dia

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# 1 Diabetes Prediction on Pima Indians Diabetes Database using Naive Bayes

The Pima Indian Diabetes Database is from National Institute of Diabetes and Digestive and Kidney Diseases. It consists of nine variables, out of which 'outcome' is the target variable. The objective of this dataset is to aid in predicting if a person is likely to have Diabetes or not.

Data Desription

Predictor Variables

1. Preganancies - Number of times the patient got pregnant
2. Glucose - Plasma glucose concentration
3. Blood Preassure - Diastolic Blood Preassure (mmHg)
4. Skin Thickness - Triceps skin fold thickness (mm)
5. Insulin - 2-Hour serum insulin (mu U/ml)
6. BMI: Body mass index (weight in kg/(height in m)^2)
7. DiabetesPedigreeFunction: Diabetes pedigree function
8. Age: Age (years)
9. Outcome: Class variable (0 or 1)

[4]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

[5]:
```
data = pd.read_csv('diabetes.csv')
```

[6]:
```
data.head()
```

[6]:
```
   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
```

[7]:
```
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
```

[8]:
```
data.shape
```

[8]:
```
(768, 9)
```

## 1.1 Missing Value Detection and Treatment

The following values in a data set are considered to be missing values -

1. Blank Values
2. NaN
3. null
4. Some countinuous columns might have 0's to indicate missing data.

[9]:
```
data.isnull()
```

[9]:
```
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin    BMI  \
0          False    False          False          False    False  False
1          False    False          False          False    False  False
2          False    False          False          False    False  False
3          False    False          False          False    False  False
4          False    False          False          False    False  False
..           …        …            …              …        …      …
763        False    False          False          False    False  False
764        False    False          False          False    False  False
```

```
765        False     False           False           False     False  False
766        False     False           False           False     False  False
767        False     False           False           False     False  False

     DiabetesPedigreeFunction    Age  Outcome
0                       False  False    False
1                       False  False    False
2                       False  False    False
3                       False  False    False
4                       False  False    False
..                        ...    ...      ...
763                     False  False    False
764                     False  False    False
765                     False  False    False
766                     False  False    False
767                     False  False    False

[768 rows x 9 columns]
```

[10]:
```
data.isnull().sum()
```

[10]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

[11]:
```
data.describe()
```

[11]:
```
       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
```

From the above description of the data, we can see that columns - Pregnancies, Glucose, Blood Preassure, Skin Thickness, Insulin and BMI have minimum values of 0. It makes sense to have 0 prgnancies, but the it does not make sense for other mentioned variables to have a minimum value of 0. So we can conclude that Glucose, Blood Preassure, Skin Thickness, Insulin and BMI have missing data. The 0's in these columns should be replaced with the median, since the median is least affected by outliers.

[12]:
```
from numpy import nan
data['Glucose'] = data['Glucose'].replace(0,np.nan)
data['BMI'] = data['BMI'].replace(0,np.nan)
data['SkinThickness'] = data['SkinThickness'].replace(0,np.nan)
data['BloodPressure'] = data['BloodPressure'].replace(0,np.nan)
data['Insulin'] = data['Insulin'].replace(0,np.nan)
```

[13]:
```
data.head()
```

[13]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6    148.0           72.0           35.0      NaN  33.6
1            1     85.0           66.0           29.0      NaN  26.6
2            8    183.0           64.0            NaN      NaN  23.3
3            1     89.0           66.0           23.0     94.0  28.1
4            0    137.0           40.0           35.0    168.0  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
```

[14]:
```
data.isnull().sum()
```

[14]:
```
Pregnancies                   0
Glucose                       5
BloodPressure                35
SkinThickness               227
Insulin                     374
BMI                          11
DiabetesPedigreeFunction      0
Age                           0
```

```
Outcome                     0
dtype: int64
```

[15]:
```
data.median()
```

[15]:
```
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
```

[16]:
```
data.fillna(data.median(), inplace=True)
```

[17]:
```
data.isnull().sum()
```

[17]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

## 1.2 Outlier Detection and treatment

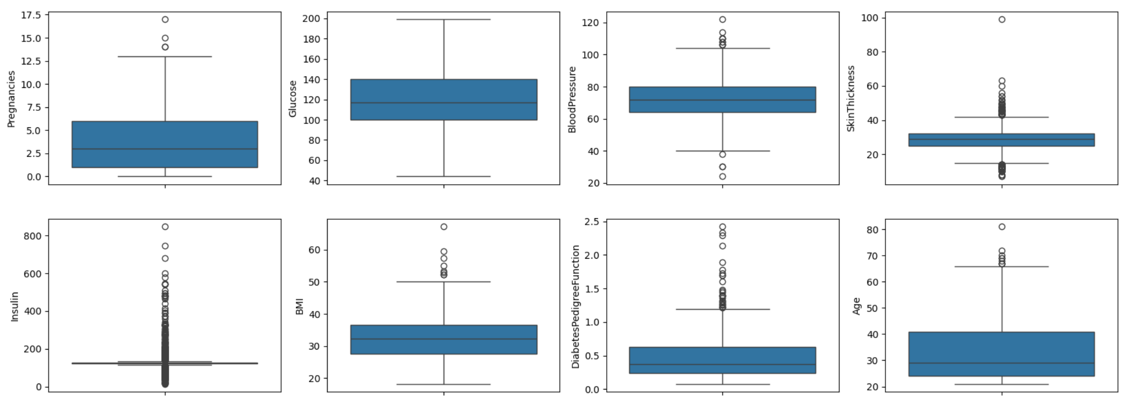
Outlier Detection

Boxplots are a great way of detecting outliers. Once the outliers have been detected, they can be imputed with the 5th and 95th percentiles.

[18]:
```
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'])
```

[18]:
```
<Axes: ylabel='Age'>
```



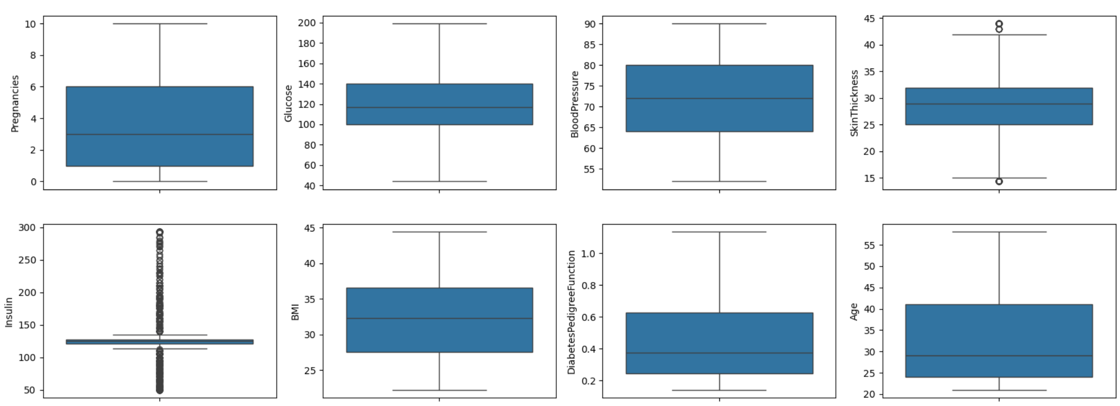

Apart from 'Glucose' all the other attributes show preasence of outliers. These lower level and upper level outliers will be replaced by the 5th and 95th percentile respectively.

[19]:
```
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))
```

[20]:
```
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'])
```

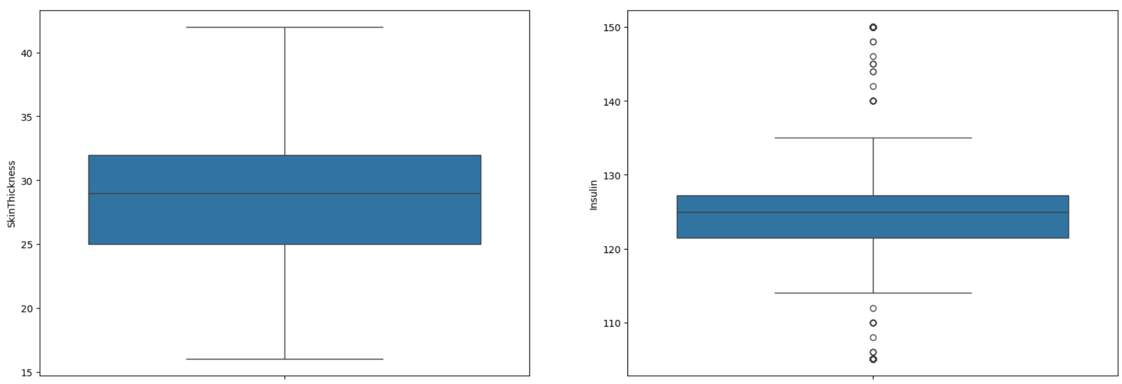
[20]:
```
<Axes: ylabel='Age'>
```




[21]:
```
# 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'])
```

[21]: <Axes: ylabel='Insulin'>



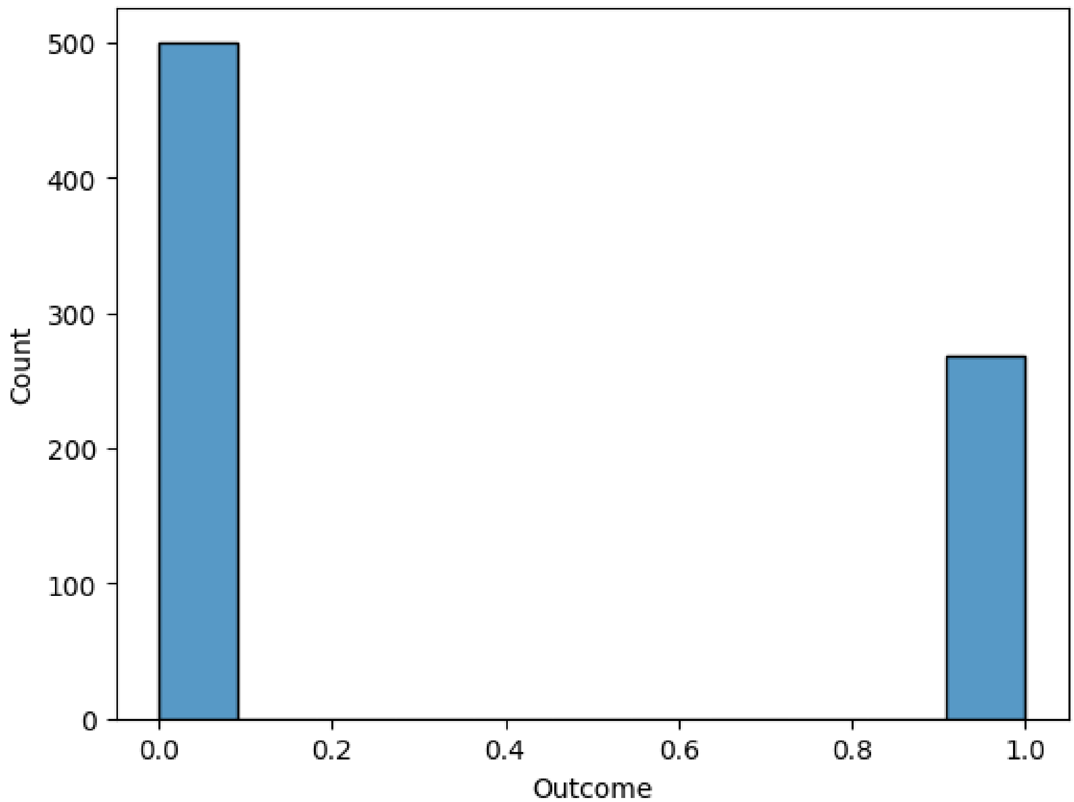

The outliers of Skin Thickness were treated by minor changes in the percentiles but the outliers of insulin require a major changes in the percentiles. This might result in too much data manipulation, which migh jepordise the models.

Attribute Insulin might have to be removed from the data set.

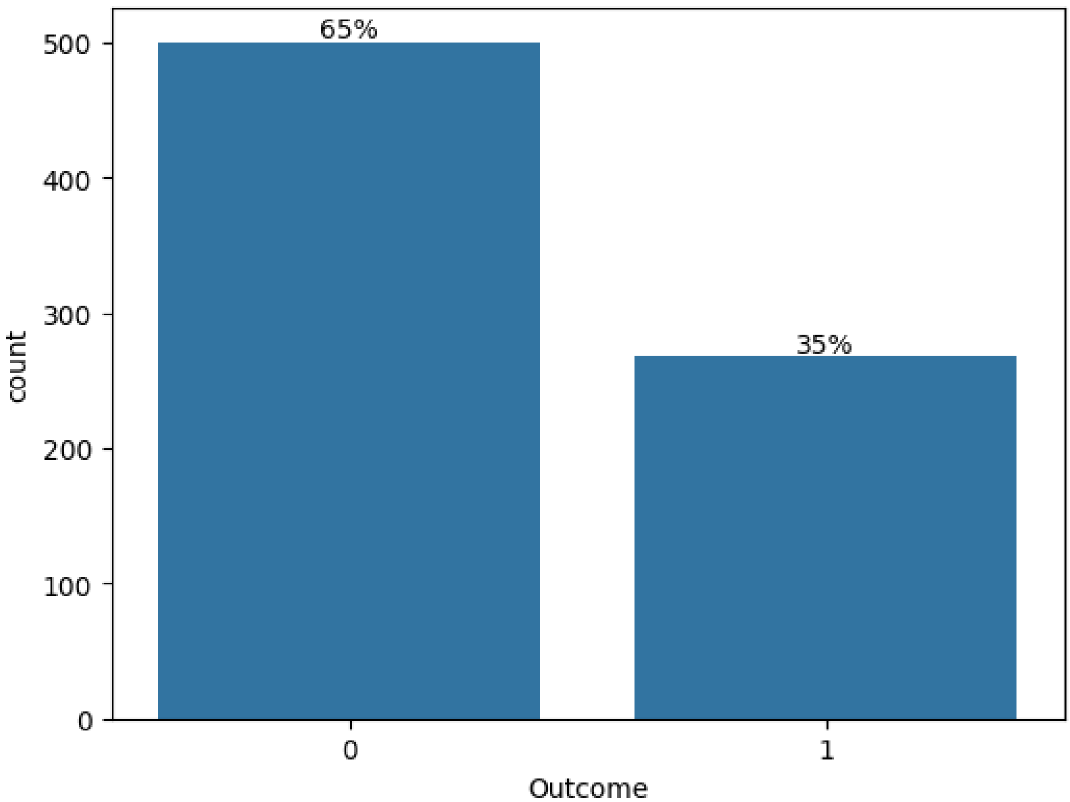
### 1.3 Data visualization

[27]:
```
sns.histplot(data['Outcome'])
```

[27]: <Axes: xlabel='Outcome', ylabel='Count'>




[24]:
```
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")
```

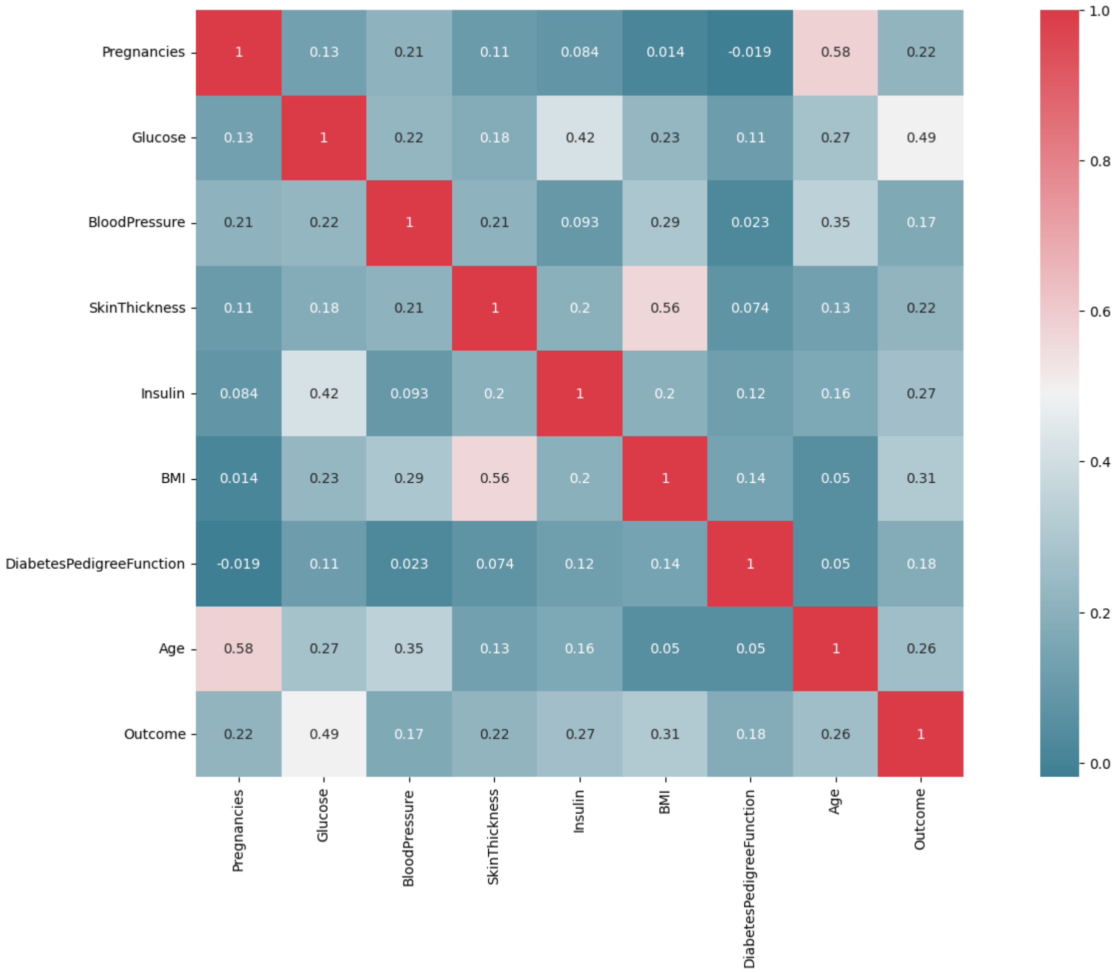



About 65% of the data contains records belonging to Non Diabetic Patients. The data set has a class imbalance and might have to be treated in future, during the model building stages.

Lets now plot a corr-plot (correlation plot). This plot will help us understand if there is multi colinearity in the data set.

[29]:
```
f, ax = plt.subplots(figsize=(20, 10))
corr = data.corr("pearson")
sns.heatmap(corr, mask=np.zeros_like(corr, dtype=bool), cmap=sns.
 ↪diverging_palette(220, 10, as_cmap=True),
            square=True, ax=ax,annot=True)
```

[29]: <Axes: >




From the above corr-plot, it can be identified that there is no high multi-colinearity in the data set.

[30]:
```python
# Pair plot analysis
sns.pairplot(data,hue='Outcome',diag_kind='kde')
```

[30]: <seaborn.axisgrid.PairGrid at 0x2620af05d90>


From the above pairplot, we can infer that most of the predictor variables are weak predictors of Outcome. The kernal density plots (diagonal) suggests that the distribution for diabetic and non diabetic are very similar and are overlapping each other significantly, hence they wont be able to differentiate between a diabetic patient and a non diabetic patient.

The scatterplots also suggest very poorly corelated data (data with not hidden patterns or relationships). Hence models built on this data might not be able to identify any hidden patterns or might identify nonsense patterns i.e. patterns that do not make sense.

[31]:
```
data.columns
```

[31]:
```
Index(['Pregnancies', 'Glucose', 'BloodPressure', 'SkinThickness', 'Insulin',
       'BMI', 'DiabetesPedigreeFunction', 'Age', 'Outcome'],
      dtype='object')
```

[32]:
```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)
```

[33]:
```python
from sklearn.naive_bayes import GaussianNB

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

[34]:
```python
model.fit(xTrain,yTrain)
```

[34]:
```
GaussianNB()
```

[35]:
```python
predicted= model.predict(xTest)
```

[36]:
```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]
```

[37]:
```python
from sklearn import metrics

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

```
Accuracy: 0.7792207792207793
```

By the Above accuracy score we can say that the prediction model bulit has good accuracy in predicting the diabetic Vs non diaetic.