Diabetes Prediction

About the dataset

This dataset is originally from the National Institute of Diabetes and Digestive and Kidney Diseases. The objective is to predict based on diagnostic measurements whether a patient has diabetes

1) Pregnancies : Number of times pregnant

2) Glucose : Plasma glucose concentration a 2 hour in an oral glucose tolerance test

3) Blood Pressure : Diastolic Blood pressure (mm Hg)

4) SkinThickness : Triceps skin fold thickness(mm)

5) Insulin : 2-hour serum insulin (mu U/ml)

6) DiabetesPedigreeFunction : Diabetes Pedigree Function

7) Age : Age

8) Outcome : 1 - Diabetes, 0 - No diabetes

In [1]:
```
# import needed libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import warnings
warnings.filterwarnings('ignore')
from sklearn.model_selection import train_test_split,GridSearchCV
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report,confusion_matrix
```

In [2]:
```
# Read the dataset with pandas
dia_df = pd.read_csv('diabetes.csv')
dia_df.head()
```

Out[2]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	A
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	
4	0	137	40	35	168	43.1	2.288	

In [3]:
```
# Get the quick info about dataset
dia_df.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 [4]:
```
# Disripition of data set
dia_df.describe()
```

Out[4]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPe
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	

Data Preprocessing

In [5]:
```
# Seeking the null values
dia_df.isnull().sum()
```

Out[5]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [6]:
```
dia_df.nunique()
```

Out[6]:
```
Pregnancies                 17
Glucose                    136
BloodPressure               47
SkinThickness               51
Insulin                    186
BMI                        248
DiabetesPedigreeFunction   517
Age                         52
Outcome                      2
dtype: int64
```

In [7]:
```
# detecting the number of rows that contains 0 in Insulin cloumn
(dia_df[dia_df.Insulin==0])
```

Out[7]:

	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
5	5	116	74	0	0	25.6	0.201
7	10	115	0	0	0	35.3	0.134
...	...	...	...	...	...	...	...
761	9	170	74	31	0	44.0	0.403
762	9	89	62	0	0	22.5	0.142
764	2	122	70	27	0	36.8	0.340
766	1	126	60	0	0	30.1	0.349
767	1	93	70	31	0	30.4	0.315

374 rows × 9 columns

In [8]:
```
# Imputing the value with mean value
dia_df.Insulin.replace(to_replace=0,value=dia_df.Insulin.mean(),inplace=True)
```

In [9]:
```
# detecting the number of rows that contains 0 in Skin Thickness cloumn
dia_df[dia_df['SkinThickness']==0]
```

Out[9]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctic
2	8	183	64	0	79.799479	23.3	0.6
5	5	116	74	0	79.799479	25.6	0.2
7	10	115	0	0	79.799479	35.3	0.1
9	8	125	96	0	79.799479	0.0	0.2
10	4	110	92	0	79.799479	37.6	0.1
...	...	...	...	...	...	...	
757	0	123	72	0	79.799479	36.3	0.2
758	1	106	76	0	79.799479	37.5	0.1
759	6	190	92	0	79.799479	35.5	0.2
762	9	89	62	0	79.799479	22.5	0.1
766	1	126	60	0	79.799479	30.1	0.3

227 rows × 9 columns

In [10]:
```
# Imputing the value with mean value
dia_df.SkinThickness.replace(to_replace=0,value=dia_df.SkinThickness.mean(),inplac
```

In [11]:
```
# detecting the number of rows that contains 0 in  cloumn
dia_df[dia_df['BMI']==0]
```

Out[11]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctic
9	8	125	96	20.536458	79.799479	0.0	0.2
49	7	105	0	20.536458	79.799479	0.0	0.3
60	2	84	0	20.536458	79.799479	0.0	0.3
81	2	74	0	20.536458	79.799479	0.0	0.1
145	0	102	75	23.000000	79.799479	0.0	0.5
371	0	118	64	23.000000	89.000000	0.0	1.7
426	0	94	0	20.536458	79.799479	0.0	0.2
494	3	80	0	20.536458	79.799479	0.0	0.1
522	6	114	0	20.536458	79.799479	0.0	0.1
684	5	136	82	20.536458	79.799479	0.0	0.6
706	10	115	0	20.536458	79.799479	0.0	0.2

In [12]:
```
# Imputing the value with mean value
dia_df['BMI'].replace(to_replace=0,value=dia_df['BMI'].mean(),inplace=True)
```

Detecting and removing the outliers

```
q3 = dia_df.BloodPressure.quantile(0.75)
```

In [14]:
```
IQR = q3-q1
upper = q3+1.5*IQR
lower = q1-1.5*IQR
```

In [15]:
```
upper,lower
```

Out[15]:
```
(107.0, 35.0)
```

In [16]:
```
dia_df = dia_df[(dia_df.BloodPressure>lower)&(dia_df.BloodPressure<upper)]
```

In [17]:
```
dia_df
```

Out[17]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunct
0	6	148	72	35.000000	79.799479	33.6	0.
1	1	85	66	29.000000	79.799479	26.6	0.
2	8	183	64	20.536458	79.799479	23.3	0.
3	1	89	66	23.000000	94.000000	28.1	0.
4	0	137	40	35.000000	168.000000	43.1	2.
...	...	...	...	...	...	...	
763	10	101	76	48.000000	180.000000	32.9	0.
764	2	122	70	27.000000	79.799479	36.8	0.
765	5	121	72	23.000000	112.000000	26.2	0.
766	1	126	60	20.536458	79.799479	30.1	0.
767	1	93	70	31.000000	79.799479	30.4	0.

723 rows × 9 columns

In [18]:
```
# removing outliers in glucose cloumn using IQR
q1=dia_df.Glucose.quantile(0.25)
q3=dia_df.Glucose.quantile(0.75)
```

In [19]:
```
IQR = q3-q1
upper,lower = q3+1.5*IQR, q1-1.5*IQR
upper,lower
```

Out[19]:
```
(204.0, 36.0)
```

In [20]:
```
dia_df = dia_df[(dia_df.Glucose>lower)&(dia_df.Glucose<upper)]
```

In [21]:
```
dia_df
```

Out[21]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunct
0	6	148	72	35.000000	79.799479	33.6	0.
1	1	85	66	29.000000	79.799479	26.6	0.
2	8	183	64	20.536458	79.799479	23.3	0.
3	1	89	66	23.000000	94.000000	28.1	0.
4	0	137	40	35.000000	168.000000	43.1	2.
...	...	...	...	...	...	...	
763	10	101	76	48.000000	180.000000	32.9	0.
764	2	122	70	27.000000	79.799479	36.8	0.
765	5	121	72	23.000000	112.000000	26.2	0.
766	1	126	60	20.536458	79.799479	30.1	0.
767	1	93	70	31.000000	79.799479	30.4	0.

718 rows × 9 columns

Exploratory Data Analysis

Distribution of variables

In [22]:
```
dia_df.head()
```

Out[22]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
0	6	148	72	35.000000	79.799479	33.6	0.62
1	1	85	66	29.000000	79.799479	26.6	0.35
2	8	183	64	20.536458	79.799479	23.3	0.67
3	1	89	66	23.000000	94.000000	28.1	0.16
4	0	137	40	35.000000	168.000000	43.1	2.28

In [23]:
```
fig, ax = plt.subplots(1,3,figsize=(19,6))
sns.histplot(dia_df.Pregnancies,ax=ax[0])
sns.distplot(dia_df.Glucose,ax=ax[1])
sns.histplot(dia_df.BloodPressure,ax=ax[2])
```

Out[23]:
```
<Axes: xlabel='BloodPressure', ylabel='Count'>
```

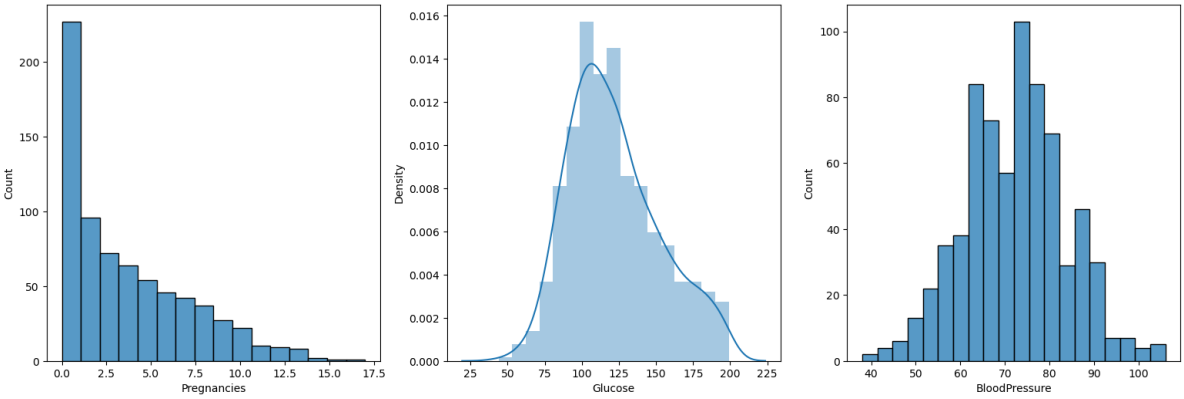


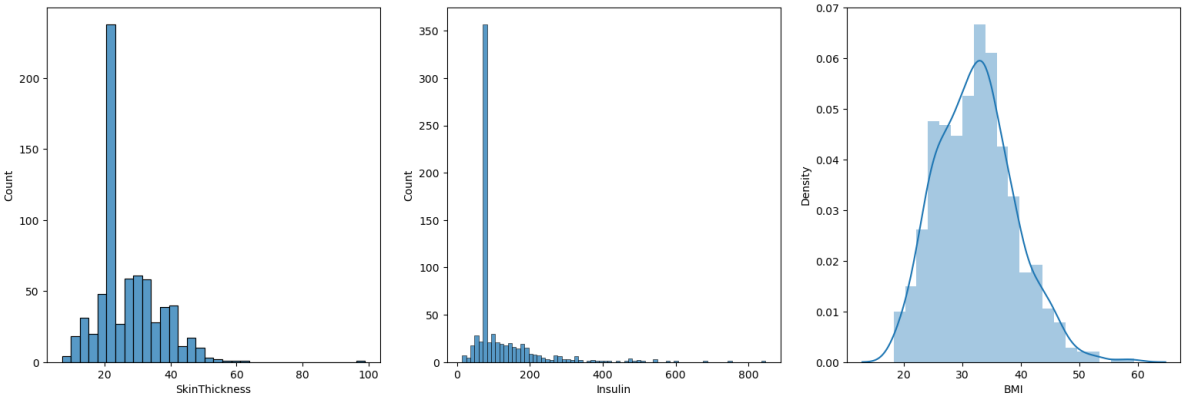
Chart 1 illustrates number of pregnancies. Many of the females don't get pregnant or atleast one

Chart 2 Demonstrates glucose level of the patients. Most of the patients have glucose level range between 80 to 130

Chart 3 describes the boold pressure of the patients. Most of the patients have blood pressure range between 65 to 80 mmHg

In [24]:
```
fig, ax = plt.subplots(1,3,figsize=(19,6))
sns.histplot(dia_df.SkinThickness,ax=ax[0])
sns.histplot(dia_df.Insulin,ax=ax[1])
sns.distplot(dia_df.BMI,ax=ax[2])
```

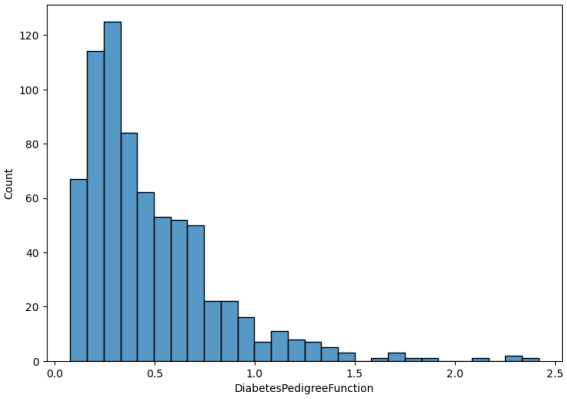
Out[24]:
```
<Axes: xlabel='BMI', ylabel='Density'>
```

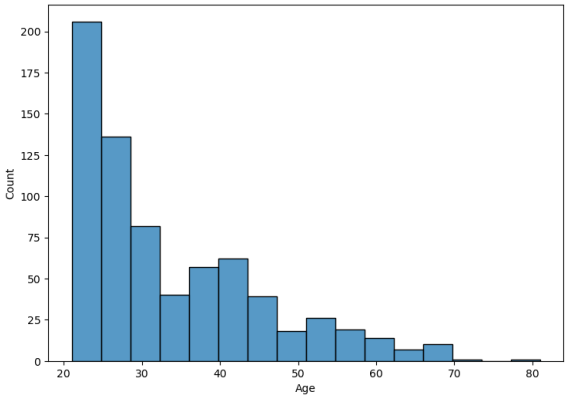


These charts demonstrates the distribution of skin thickness, insulin, BMI of the patients respectively. Most of the patients have the skin thickness 20, insulin range between 0 to 200 and BMI range between 25 to 37.

In [25]:
```
fig, ax = plt.subplots(1,2,figsize=(19,6))
sns.histplot(dia_df.DiabetesPedigreeFunction,ax=ax[0])
sns.histplot(dia_df.Age,ax=ax[1])
```

Out[25]:
```
<Axes: xlabel='Age', ylabel='Count'>
```

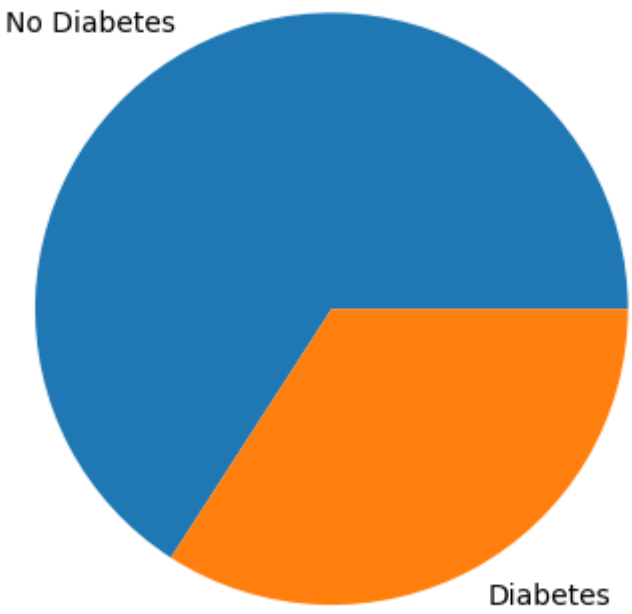




These charts demonstrates the distribution of Diabetes pedigree function, Age, result of having diabetes of the patients respectively. Most of the patients have the Diabetes pedigree function range between 0 to 0.5, age range between 21 to 30.

In [26]:
```
plt.pie(x=dia_df['Outcome'].value_counts(),labels=['No Diabetes','Diabetes'])
```

Out[26]:
```
([<matplotlib.patches.Wedge at 0x2822f75c610>,
  <matplotlib.patches.Wedge at 0x2822f75c550>],
 [Text(-0.5262135668456065, 0.9659706424460448, 'No Diabetes'),
  Text(0.5262135668456059, -0.9659706424460451, 'Diabetes')])
```

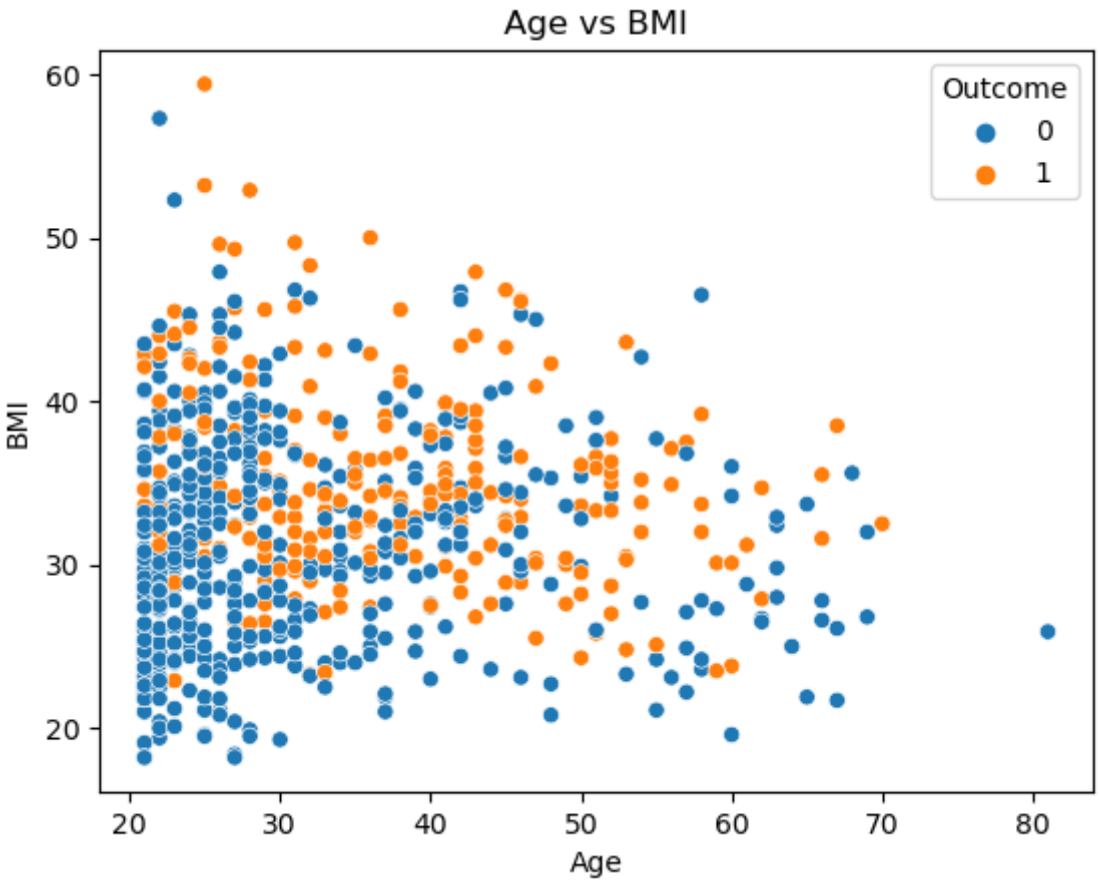


Most of the females don't have diabetes.

Relationship with target variable

In [27]:
```
sns.scatterplot(x='Age',y='BMI',data=dia_df,hue='Outcome').set(title='Age vs BMI')
```

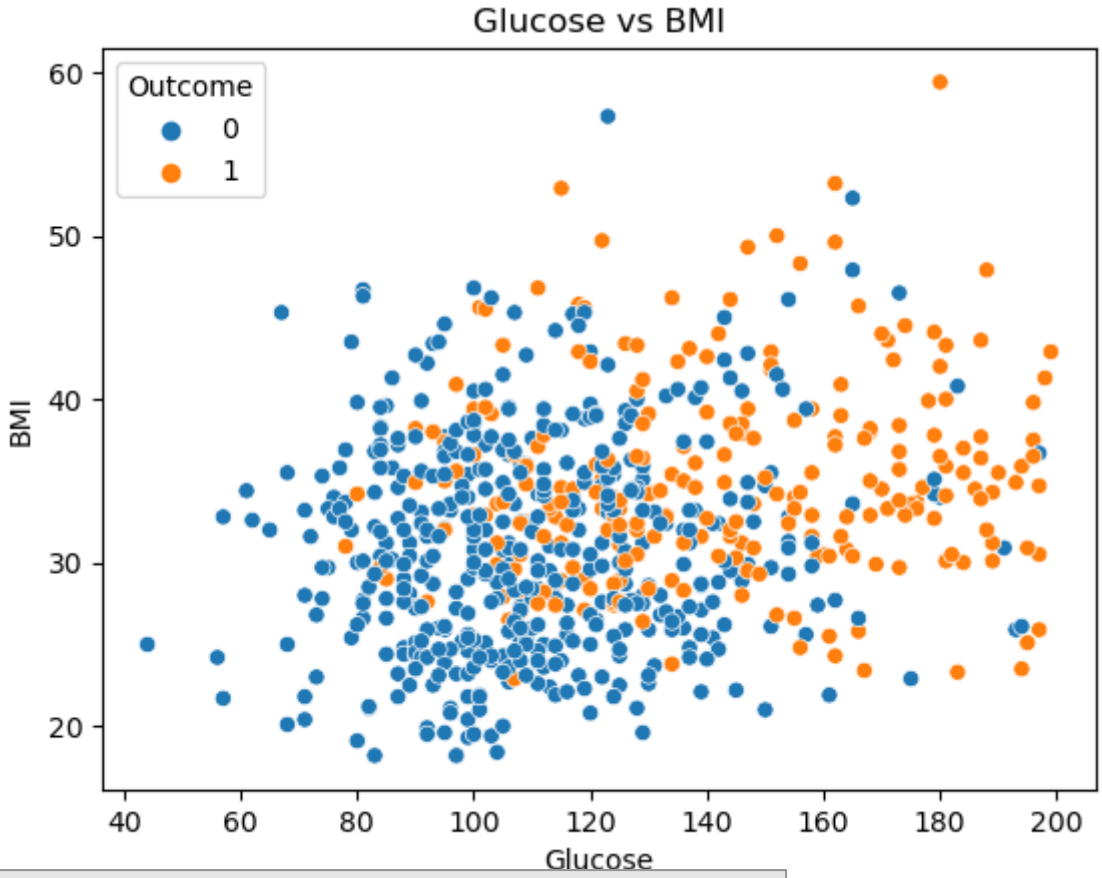
Out[27]:
```
[Text(0.5, 1.0, 'Age vs BMI')]
```



In this plot we can know lower the BMI lower the risk of diabetes.

In [28]:
```
sns.scatterplot(x='Glucose',y='BMI',data=dia_df,hue='Outcome').set(title='Glucose
```

Out[28]:
```
[Text(0.5, 1.0, 'Glucose vs BMI')]
```

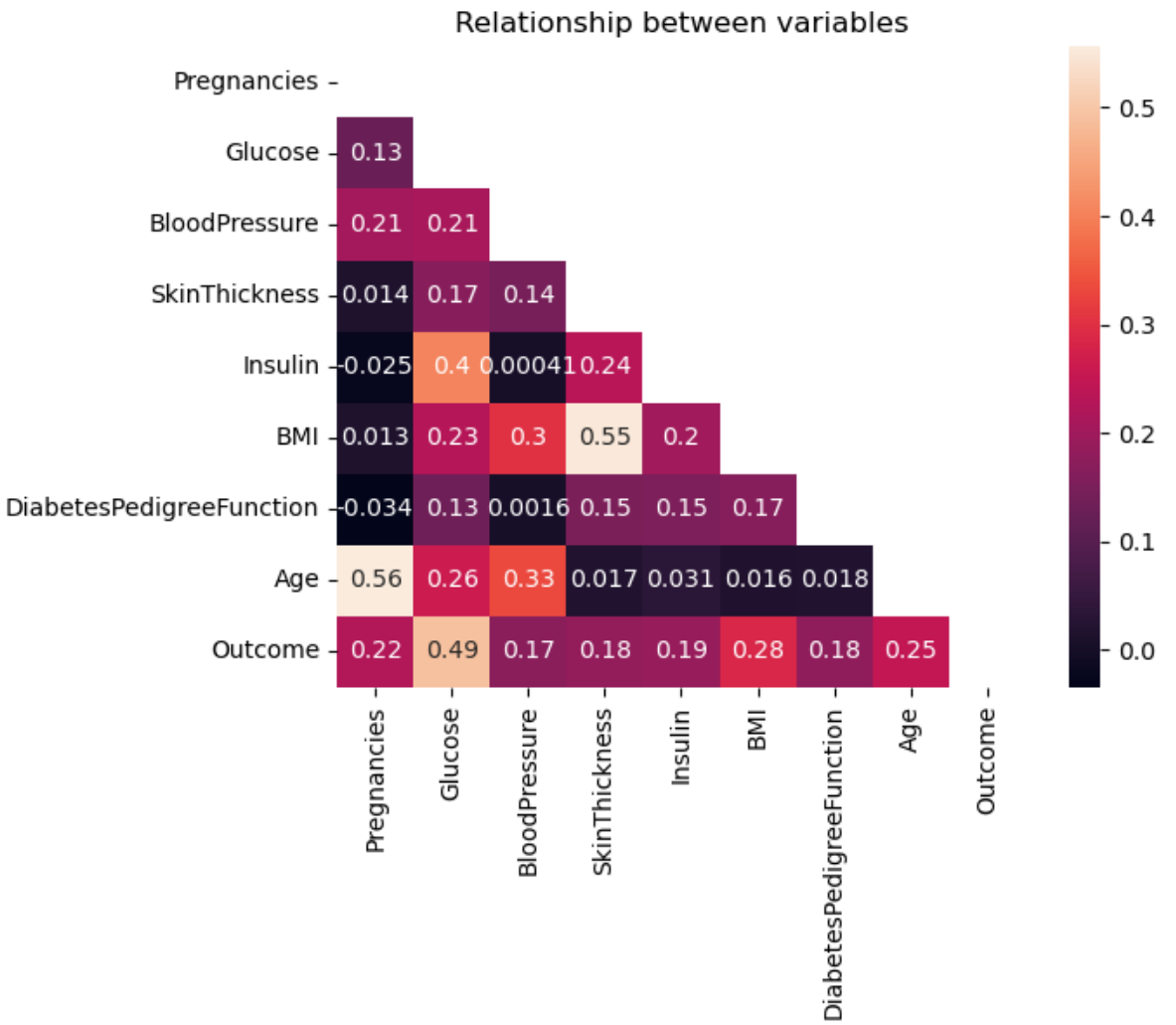


This Chart clearly shows glucose level strongly affects the outcome of diabetes

Heatmap

In [29]:
```
sns.heatmap(dia_df.corr(),annot = True,
            mask = np.triu(np.ones_like(dia_df.corr()))).set(title='Relationship be
```

Out[29]:
```
[Text(0.5, 1.0, 'Relationship between variables')]
```



Model Building

In [30]:
```
# Seprate the target variable
x = dia_df.drop('Outcome',axis=1)
y = dia_df.Outcome
```

In [31]:
```
# train test split
x_train,x_test,y_train,y_test = train_test_split(x,y,test_size=0.2,random_state=42
x_train.shape
```

Out[31]:
```
(574, 8)
```

Models to be used 1) Decision Tree Classifier 2) Random Forest Classifier

Decision Tree Classifier

In [32]:
```
DTC = DecisionTreeClassifier()
```

In [33]:
```
# parameters needed for hyperparameter tuning
params = {
    'min_samples_leaf':[2,4,6,8,10],
    'min_samples_split':[2,4,6,8,10],
    'max_depth':[2,5,10,20],
    'criterion':['gini','entropy'],
    'random_state':[0,42]
}
```

In [34]:
```
# Grid Search CV
clf = GridSearchCV(DTC,params,cv=5)
clf.fit(x_train,y_train)
clf.best_params_
```

Out[34]:
```
{'criterion': 'entropy',
 'max_depth': 5,
 'min_samples_leaf': 4,
 'min_samples_split': 2,
 'random_state': 0}
```

In [35]:
```
# Training score
clf.best_estimator_.score(x_train,y_train)
```

Out[35]:
```
0.8101045296167247
```

In [36]:
```
# Test score
clf.best_estimator_.score(x_test,y_test)
```

Out[36]:
```
0.75
```

In [37]:
```
# Predicted values
d_pred = clf.best_estimator_.predict(x_test)
```

Random Forest Classifier

In [38]:
```
RFC = RandomForestClassifier()
```

In [39]:
```
# parameters needed for hyperparameter tuning
params = {
    'min_samples_leaf':[2,6,10],
    'min_samples_split':[10,20],
    'max_depth':[10,20],
    'criterion':['gini','entropy'],
    'random_state':[0,42]
}
```

In [40]:
```
# Grid Search CV
clf = GridSearchCV(RFC,params,cv=5)
clf.fit(x_train,y_train)
clf.best_params_
```

Out[40]:
```
{'criterion': 'gini',
 'max_depth': 20,
 'min_samples_leaf': 6,
 'min_samples_split': 20,
 'random_state': 42}
```

In [41]:
```
# Training score
clf.best_estimator_.score(x_train,y_train)
```

Out[41]:
```
0.8588850174216028
```

In [42]:
```
# Test score
clf.best_estimator_.score(x_test,y_test)
```

Out[42]:
```
0.7847222222222222
```

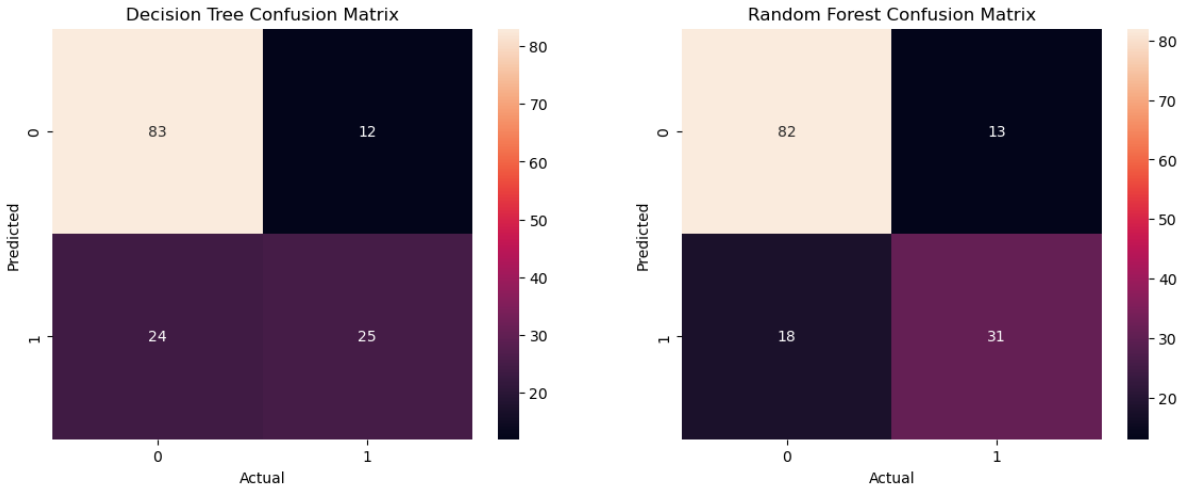
In [43]:
```
# Predicted values
r_pred = clf.best_estimator_.predict(x_test)
```

Model Evaluation

Confusion Matrix heatmap

In [52]:
```
fig,ax = plt.subplots(1,2,figsize=(14,5))
sns.heatmap(confusion_matrix(y_test,d_pred),annot=True,ax=ax[0]).set(title='Decisi
sns.heatmap(confusion_matrix(y_test,r_pred),annot=True,ax=ax[1]).set(title='Random
```

Out[52]:
```
[Text(0.5, 1.0, 'Random Forest Confusion Matrix'),
 Text(0.5, 25.722222222222214, 'Actual'),
 Text(737.5404040404039, 0.5, 'Predicted')]
```



Classification report

In [56]:
```
# Decision Tree
d = classification_report(y_test,d_pred,output_dict=True)
pd.DataFrame(d).transpose()
```

Out[56]:

	precision	recall	f1-score	support
0	0.775701	0.873684	0.821782	95.00
1	0.675676	0.510204	0.581395	49.00
accuracy	0.750000	0.750000	0.750000	0.75
macro avg	0.725688	0.691944	0.701589	144.00
weighted avg	0.741665	0.750000	0.739984	144.00

In [57]:
```
# Random Forest
r = classification_report(y_test,r_pred,output_dict=True)
pd.DataFrame(r).transpose()
```

Out[57]:

	precision	recall	f1-score	support
0	0.820000	0.863158	0.841026	95.000000
1	0.704545	0.632653	0.666667	49.000000
accuracy	0.784722	0.784722	0.784722	0.784722
macro avg	0.762273	0.747905	0.753846	144.000000
weighted avg	0.780713	0.784722	0.781695	144.000000