Data Science Capstone Project 2 - Healthcare

DESCRIPTION

Problem Statement

• NIDDK (National Institute of Diabetes and Digestive and Kidney Diseases) research creates knowledge about and treatments for the most chronic, costly, and consequential diseases.

• The dataset used in this project is originally from NIDDK. The objective is to predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset.

• Build a model to accurately predict whether the patients in the dataset have diabetes or not. Dataset Description

The datasets consist of several medical predictor variables and one target variable (Outcome). Predictor variables includes the number of pregnancies the patient has had, their BMI, insulin level, age, and more.

In [1]:
```
#Importing Required Libraries

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from matplotlib import style
import seaborn as sns
sns.set()
%matplotlib inline
import warnings
warnings.filterwarnings('ignore')
```

In [2]:
```
diabetes = pd.read_csv('health care diabetes.csv')
```

In [3]:
```
diabetes.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]:
```
diabetes.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
Pregnancies                 768 non-null int64
Glucose                     768 non-null int64
BloodPressure               768 non-null int64
SkinThickness               768 non-null int64
Insulin                     768 non-null int64
BMI                         768 non-null float64
DiabetesPedigreeFunction    768 non-null float64
Age                         768 non-null int64
Outcome                     768 non-null int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

In [5]:
```
diabetes.describe().T
```

Out[5]:

	count	mean	std	min	25%	50%	75%	max
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	99.00
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	846.00
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	67.10
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

Project Task: Week 1

Data Exploration:

1. Perform descriptive analysis. Understand the variables and their corresponding values. On the columns below, a value of zero does not make sense and thus indicates missing value:

• Glucose • BloodPressure • SkinThickness • Insulin • BMI

In [6]:
```
#copying the same dataframe
diabetes_nan= diabetes.copy(deep = True)
```

In [7]:
```
#Converting all zeros to 'NaN' or null value
diabetes_nan[['Glucose','BloodPressure','SkinThickness','Insulin','BMI']] = diabetes_nan[['Glucos
e','BloodPressure','SkinThickness','Insulin','BMI']].replace(0,np.NaN)
```

In [8]:
```
#Dataframe
diabetes_nan.head()
```

Out[8]:

	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 [9]:
```
## showing the count of NaN or Nulls
print(diabetes_nan.isnull().sum())
```

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

In [10]:
```
#Convertion of Nulls to mean value
diabetes_nan['Glucose'].fillna(diabetes_nan['Glucose'].mean(), inplace = True)
diabetes_nan['BloodPressure'].fillna(diabetes_nan['BloodPressure'].mean(), inplace = True)
diabetes_nan['SkinThickness'].fillna(diabetes_nan['SkinThickness'].median(), inplace = True)
diabetes_nan['Insulin'].fillna(diabetes_nan['Insulin'].median(), inplace = True)
diabetes_nan['BMI'].fillna(diabetes_nan['BMI'].median(), inplace = True)
```

In [11]:
```
## showing the count of Nans
print(diabetes_nan.isnull().sum())
```

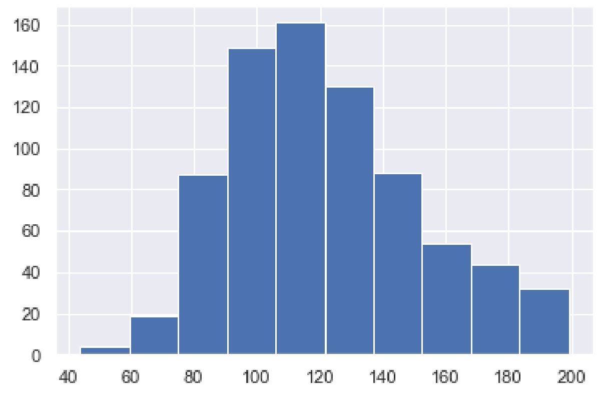
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

As value 0 doesn't make sense with 5 mentioned variables to analyze the data, we have filled the missing values with mean or average data points

2. Visually explore these variables using histograms. Treat the missing values accordingly.

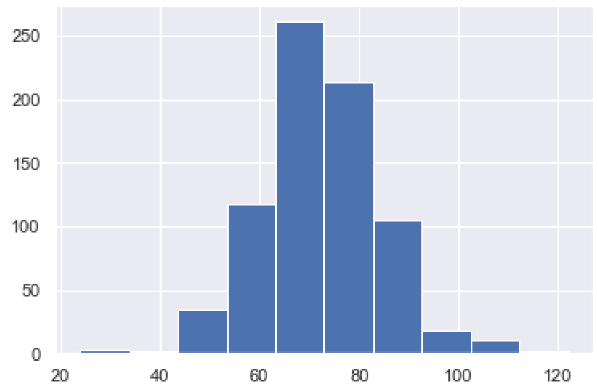
In [12]:
```
#Histogram of 'Glucose'
plt.hist(diabetes_nan['Glucose'])
```

Out[12]:
```
(array([  4.,  19.,  87., 149., 161., 130.,  88.,  54.,  44.,  32.]),
 array([ 44. ,  59.5,  75. ,  90.5, 106. , 121.5, 137. , 152.5, 168. ,
        183.5, 199. ]),
 <a list of 10 Patch objects>)
```

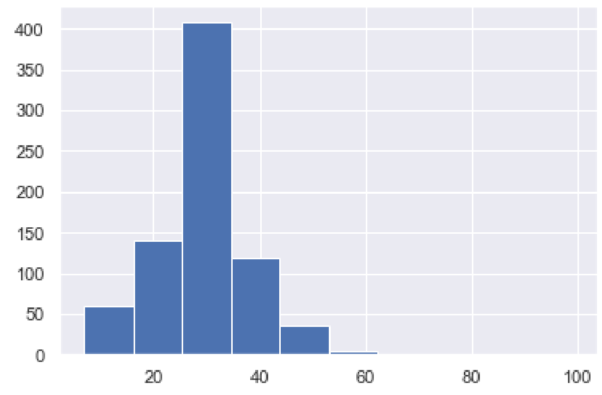


In [13]:
```
#Histogram of 'Blood Pressure'
plt.hist(diabetes_nan['BloodPressure'])
```

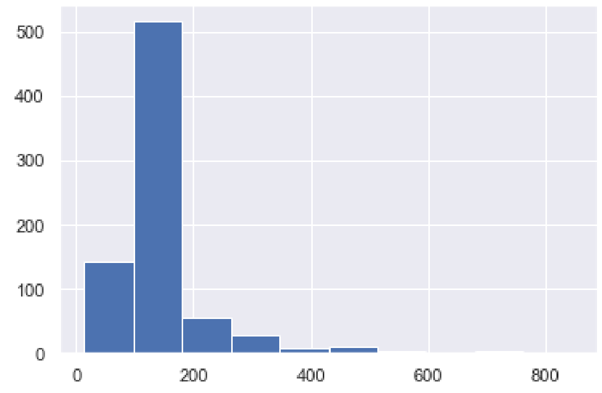
Out[13]:
```
(array([  3.,   2.,  35., 118., 261., 214., 105.,  18.,  10.,   2.]),
 array([ 24. ,  33.8,  43.6,  53.4,  63.2,  73. ,  82.8,  92.6, 102.4,
        112.2, 122. ]),
 <a list of 10 Patch objects>)
```



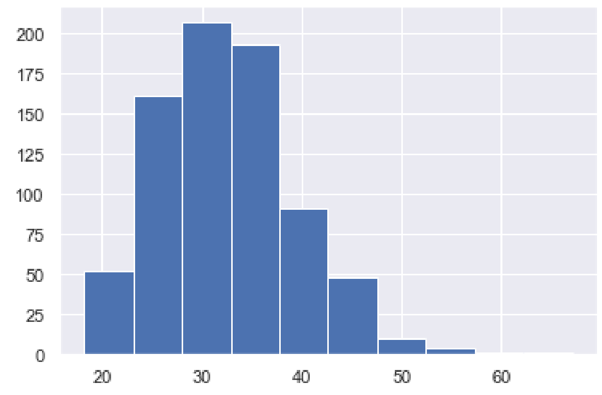
```
In [14]: #Histogram of 'Skin Thickness'
         plt.hist(diabetes_nan['SkinThickness'])

Out[14]: (array([ 59., 141., 408., 118.,  36.,   4.,   1.,   0.,   0.,   1.]),
          array([ 7. , 16.2, 25.4, 34.6, 43.8, 53. , 62.2, 71.4, 80.6, 89.8, 99. ]),
          <a list of 10 Patch objects>)
```



```
In [15]: #Histogram of 'Insulin'
         plt.hist(diabetes_nan['Insulin'])

Out[15]: (array([142., 517.,  55.,  29.,   7.,  10.,   4.,   1.,   2.,   1.]),
          array([ 14. ,  97.2, 180.4, 263.6, 346.8, 430. , 513.2, 596.4, 679.6,
                 762.8, 846. ]),
          <a list of 10 Patch objects>)
```

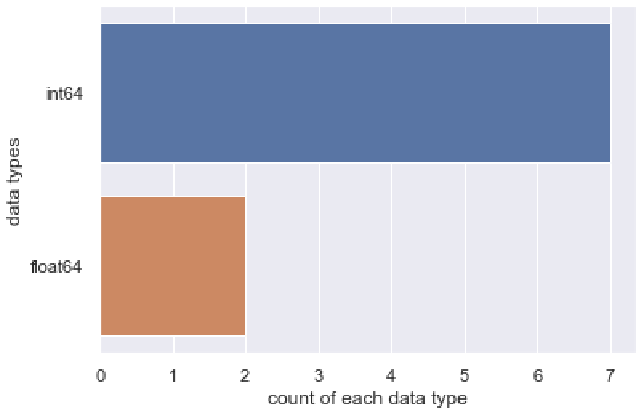


```
In [16]: #Histogram of 'BMI'
         plt.hist(diabetes_nan['BMI'])

Out[16]: (array([ 52., 161., 207., 193.,  91.,  48.,  10.,   4.,   1.,   1.]),
          array([18.2 , 23.09, 27.98, 32.87, 37.76, 42.65, 47.54, 52.43, 57.32,
                 62.21, 67.1 ]),
          <a list of 10 Patch objects>)
```



3. There are integer and float data type variables in this dataset. Create a count (frequency) plot describing the data types and the count of variables.

In [17]:
```
sns.countplot(y=diabetes.dtypes.map(str),data=diabetes)
plt.xlabel("count of each data type")
plt.ylabel("data types")
plt.show()
```



Project Task: Week 2

Data Exploration:

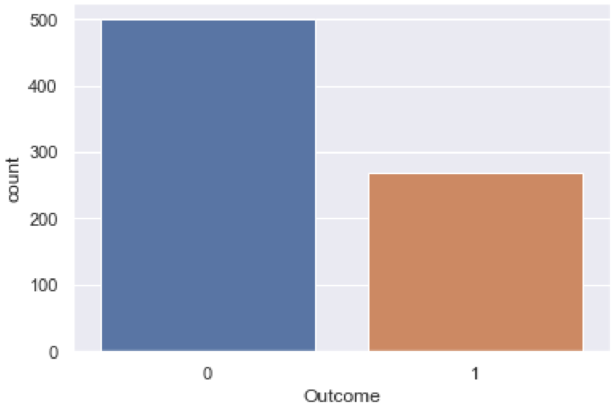
1. Check the balance of the data by plotting the count of outcomes by their value. Describe your findings and plan future course of action.

In [18]:
```
## checking the balance of the data by plotting the count of outcomes by their value
print(diabetes.Outcome.value_counts())
```

```
0    500
1    268
Name: Outcome, dtype: int64
```

In [19]:
```
sns.countplot(diabetes.Outcome)
```

Out[19]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x1ef94f9f888>
```

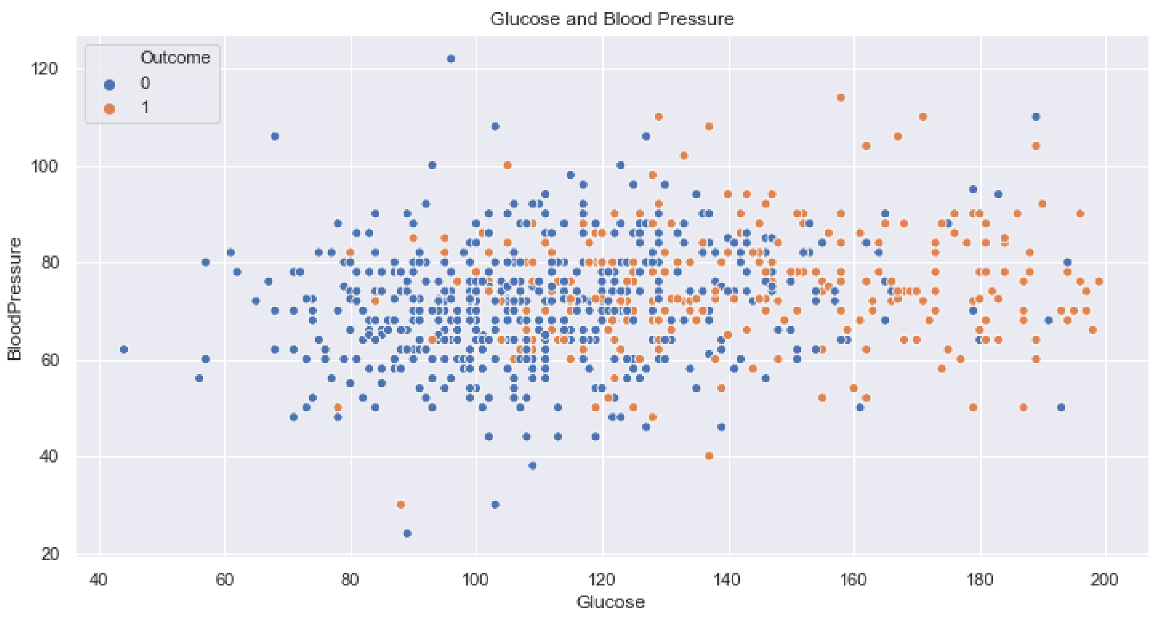


The above graph shows that the data is biased towards datapoints having outcome value as 0 where it means that diabetes was not present actually. The number of non-diabetics is almost twice the number of diabetic patients

2. Create scatter charts between the pair of variables to understand the relationships. Describe your findings.

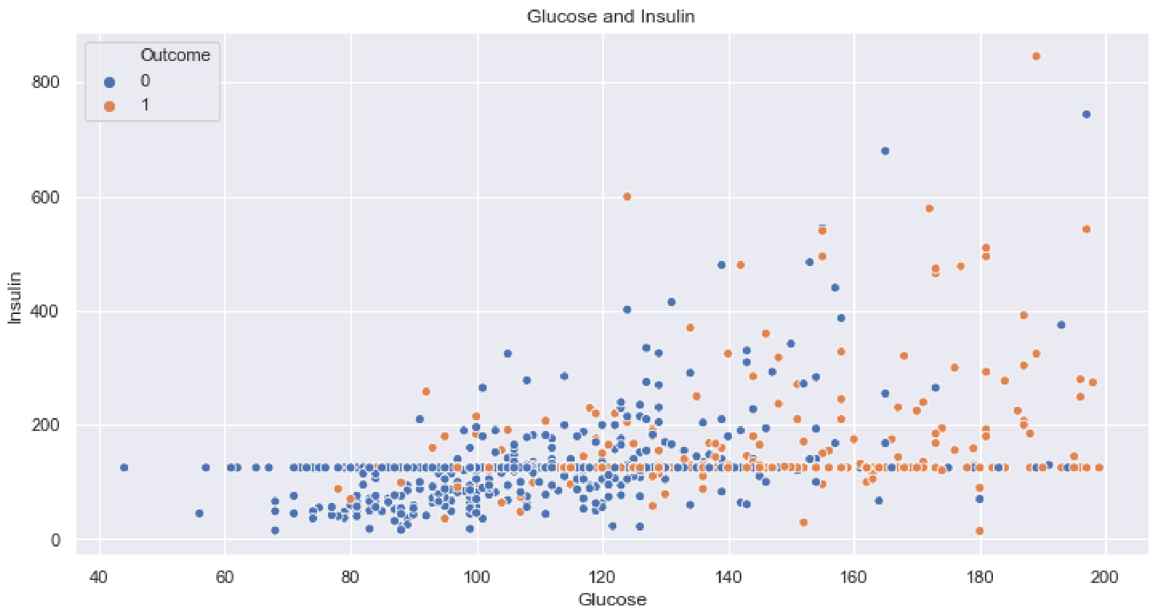
In [20]:
```
#copying the clean dataset to 'diabetes_data'
diabetes_data = diabetes_nan.copy(deep = True)
```

In [21]:
```
plt.figure(figsize= (12,6))
plt.title("Glucose and Blood Pressure")
sns.scatterplot(x= "Glucose" ,y= "BloodPressure",
               hue="Outcome",
               data=diabetes_data);
```

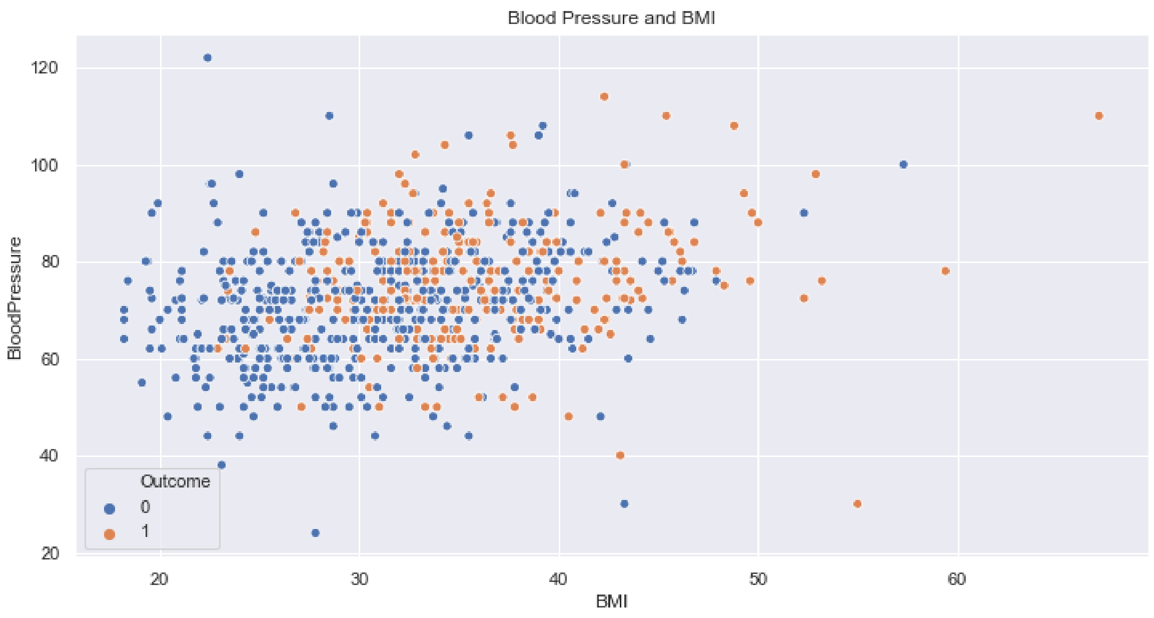


The above scatter plot between Glucose and Blood Pressure shows that Patients with high blood pressure and higher glucose level have more chances to be diabetic.

In [22]:
```
plt.figure(figsize= (12,6))
plt.title("Glucose and Insulin")
sns.scatterplot(x= "Glucose" ,y= "Insulin",
               hue="Outcome",
               data=diabetes_data);
```

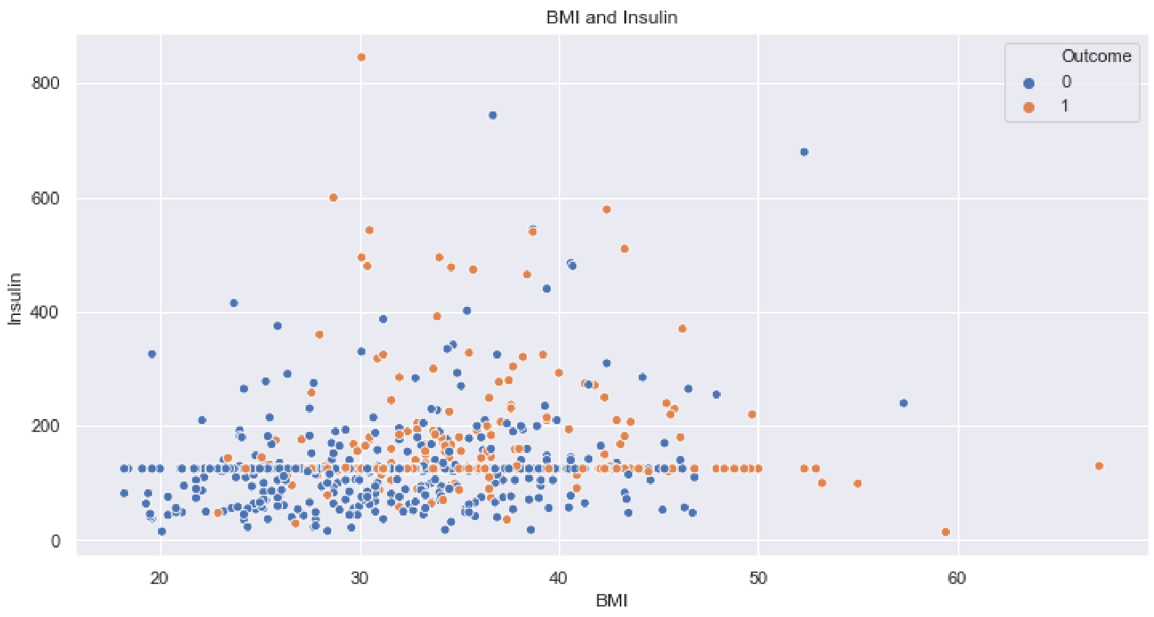


In [22]:
```python
plt.figure(figsize= (12,6))
plt.title("Blood Pressure and BMI")
sns.scatterplot(x= "BMI" ,y= "BloodPressure",
              hue="Outcome",
              data=diabetes_data);
```

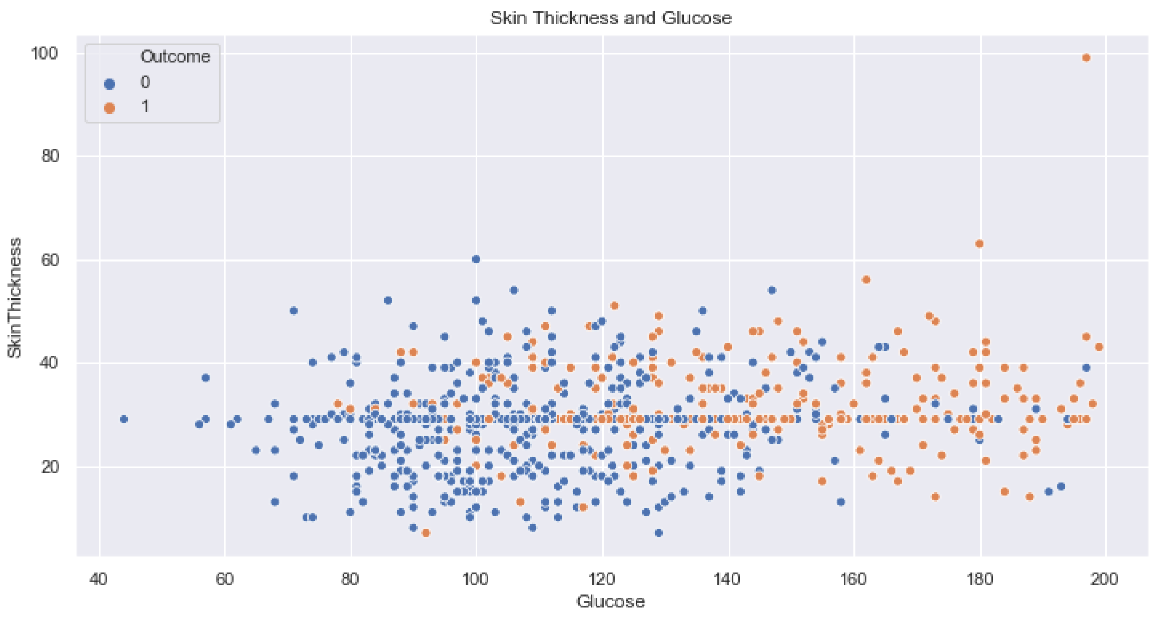


Diabetic patients with high blood pressure tend to have high BMI

In [23]:
```python
plt.figure(figsize= (12,6))
plt.title("BMI and Insulin")
sns.scatterplot(x= "BMI" ,y= "Insulin",
              hue="Outcome",
              data=diabetes_data);
```

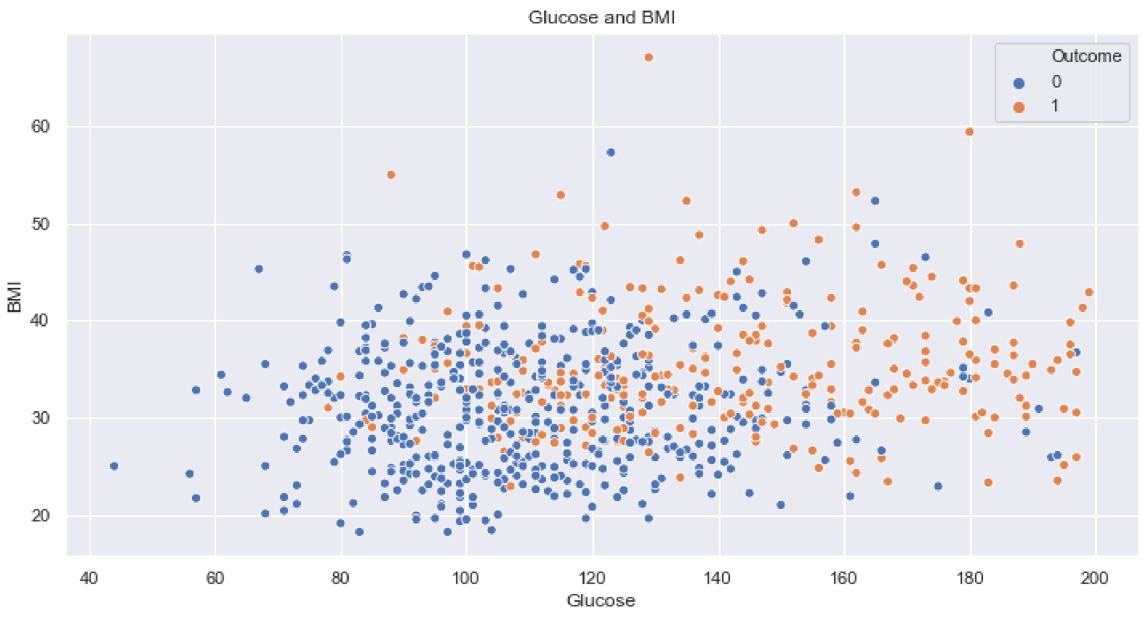


```
In [24]: plt.figure(figsize= (12,6))
         plt.title("Skin Thickness and Glucose")
         sns.scatterplot(x= "Glucose" ,y= "SkinThickness",
                         hue="Outcome",
                         data=diabetes_data);
```



Skin thickness doesn't seem to be an indicator for diabetes

```
In [25]: plt.figure(figsize= (12,6))
         plt.title("Glucose and BMI")
         sns.scatterplot(x= "Glucose" ,y= "BMI",
                         hue="Outcome",
                         data=diabetes_data);
```



Patients with higher glucose levels have chances to be diabetic

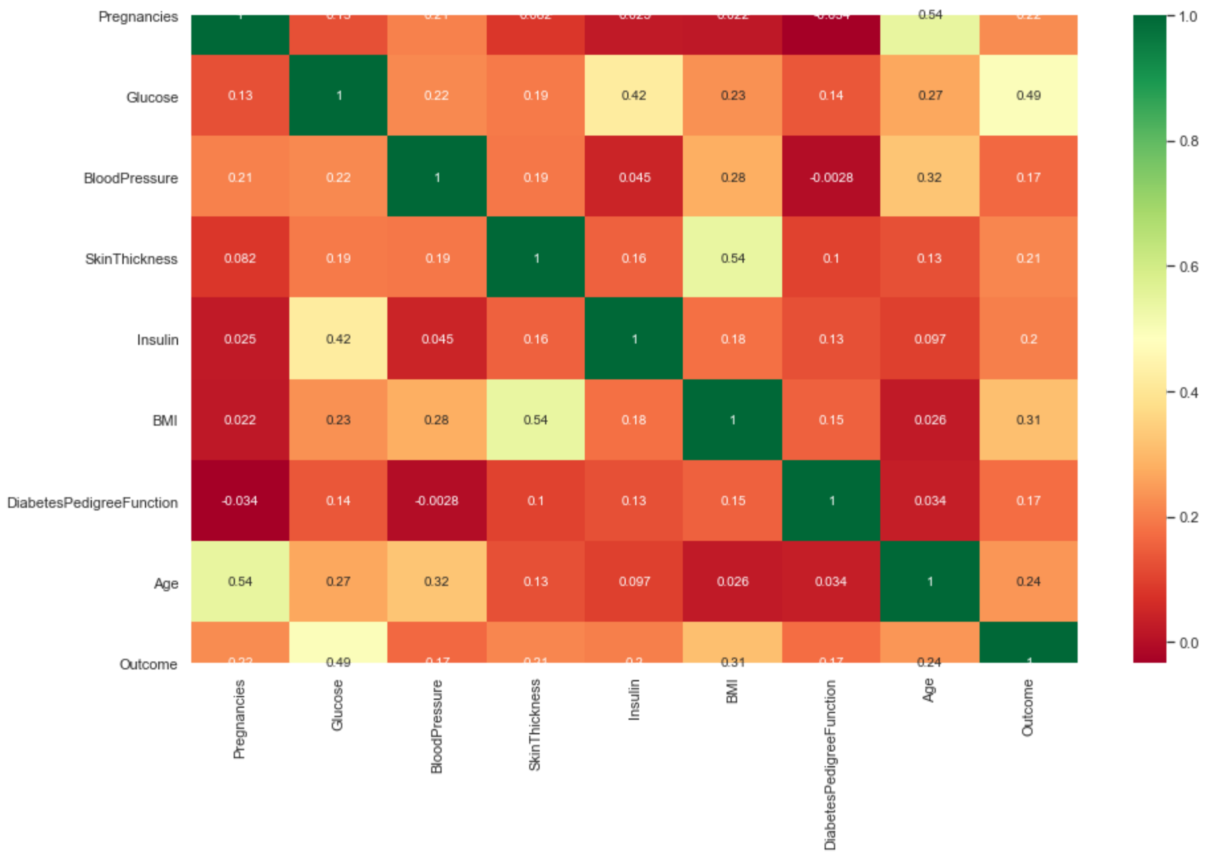
3. Perform correlation analysis. Visually explore it using a heat map.

```
In [26]: diabetes_data.corr()
```

Out[26]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunct
Pregnancies	1.000000	0.127911	0.208522	0.081770	0.025047	0.021559	-0.033
Glucose	0.127911	1.000000	0.218367	0.192686	0.419064	0.231128	0.137
BloodPressure	0.208522	0.218367	1.000000	0.191853	0.045087	0.281199	-0.002
SkinThickness	0.081770	0.192686	0.191853	1.000000	0.155610	0.543205	0.102
Insulin	0.025047	0.419064	0.045087	0.155610	1.000000	0.180241	0.126
BMI	0.021559	0.231128	0.281199	0.543205	0.180241	1.000000	0.153
DiabetesPedigreeFunction	-0.033523	0.137060	-0.002763	0.102188	0.126503	0.153438	1.000
Age	0.544341	0.266534	0.324595	0.126107	0.097101	0.025597	0.033
Outcome	0.221898	0.492928	0.166074	0.214873	0.203790	0.312038	0.173

```
In [27]: plt.figure(figsize=(15,9))
         p=sns.heatmap(diabetes_data.corr(), annot=True,cmap ='RdYlGn')
```



Project Task: Week 3

Data Modeling:

1. Devise strategies for model building. It is important to decide the right validation framework. Express your thought process.

2. Apply an appropriate classification algorithm to build a model. Compare various models with the results from KNN algorithm.

In [36]:
```
#Importing libraries for modelling
from sklearn import svm
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import train_test_split
from sklearn.model_selection import KFold
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn import metrics
import warnings
warnings.filterwarnings('ignore')
```

In [29]:
```
diabetes_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
Pregnancies                 768 non-null int64
Glucose                     768 non-null float64
BloodPressure               768 non-null float64
SkinThickness               768 non-null float64
Insulin                     768 non-null float64
BMI                         768 non-null float64
DiabetesPedigreeFunction    768 non-null float64
Age                         768 non-null int64
Outcome                     768 non-null int64
dtypes: float64(6), int64(3)
memory usage: 54.1 KB
```

As observed above we have 768 entries and 9 columns. First 8 columns represent the features and the last column represent the target. Hence splitting data into 2 dataframe X (feature) and y (target)

In [30]:
```
X=diabetes_data.drop(["Outcome"],axis=1)
y=diabetes_data["Outcome"]
```

In [31]:
```
X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.25,random_state=0, stratify=y)
```

In [32]:
```
model = LogisticRegression()
model.fit(X_train, y_train)
predicted = model.predict(X_test)
print("Accuracy of Logistic Regression: " ,round(metrics.accuracy_score(predicted,y_test),2))
```

```
Accuracy of Logistic Regression:  0.78
```

In [33]:
```
model = DecisionTreeClassifier()
model.fit(X_train, y_train)
predicted = model.predict(X_test)
print("Accuracy of Decision Tree Classifier: " ,round(metrics.accuracy_score(predicted,y_test),2))
```

```
Accuracy of Decision Tree Classifier:  0.69
```

In [34]:
```
types=['rbf','linear']
for i in types:
    model=svm.SVC(kernel=i)
    model.fit(X_train, y_train)
    predicted = model.predict(X_test)
    print('Accuracy for SVM kernel=',i,'is',round(metrics.accuracy_score(predicted,y_test),2))
```

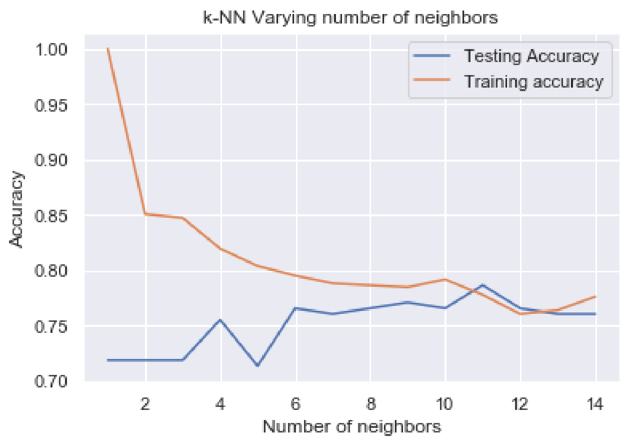
```
Accuracy for SVM kernel= rbf is 0.65
Accuracy for SVM kernel= linear is 0.76
```

In [37]:
```
model = RandomForestClassifier()
model.fit(X_train, y_train)
predicted = model.predict(X_test)
print("Accuracy of Random Forest Classifier: " ,round(metrics.accuracy_score(predicted,y_test),2))
```

```
Accuracy of Random Forest Classifier:  0.78
```

In [38]:
```
#Setup arrays to store training and test accuracies
neighbors = np.arange(1,15)
train_accuracy =np.empty(len(neighbors))
test_accuracy = np.empty(len(neighbors))

for i,k in enumerate(neighbors):
    #Setup a knn classifier with k neighbors
    knn = KNeighborsClassifier(n_neighbors=k)

    #Fit the model
    knn.fit(X_train, y_train)

    #Compute accuracy on the training set
    train_accuracy[i] = knn.score(X_train, y_train)

    #Compute accuracy on the test set
    test_accuracy[i] = knn.score(X_test, y_test)
```

In [39]:
```
#Generate plot
plt.title('k-NN Varying number of neighbors')
plt.plot(neighbors, test_accuracy, label='Testing Accuracy')
plt.plot(neighbors, train_accuracy, label='Training accuracy')
plt.legend()
plt.xlabel('Number of neighbors')
plt.ylabel('Accuracy')
plt.show()
```



As we get maximum testing accuracy 11, lets create KNN model with number of classifiers =11

In [40]:
```
knn = KNeighborsClassifier(n_neighbors=11)
knn.fit(X_train,y_train)
print("Accuracy of KNN: " ,round(knn.score(X_test,y_test),2))
```

```
Accuracy of KNN:  0.79
```

Comparison of all models

In [41]:
```
abc=[]
classifiers=['Linear Svm','Radial Svm','Logistic Regression','Decision Tree','Random Forest','KNN'
]
models=[svm.SVC(kernel='linear'),svm.SVC(kernel='rbf'),LogisticRegression(),DecisionTreeClassifier
(),RandomForestClassifier(),KNeighborsClassifier(n_neighbors=11)]
for i in models:
    model = i
    model.fit(X_train,y_train)
    prediction=model.predict(X_test)
    abc.append(metrics.accuracy_score(prediction,y_test))
models_dataframe=pd.DataFrame(abc,index=classifiers)
models_dataframe.columns=['Accuracy']
models_dataframe
```

Out[41]:

	Accuracy
Linear Svm	0.755208
Radial Svm	0.651042
Logistic Regression	0.776042
Decision Tree	0.713542
Random Forest	0.729167
KNN	0.786458

upon comparing all machine learning models, KNN is proving high accuracy with number of neighbours =11

Project Task: Week 4

Data Modeling:

1. Create a classification report by analyzing sensitivity, specificity, AUC (ROC curve), etc. Please be descriptive to explain what values of these parameter you have used.

Lets create confusion matrix for summarizing the performance of a classification algorithm using KNN model

In [42]:
```
#import confusion_matrix
from sklearn import metrics
from sklearn.metrics import confusion_matrix
```

In [43]:
```
y_pred = knn.predict(X_test)
confusion_matrix(y_test,y_pred)
pd.crosstab(y_test, y_pred, rownames=['Actual'], colnames=['Predicted'], margins=True)
```

Out[43]:

Predicted	0	1	All
Actual			
0	109	16	125
1	25	42	67
All	134	58	192

In [44]:
```
y_pred = knn.predict(X_test)
cnf_matrix = metrics.confusion_matrix(y_test, y_pred)
```

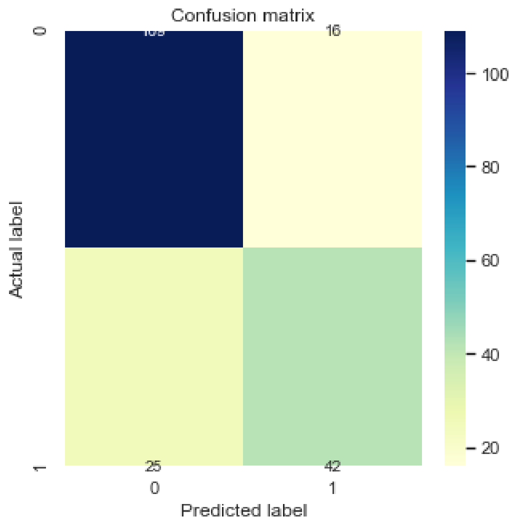
In [45]:
```
pd.DataFrame(cnf_matrix)
```

Out[45]:

	0	1
0	109	16
1	25	42

In [46]:
```
plt.figure(figsize=(5,5))
sns.heatmap(pd.DataFrame(cnf_matrix), annot=True, cmap="YlGnBu" ,fmt='g')
plt.title('Confusion matrix',y=1.1)
plt.ylabel('Actual label')
plt.xlabel('Predicted label')
```

Out[46]:
```
Text(0.5, 21.5, 'Predicted label')
```



According to the confusion matrix :

- True Positive (TP) = 109 , which indicates Dr. has correctly predicted that the patient has disease
- False Positive (FP) = 16 , Type I error
- True Negative (TN) = 42 , which indicates Dr. has correctly predicted that the patient doesn't have the disease
- False Negative (FN)= 25 , Type II error

Classification Report

```
 -Summary of the precision, recall, F1 score for each class. Scikit-learn provides facility to calculat
e Classification report using the classification_report method.
```

Precision Score

```
-The ratio of correctly predicted positive observations to the total predicted positive observations.
-Precision = TP/TP+FP
```

Recall (Sensitivity)

```
-The ratio of correctly predicted positive observations to the all observations
-Recall = TP/TP+FN
```

F1 score

```
- F1 Score is the weighted average of Precision and Recall. Therefore, this score takes both false posi
tives and false  negatives into account.
- F1 = 2 x (precision x recall)/(precision + recall)
```

In [47]:
```
#import classification_report
from sklearn.metrics import classification_report
```

In [48]:
```
print(classification_report(y_test,y_pred))
```

```
              precision    recall  f1-score   support

           0       0.81      0.87      0.84       125
           1       0.72      0.63      0.67        67

    accuracy                           0.79       192
   macro avg       0.77      0.75      0.76       192
weighted avg       0.78      0.79      0.78       192
```

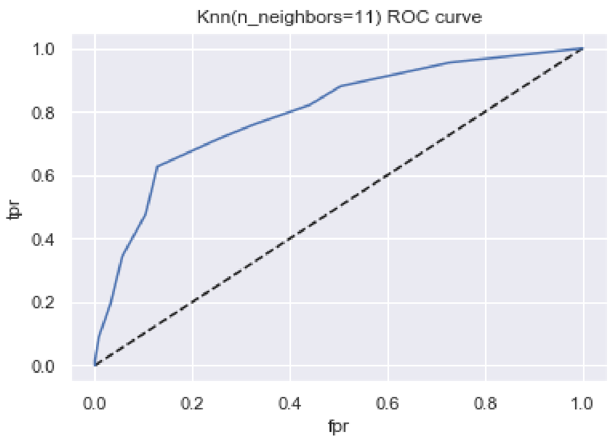
So, we have got 78% f1-score

AUC(RUC) Curve

In [49]:
```
from sklearn.metrics import roc_curve
```

In [50]:
```
y_pred_proba = knn.predict_proba(X_test)[:,1]
fpr, tpr, thresholds = roc_curve(y_test, y_pred_proba)
```

In [51]:
```
plt.plot([0,1],[0,1],'k--')
plt.plot(fpr,tpr, label='Knn')
plt.xlabel('fpr')
plt.ylabel('tpr')
plt.title('Knn(n_neighbors=11) ROC curve')
plt.show()
```



In [54]:
```
#Area under ROC curve
from sklearn.metrics import roc_auc_score
print("AUC score: " ,round(roc_auc_score(y_test,y_pred_proba),2))
```

```
AUC score:  0.8
```

ROC (Receiver Operating Characteristic) Curve tells us about how good the model can distinguish between two things (e.g If a patient has a disease or no).

It is a plot of the true positive rate against the false positive rate for the different possible cutpoints of a diagnostic test.

An ROC curve demonstrates several things:

1) It shows the tradeoff between sensitivity and specificity (any increase in sensitivity will be accompanied by a decrease in specificity).

2) The closer the curve follows the left-hand border and then the top border of the ROC space, the more accurate the test.

3)The closer the curve comes to the 45-degree diagonal of the ROC space, the less accurate the test.

4) The area under the curve is a measure of test accuracy.

Exporting dataset to create tableau report

```
In [59]: diabetes_data.to_excel(r'Diabetes Dataset.xlsx',index = False)
```