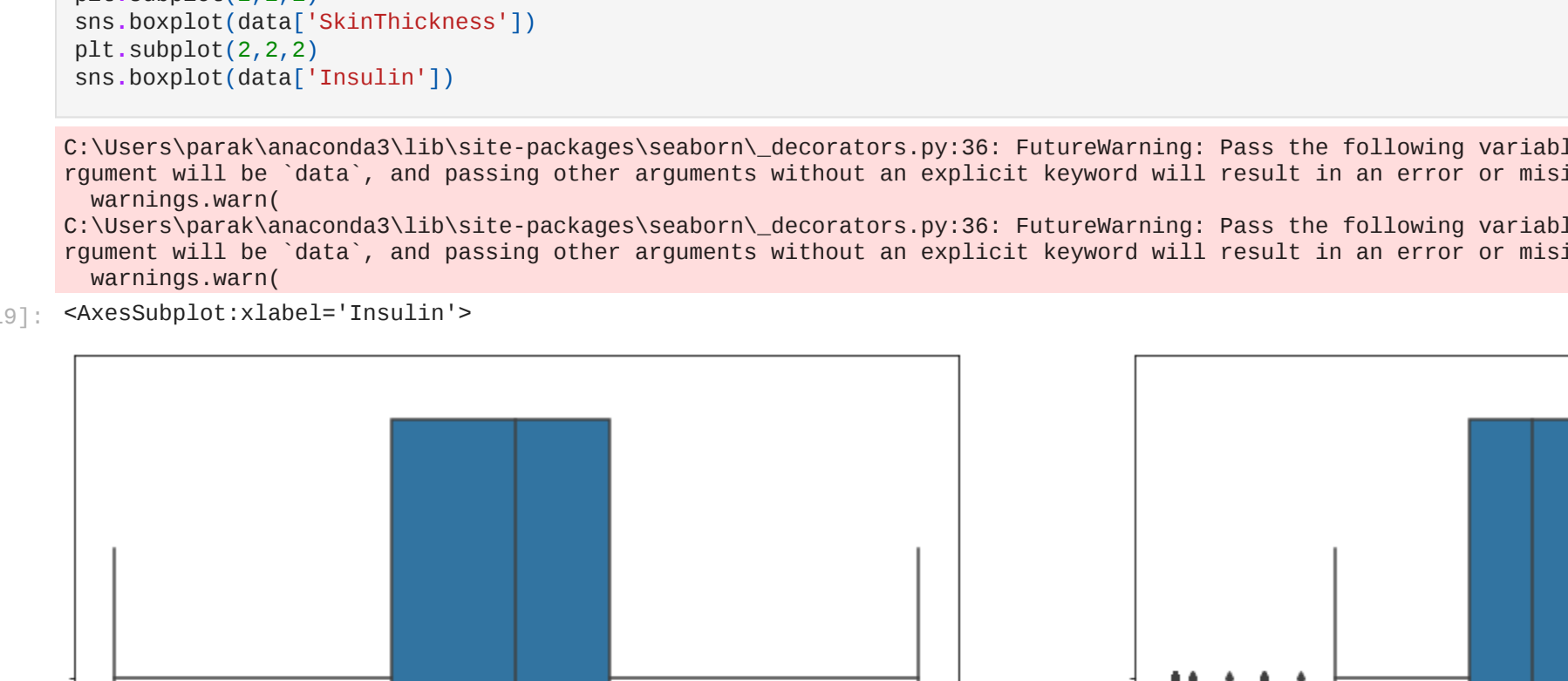
Out[18]:
```
<AxesSubplot:xlabel='Age'>
```



In [19]:
```python
# As we can see, there are still outliers in columns Skin Thickness and Insulin. Lets try manipulating the percentile values.
data['SkinThickness']=data['SkinThickness'].clip(lower=data['SkinThickness'].quantile(0.07), upper=data['SkinThickness'].quantile(0.93))
data['Insulin']=data['Insulin'].clip(lower=data['Insulin'].quantile(0.21), upper=data['Insulin'].quantile(0.80))
plt.figure(figsize= (20,15))
plt.subplot(2,2,1)
sns.boxplot(data['SkinThickness'])
plt.subplot(2,2,2)
sns.boxplot(data['Insulin'])
```

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

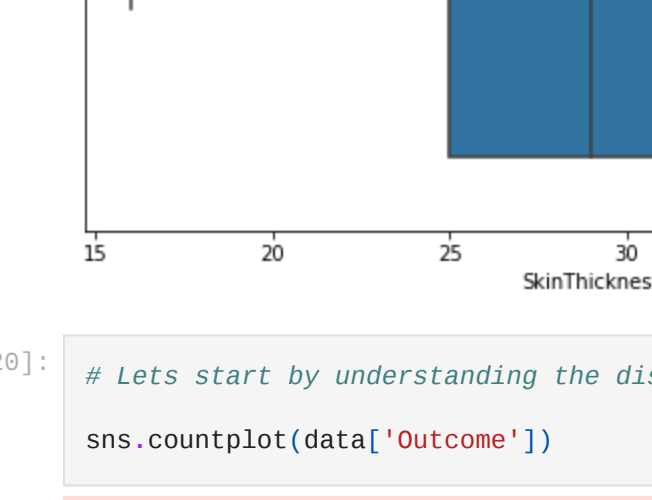
Out[19]:
```
<AxesSubplot:xlabel='Insulin'>
```



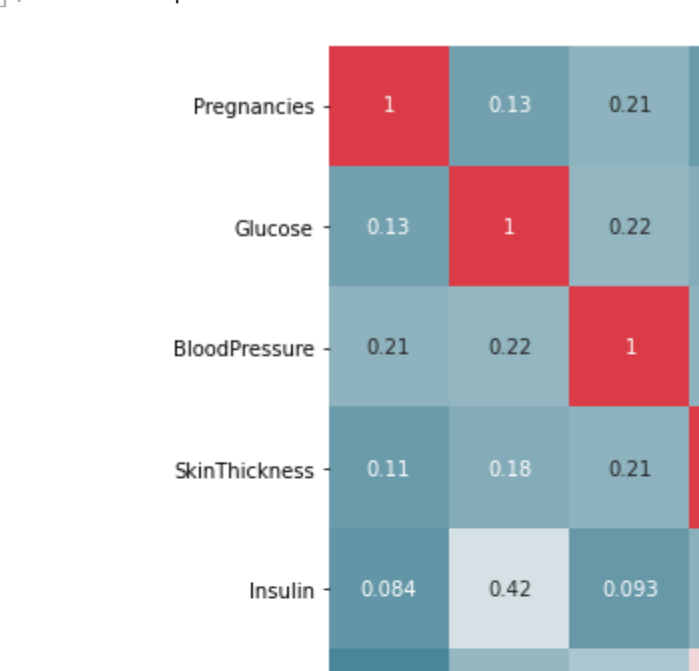
In [20]:
```python
# Lets start by understanding the distribution diabitic Vs Non Diabitic patients in the data set.

sns.countplot(data['Outcome'])
```

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

Out[20]:
```
<AxesSubplot:xlabel='Outcome', ylabel='count'>
```



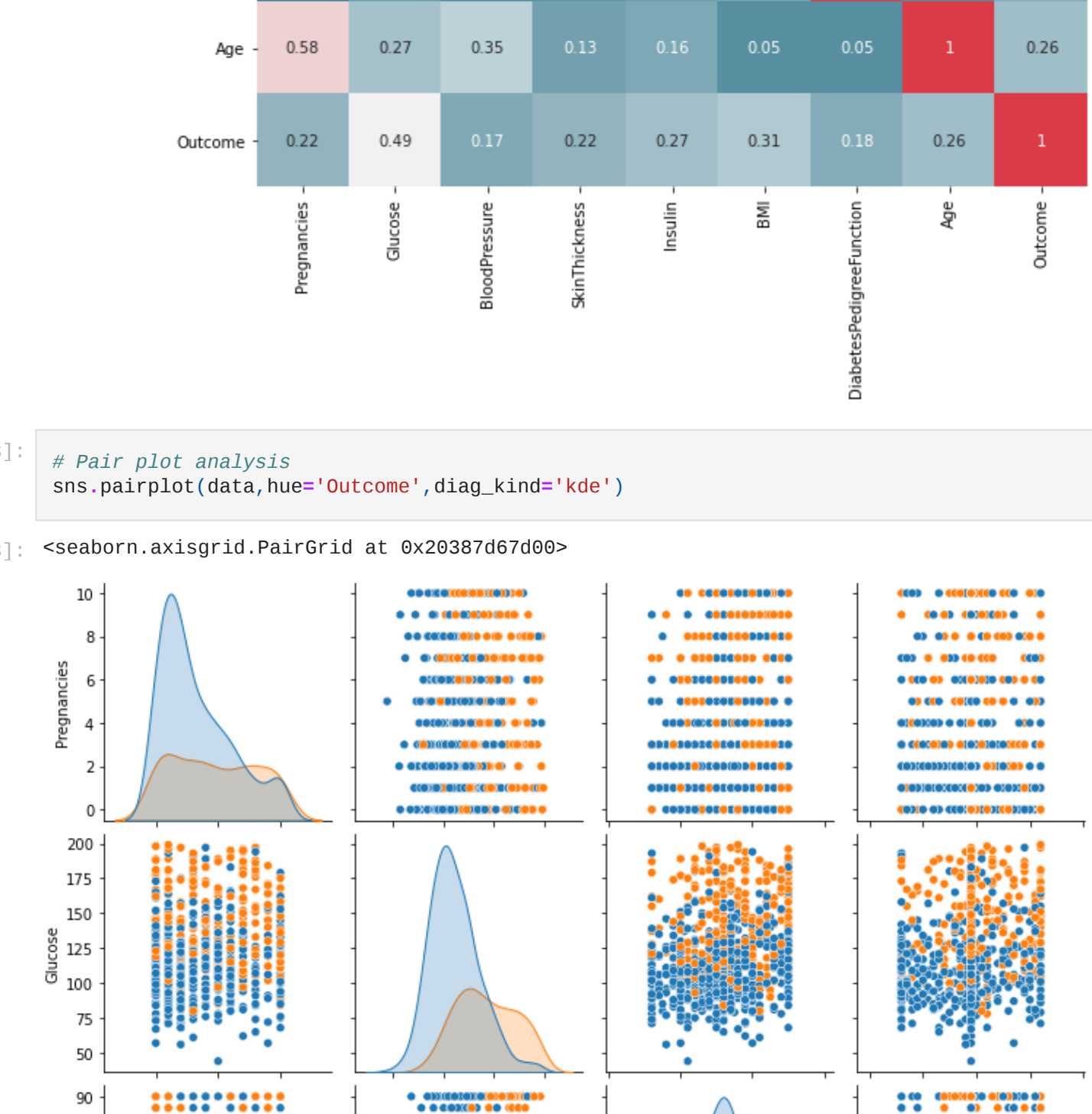
In [21]:
```python
total=float(len(data))
ax = sns.countplot(x="Outcome", data=data)
for p in ax.patches:
    height = p.get_height()
    ax.text(p.get_x()+p.get_width()/2.,
            height + 3,
            '{0:.0%}'.format(height/total),
            ha="center")
```



In [22]:
```python
f, ax = plt.subplots(figsize=(20, 10))
corr = data.corr("pearson")
sns.heatmap(corr, mask=np.zeros_like(corr, dtype=np.bool), cmap=sns.diverging_palette(220, 10, as_cmap=True),
            square=True, ax=ax,annot=True)
```

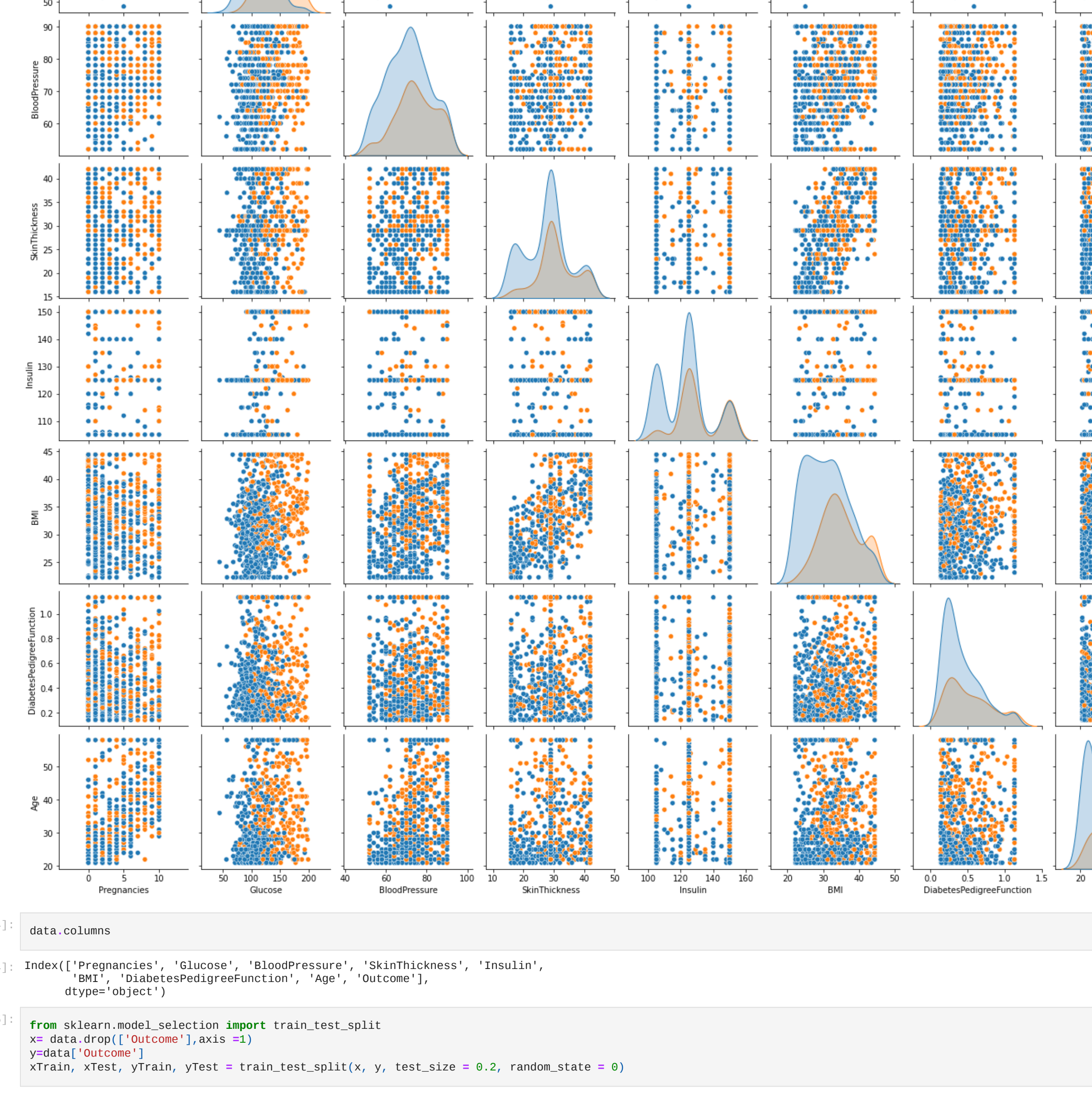
```
<ipython-input-22-24a80e48906b>:3: DeprecationWarning: `np.bool` is a deprecated alias for the builtin `bool`. To silence this warning, use `bool` by itself. Doing this will not mo
dify any behavior and is safe. If you specifically wanted the numpy scalar type, use `np.bool_` here.
Deprecated in NumPy 1.20; for more details and guidance: https://numpy.org/devdocs/release/1.20.0-notes.html#deprecations
  sns.heatmap(corr, mask=np.zeros_like(corr, dtype=np.bool), cmap=sns.diverging_palette(220, 10, as_cmap=True),
```

Out[22]:
```
<AxesSubplot:>
```



In [23]:
```python
# Pair plot analysis
sns.pairplot(data,hue='Outcome',diag_kind='kde')
```

Out[23]:
```
<seaborn.axisgrid.PairGrid at 0x20387d67d00>
```



In [24]:
```python
data.columns
```

Out[24]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

In [25]:
```python
from sklearn.model_selection import train_test_split
x= data.drop(['Outcome'],axis =1)
y=data['Outcome']
xTrain, xTest, yTrain, yTest = train_test_split(x, y, test_size = 0.2, random_state = 0)
```

In [26]:
```python
from sklearn.naive_bayes import GaussianNB

#Create a Gaussian Classifier
model = GaussianNB()
```

In [27]:
```python
model.fit(xTrain,yTrain)
```

Out[27]:
```
GaussianNB()
```

In [28]:
```python
predicted= model.predict(xTest)
```

In [29]:
```python
print("Predicted Value:", predicted)
```

```
Predicted Value: [1 0 0 1 0 0 1 1 0 1 1 1 0 0 0 0 1 0 1 0 1 0 0 0 0 0 0 1 0 0 1 0 0 1 0 1 1
 0 0 1 0 0 0 1 1 0 0 0 0 0 0 0 1 1 0 0 0 0 0 0 1 1 0 1 1 1 1 0 0 0 0 0 0 1
 1 0 0 1 0 0 0 1 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 1 1 0 1 0 0 0 1 0 0 0 0 1 0
 1 1 1 1 1 0 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 1 0 1 0 0 0 0 0 1 0 0 0 0 0 0
 0 0 0 1 0 0]
```

In [30]:
```python
from sklearn import metrics

# Model Accuracy, how often is the classifier correct?
print("Accuracy:",metrics.accuracy_score(yTest, predicted))
```

```
Accuracy: 0.7792207792207793
```

In [ ]: