Capstone Project

Healthcare

Submitted in Partial Fulfillment of the Award of the Degree of

Data Scientist

Submitted By

Besty Haris

In [1]:

```
#import the preliminary libraries
import numpy as np
import pandas as pd


import matplotlib.pyplot as plt
from matplotlib import style
import seaborn as sns
```

DESCRIPTION

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 consists 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 [2]:

```
data = pd.read_csv('D:Simplilearn/SimpliCapstone/Data-Science-Capstone-Healthcare-maste
r/Data-Science-Capstone-Healthcare-master/health care diabetes.csv')
```

In [3]:

```
data.head()
```

Out[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunc
0	6	148	72	35	0	33.6	0.
1	1	85	66	29	0	26.6	0.
2	8	183	64	0	0	23.3	0.
3	1	89	66	23	94	28.1	0.
4	0	137	40	35	168	43.1	2.

Project Task: Week 1

Data Exploration:

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

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

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.

Data Exploration:

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

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

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

In [4]:

```
data.isnull().any()
```

Out[4]:

```
Pregnancies                 False
Glucose                     False
BloodPressure               False
SkinThickness               False
Insulin                     False
BMI                         False
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

In [5]:

```
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 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 [6]:

```
Positive = data[data['Outcome']==1]
Positive.head(5)
```

Out[6]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunc
0	6	148	72	35	0	33.6	0.
2	8	183	64	0	0	23.3	0.
4	0	137	40	35	168	43.1	2.
6	3	78	50	32	88	31.0	0.
8	2	197	70	45	543	30.5	0.

In [7]:

```
data['Glucose'].value_counts().head(7)
```

Out[7]:

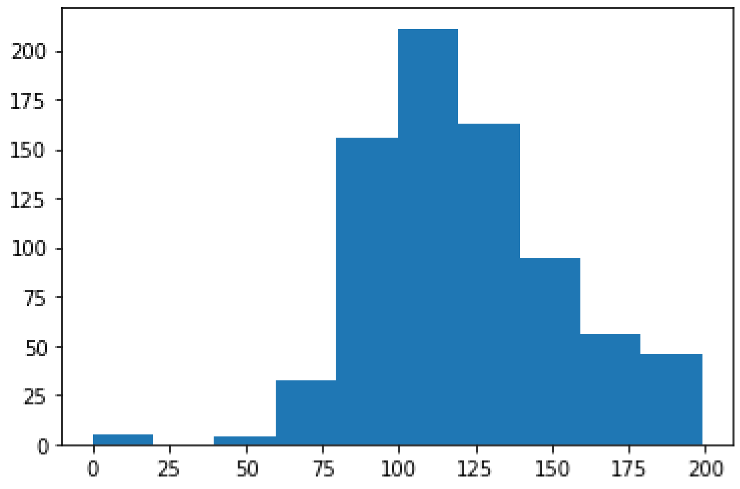
```
100    17
99     17
129    14
125    14
111    14
106    14
95     13
Name: Glucose, dtype: int64
```

In [8]:

```
plt.hist(data['Glucose'])
```

Out[8]:

```
(array([  5.,   0.,   4.,  32., 156., 211., 163.,  95.,  56.,  46.]),
 array([  0. ,  19.9,  39.8,  59.7,  79.6,  99.5, 119.4, 139.3, 159.2,
        179.1, 199. ]),
 <a list of 10 Patch objects>)
```



In [9]:

```
data['BloodPressure'].value_counts().head(7)
```

Out[9]:

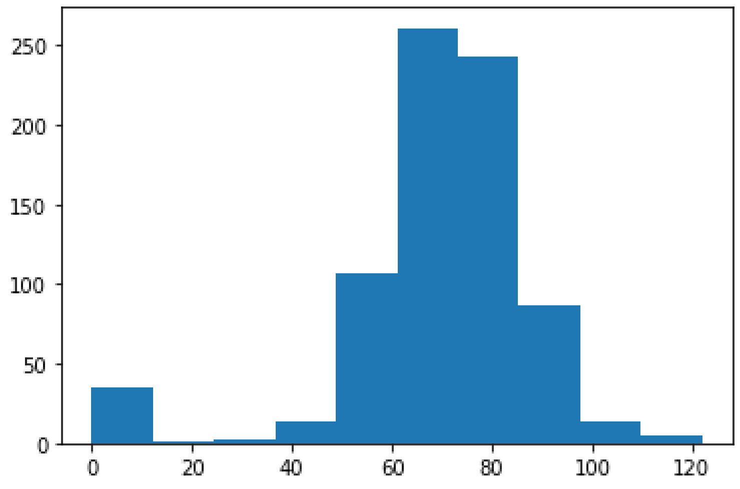
```
70    57
74    52
68    45
78    45
72    44
64    43
80    40
Name: BloodPressure, dtype: int64
```

In [10]:

```
plt.hist(data['BloodPressure'])
```

Out[10]:

```
(array([ 35.,   1.,   2.,  13., 107., 261., 243.,  87.,  14.,   5.]),
 array([  0. ,  12.2,  24.4,  36.6,  48.8,  61. ,  73.2,  85.4,  97.6,
        109.8, 122. ]),
 <a list of 10 Patch objects>)
```



In [11]:

```
data['SkinThickness'].value_counts().head(7)
```

Out[11]:

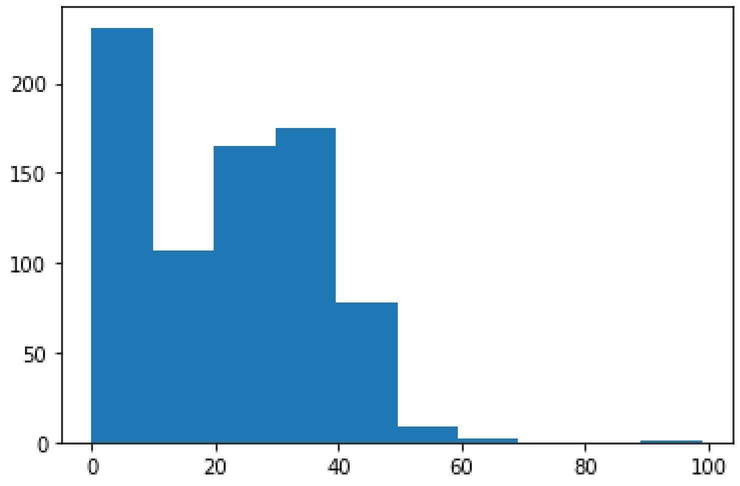
```
0     227
32     31
30     27
27     23
23     22
33     20
18     20
Name: SkinThickness, dtype: int64
```

In [12]:

```
plt.hist(data['SkinThickness'])
```

Out[12]:

```
(array([231., 107., 165., 175.,  78.,   9.,   2.,   0.,   0.,   1.]),
 array([ 0. ,  9.9, 19.8, 29.7, 39.6, 49.5, 59.4, 69.3, 79.2, 89.1, 99.
]),
 <a list of 10 Patch objects>)
```



In [13]:

```
data['Insulin'].value_counts().head(7)
```

Out[13]:

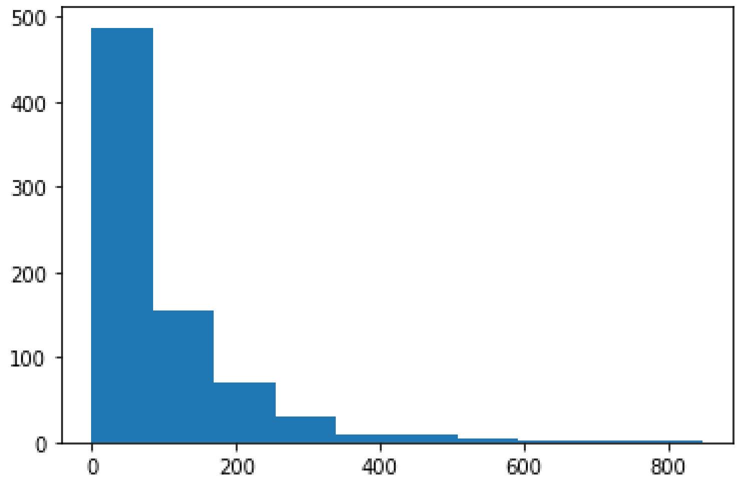
```
0      374
105     11
140      9
130      9
120      8
100      7
94       7
Name: Insulin, dtype: int64
```

In [14]:

```
plt.hist(data['Insulin'])
```

Out[14]:

```
(array([487., 155.,  70.,  30.,   8.,   9.,   5.,   1.,   2.,   1.]),
 array([  0. ,  84.6, 169.2, 253.8, 338.4, 423. , 507.6, 592.2, 676.8,
        761.4, 846. ]),
 <a list of 10 Patch objects>)
```



In [15]:

```
data['BMI'].value_counts().head(7)
```

Out[15]:

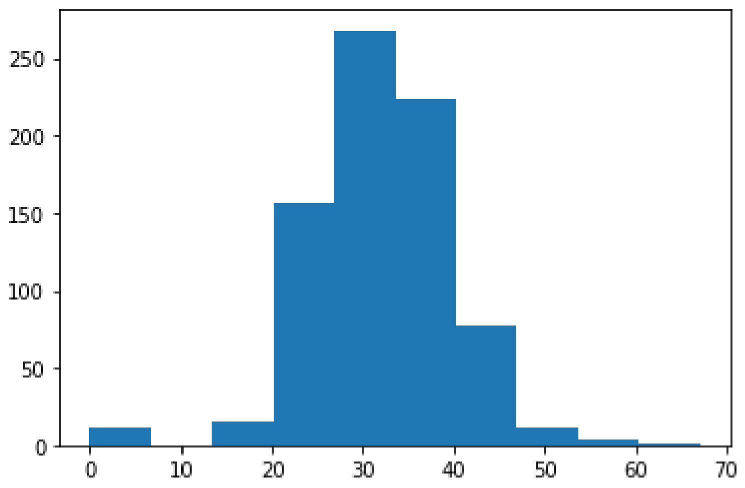
```
32.0    13
31.6    12
31.2    12
0.0     11
33.3    10
32.4    10
32.8     9
Name: BMI, dtype: int64
```

In [16]:

```
plt.hist(data['BMI'])
```

Out[16]:

```
(array([ 11.,   0.,  15., 156., 268., 224.,  78.,  12.,   3.,   1.]),
 array([ 0.  ,  6.71, 13.42, 20.13, 26.84, 33.55, 40.26, 46.97, 53.68,
        60.39, 67.1 ]),
 <a list of 10 Patch objects>)
```



In [17]:

```
data.describe().transpose()
```

Out[17]:

	count	mean	std	min	25%	50%	75
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.0000
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.2500
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.0000
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.0000
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.2500
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.6000
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.6262
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.0000
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.0000

Week 2

Data Modeling:

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

Apply an appropriate classification algorithm to build a model.

Compare various models with the results from KNN algorithm.

Create a classification report by analyzing sensitivity, specificity, AUC (ROC curve), etc.

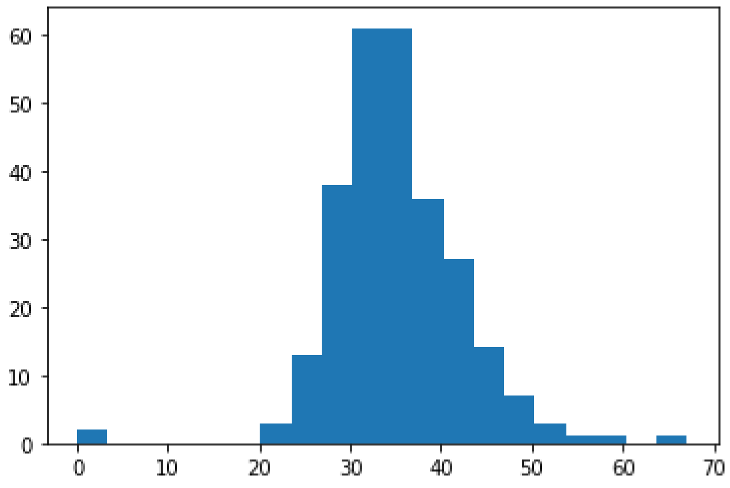
Please be descriptive to explain what values of these parameter you have used.

In [18]:

```
plt.hist(Positive['BMI'],histtype='stepfilled',bins=20)
```

Out[18]:

```
(array([ 2.,  0.,  0.,  0.,  0.,  0.,  3., 13., 38., 61., 61., 36., 27.,
        14.,  7.,  3.,  1.,  1.,  0.,  1.]),
 array([ 0.   ,  3.355,  6.71 , 10.065, 13.42 , 16.775, 20.13 , 23.485,
        26.84 , 30.195, 33.55 , 36.905, 40.26 , 43.615, 46.97 , 50.325,
        53.68 , 57.035, 60.39 , 63.745, 67.1  ]),
 <a list of 1 Patch objects>)
```



In [19]:

```
Positive['BMI'].value_counts().head(7)
```

Out[19]:

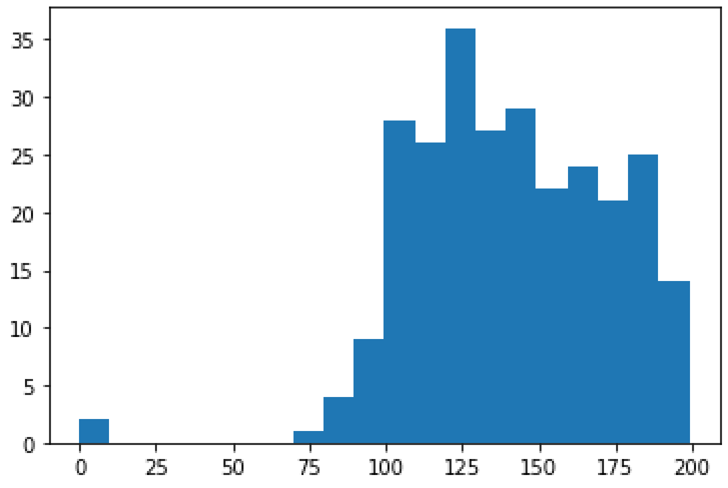
```
32.9    8
31.6    7
33.3    6
30.5    5
32.0    5
31.2    5
32.4    4
Name: BMI, dtype: int64
```

In [20]:

```
plt.hist(Positive['Glucose'],histtype='stepfilled',bins=20)
```

Out[20]:

```
(array([ 2.,  0.,  0.,  0.,  0.,  0.,  0.,  1.,  4.,  9., 28., 26., 36.,
        27., 29., 22., 24., 21., 25., 14.]),
 array([  0.  ,   9.95,  19.9 ,  29.85,  39.8 ,  49.75,  59.7 ,  69.65,
         79.6 ,  89.55,  99.5 , 109.45, 119.4 , 129.35, 139.3 , 149.25,
        159.2 , 169.15, 179.1 , 189.05, 199.  ]),
 <a list of 1 Patch objects>)
```



In [21]:

```
Positive['Glucose'].value_counts().head(7)
```

Out[21]:

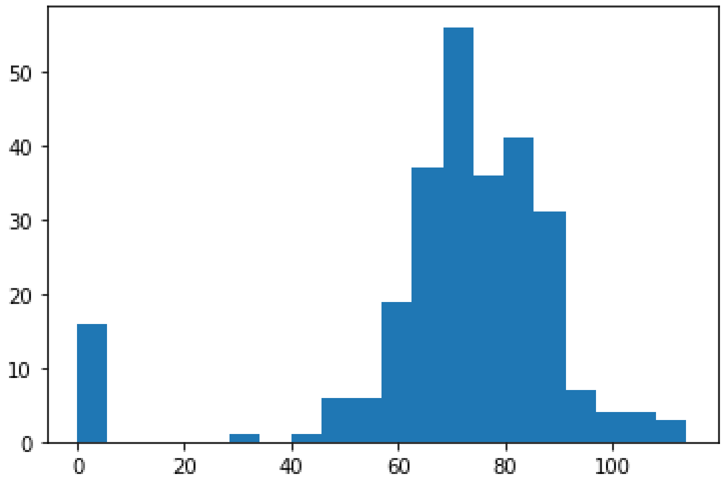
```
125    7
158    6
128    6
115    6
129    6
146    5
162    5
Name: Glucose, dtype: int64
```

In [22]:

```
plt.hist(Positive['BloodPressure'],histtype='stepfilled',bins=20)
```

Out[22]:

```
(array([16.,  0.,  0.,  0.,  0.,  1.,  0.,  1.,  6.,  6., 19., 37., 56.,
        36., 41., 31.,  7.,  4.,  4.,  3.]),
 array([  0. ,   5.7,  11.4,  17.1,  22.8,  28.5,  34.2,  39.9,  45.6,
         51.3,  57. ,  62.7,  68.4,  74.1,  79.8,  85.5,  91.2,  96.9,
        102.6, 108.3, 114. ]),
 <a list of 1 Patch objects>)
```



In [23]:

```
Positive['BloodPressure'].value_counts().head(7)
```

Out[23]:

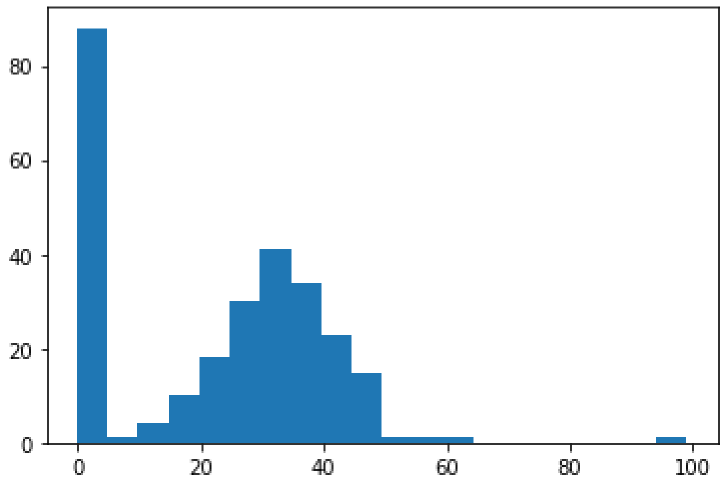
```
70    23
76    18
78    17
74    17
72    16
0     16
82    13
Name: BloodPressure, dtype: int64
```

In [24]:

```
plt.hist(Positive['SkinThickness'],histtype='stepfilled',bins=20)
```

Out[24]:

```
(array([88.,  1.,  4., 10., 18., 30., 41., 34., 23., 15.,  1.,  1.,  1.,
         0.,  0.,  0.,  0.,  0.,  0.,  1.]),
 array([ 0.  ,  4.95,  9.9 , 14.85, 19.8 , 24.75, 29.7 , 34.65, 39.6 ,
        44.55, 49.5 , 54.45, 59.4 , 64.35, 69.3 , 74.25, 79.2 , 84.15,
        89.1 , 94.05, 99.  ]),
 <a list of 1 Patch objects>)
```



In [25]:

```
Positive['SkinThickness'].value_counts().head(7)
```

Out[25]:

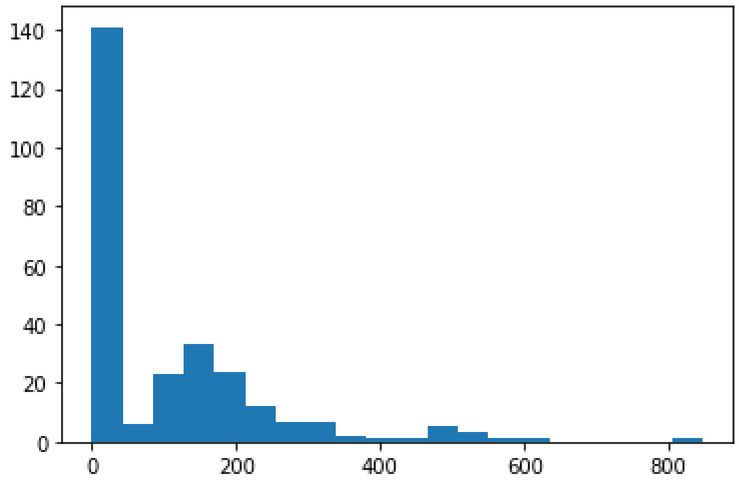
```
0     88
32    14
33     9
30     9
39     8
35     8
36     8
Name: SkinThickness, dtype: int64
```

In [26]:

```
plt.hist(Positive['Insulin'],histtype='stepfilled',bins=20)
```

Out[26]:

```
(array([141.,   6.,  23.,  33.,  24.,  12.,   7.,   7.,   2.,   1.,   1.,
          5.,   3.,   1.,   1.,   0.,   0.,   0.,   0.,   1.]),
 array([  0. ,  42.3,  84.6, 126.9, 169.2, 211.5, 253.8, 296.1, 338.4,
        380.7, 423. , 465.3, 507.6, 549.9, 592.2, 634.5, 676.8, 719.1,
        761.4, 803.7, 846. ]),
 <a list of 1 Patch objects>)
```



In [27]:

```
Positive['Insulin'].value_counts().head(7)
```

Out[27]:

```
0      138
130      6
180      4
156      3
175      3
194      2
125      2
Name: Insulin, dtype: int64
```

In [28]:

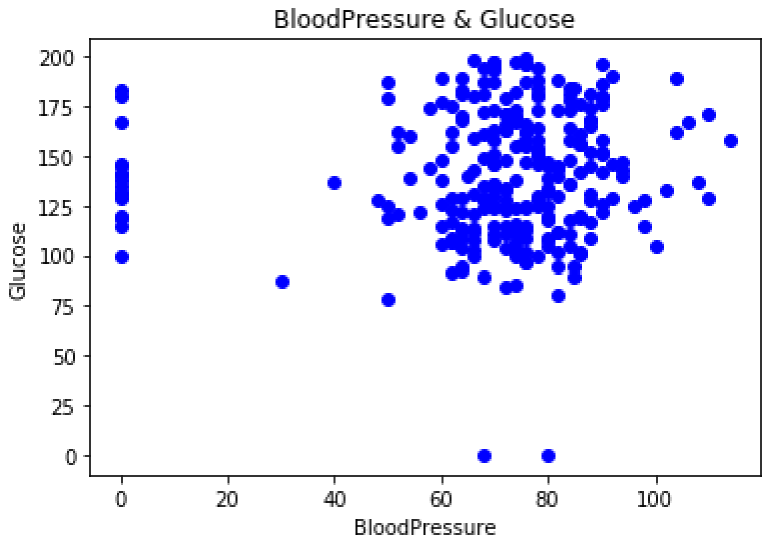
```
#Scatter plot
```

In [29]:

```
BloodPressure = Positive['BloodPressure']
Glucose = Positive['Glucose']
SkinThickness = Positive['SkinThickness']
Insulin = Positive['Insulin']
BMI = Positive['BMI']
```

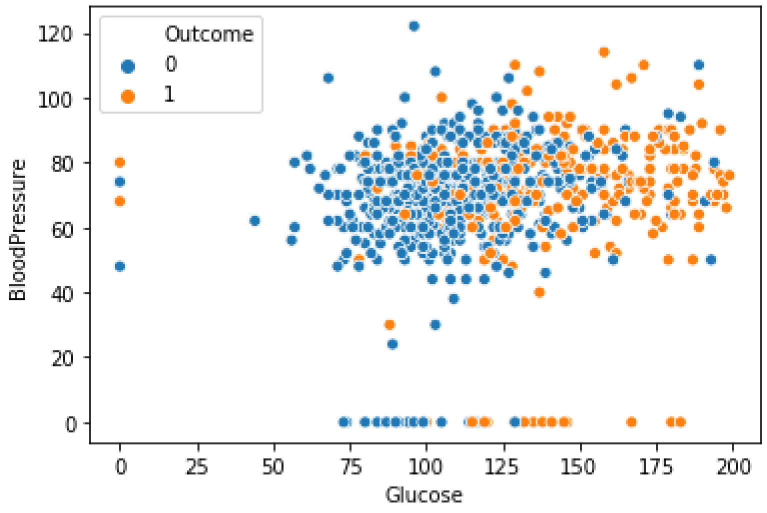
In [30]:

```
plt.scatter(BloodPressure, Glucose, color=['b'])
plt.xlabel('BloodPressure')
plt.ylabel('Glucose')
plt.title('BloodPressure & Glucose')
plt.show()
```



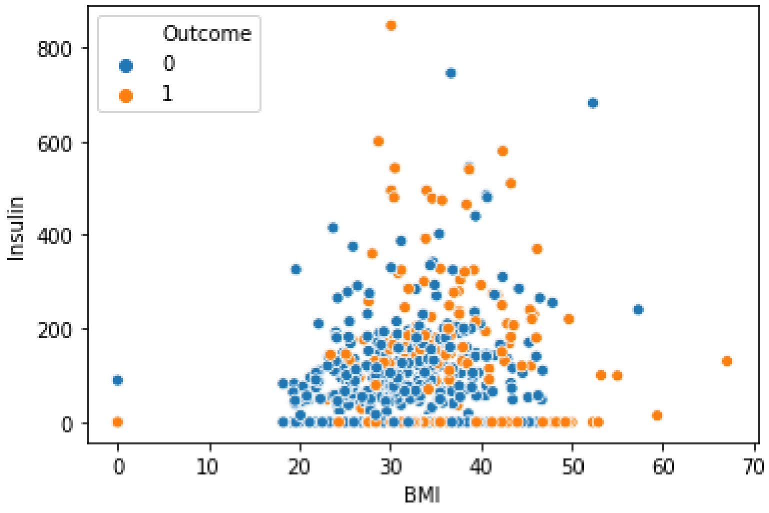
In [31]:

```
g =sns.scatterplot(x= "Glucose" ,y= "BloodPressure",
              hue="Outcome",
              data=data);
```



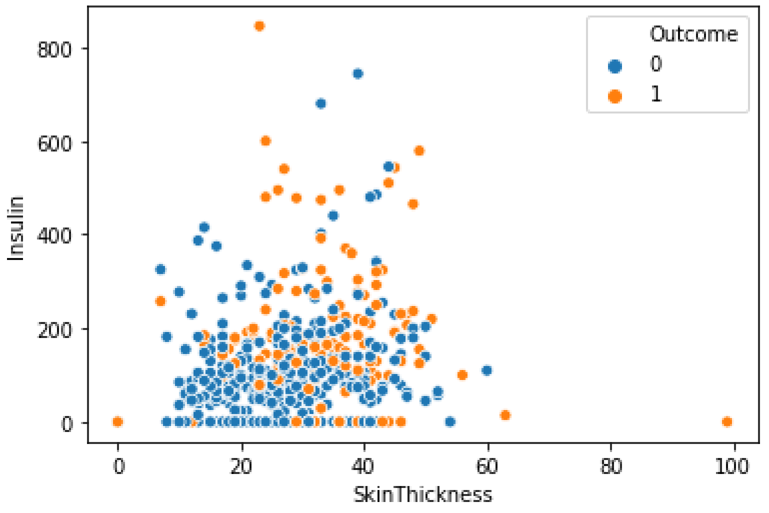
In [32]:

```
B =sns.scatterplot(x= "BMI" ,y= "Insulin",
              hue="Outcome",
              data=data);
```



In [33]:

```
S =sns.scatterplot(x= "SkinThickness" ,y= "Insulin",
              hue="Outcome",
              data=data);
```



In [34]:

```
### correlation matrix
data.corr()
```

Out[34]:

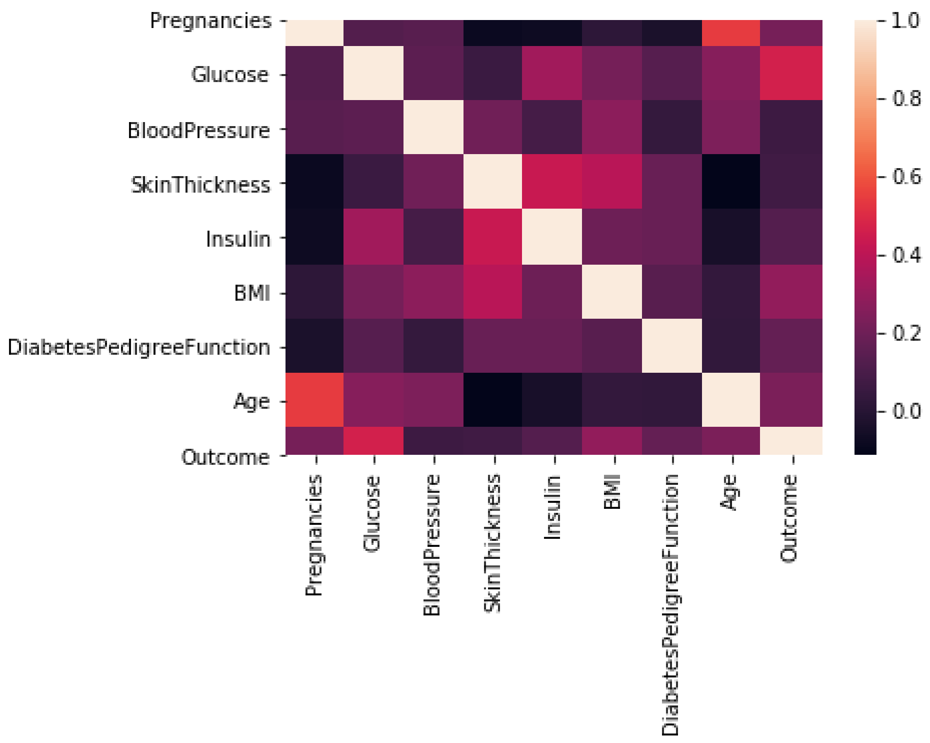
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.

In [35]:

```
### create correlation heat map
sns.heatmap(data.corr())
```

Out[35]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x1b86a3af0c8>
```

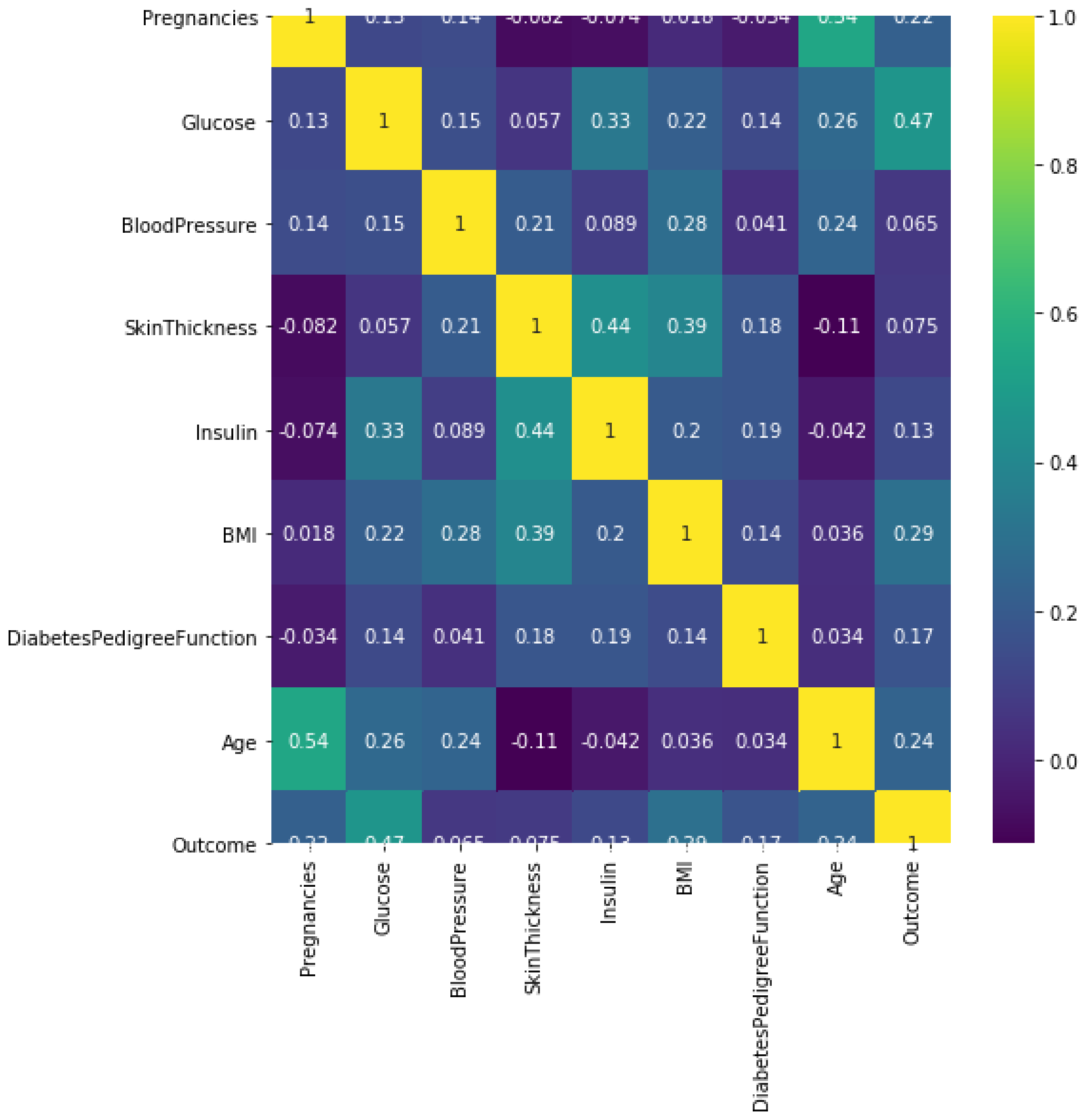


In [36]:

```
plt.subplots(figsize=(8,8))
sns.heatmap(data.corr(),annot=True,cmap='viridis')  ### gives correlation value
```

Out[36]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x1b86a47e148>
```



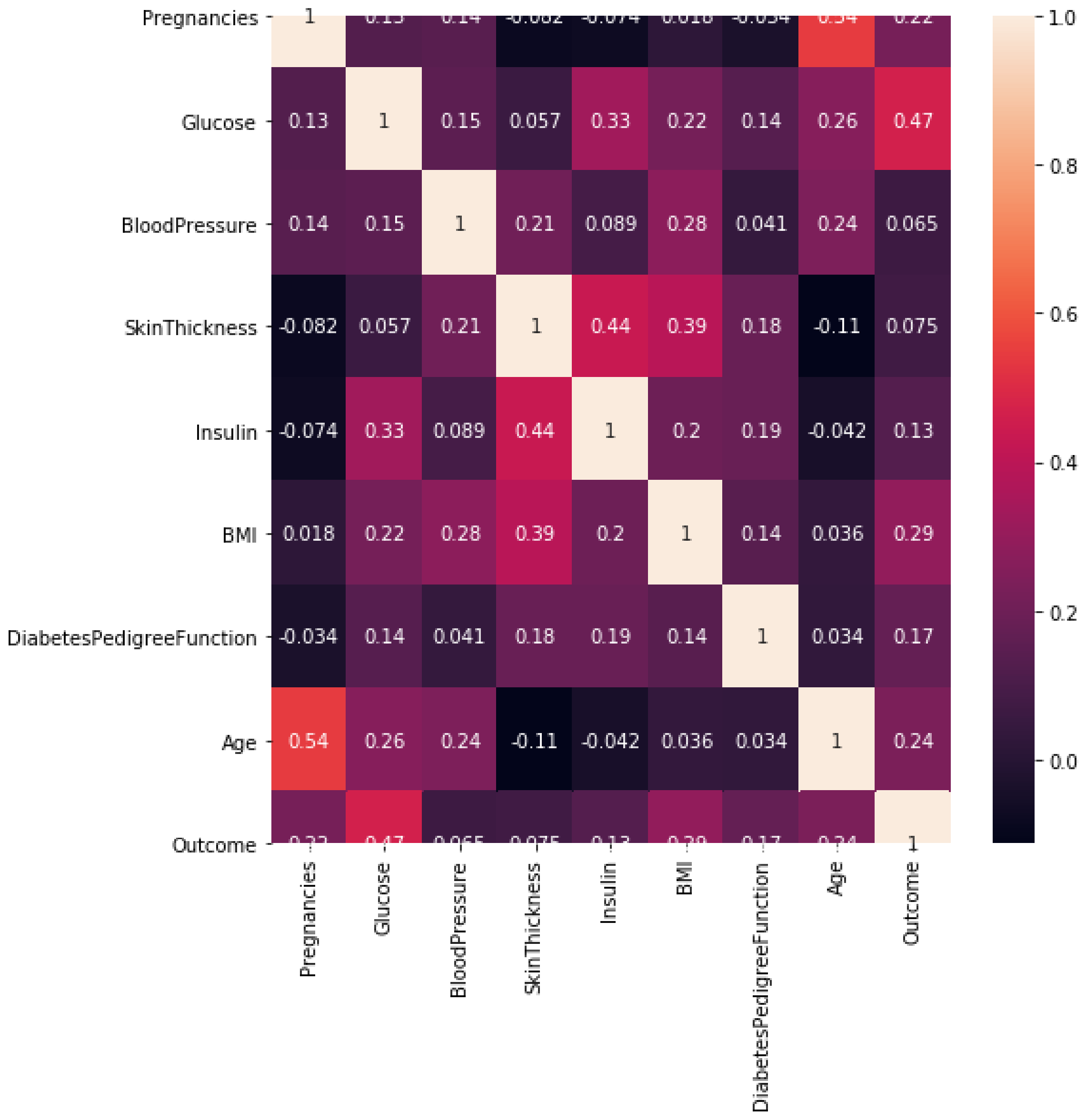
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1	0.13	0.14	-0.082	-0.074	0.018	-0.034	0.54	0.22
Glucose	0.13	1	0.15	0.057	0.33	0.22	0.14	0.26	0.47
BloodPressure	0.14	0.15	1	0.21	0.089	0.28	0.041	0.24	0.065
SkinThickness	-0.082	0.057	0.21	1	0.44	0.39	0.18	-0.11	0.075
Insulin	-0.074	0.33	0.089	0.44	1	0.2	0.19	-0.042	0.13
BMI	0.018	0.22	0.28	0.39	0.2	1	0.14	0.036	0.29
DiabetesPedigreeFunction	-0.034	0.14	0.041	0.18	0.19	0.14	1	0.034	0.17
Age	0.54	0.26	0.24	-0.11	-0.042	0.036	0.034	1	0.24
Outcome	0.22	0.47	0.065	0.075	0.13	0.29	0.17	0.24	1

In [37]:

```
plt.subplots(figsize=(8,8))
sns.heatmap(data.corr(),annot=True)  ### gives correlation value
```

Out[37]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x1b86a743088>
```



In [38]:

```
# Logistic Regreation and model building
```

In [39]:

```
data.head(5)
```

Out[39]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunc
0	6	148	72	35	0	33.6	0.
1	1	85	66	29	0	26.6	0.
2	8	183	64	0	0	23.3	0.
3	1	89	66	23	94	28.1	0.
4	0	137	40	35	168	43.1	2.

In [40]:

```
features = data.iloc[:,[0,1,2,3,4,5,6,7]].values
label = data.iloc[:,8].values
```

In [41]:

```
#Train test split
from sklearn.model_selection import train_test_split
X_train,X_test,y_train,y_test = train_test_split(features,
                                                label,
                                                test_size=0.2,
                                                random_state =10)
```

In [42]:

```
#Create model
from sklearn.linear_model import LogisticRegression
model = LogisticRegression()
model.fit(X_train,y_train)
```

```
C:\Users\ME\Anaconda3\lib\site-packages\sklearn\linear_model\logistic.py:4
32: FutureWarning: Default solver will be changed to 'lbfgs' in 0.22. Spec
ify a solver to silence this warning.
  FutureWarning)
```

Out[42]:

```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=Tru
e,
                   intercept_scaling=1, l1_ratio=None, max_iter=100,
                   multi_class='warn', n_jobs=None, penalty='l2',
                   random_state=None, solver='warn', tol=0.0001, verbose=
0,
                   warm_start=False)
```

In [43]:

```
print(model.score(X_train,y_train))
print(model.score(X_test,y_test))
```

```
0.7833876221498371
0.7337662337662337
```

In [44]:

```
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(label,model.predict(features))
cm
```

Out[44]:

```
array([[452,  48],
       [126, 142]], dtype=int64)
```

In [45]:

```
from sklearn.metrics import classification_report
print(classification_report(label,model.predict(features)))
```

```
              precision    recall  f1-score   support

           0       0.78      0.90      0.84       500
           1       0.75      0.53      0.62       268

    accuracy                           0.77       768
   macro avg       0.76      0.72      0.73       768
weighted avg       0.77      0.77      0.76       768
```

In [46]:

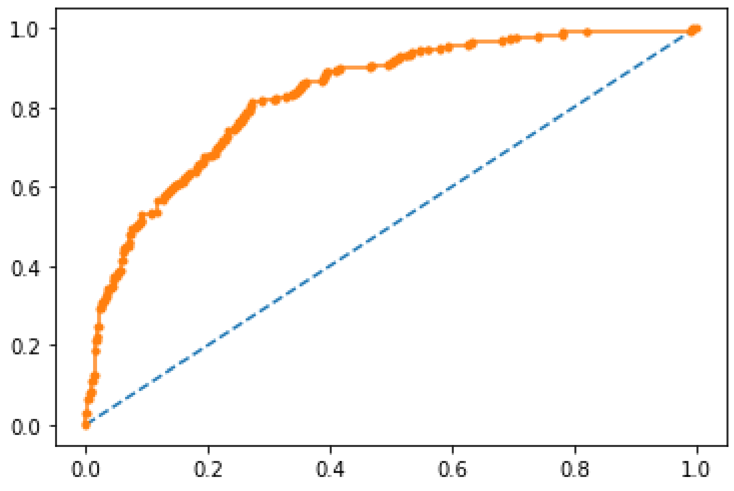
```
#Preparing ROC Curve (Receiver Operating Characteristics Curve)
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score

# predict probabilities
probs = model.predict_proba(features)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# calculate AUC
auc = roc_auc_score(label, probs)
print('AUC: %.3f' % auc)
# calculate roc curve
fpr, tpr, thresholds = roc_curve(label, probs)
# plot no skill
plt.plot([0, 1], [0, 1], linestyle='--')
# plot the roc curve for the model
plt.plot(fpr, tpr, marker='.')
```

```
AUC: 0.834
```

Out[46]:

```
[<matplotlib.lines.Line2D at 0x1b86c2e3ac8>]
```



In [47]:

```
#Applying Decission Tree Classifier
from sklearn.tree import DecisionTreeClassifier
model3 = DecisionTreeClassifier(max_depth=5)
model3.fit(X_train,y_train)
```

Out[47]:

```
DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=5,
                       max_features=None, max_leaf_nodes=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, presort=False,
                       random_state=None, splitter='best')
```

In [48]:

```
model3.score(X_train,y_train)
```

Out[48]:

```
0.8289902280130294
```

In [49]:

```
model3.score(X_test,y_test)
```

Out[49]:

```
0.7727272727272727
```

In [50]:

```
#Applying Random Forest
from sklearn.ensemble import RandomForestClassifier
model4 = RandomForestClassifier(n_estimators=11)
model4.fit(X_train,y_train)
```

Out[50]:

```
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='gin
i',
                       max_depth=None, max_features='auto', max_leaf_nodes
=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, n_estimators=11,
                       n_jobs=None, oob_score=False, random_state=None,
                       verbose=0, warm_start=False)
```

In [51]:

```
model4.score(X_train,y_train)
```

Out[51]:

```
0.990228013029316
```

In [52]:

```
model4.score(X_test,y_test)
```

Out[52]:

```
0.7337662337662337
```

In [53]:

```
#Support Vector Classifier

from sklearn.svm import SVC
model5 = SVC(kernel='rbf',
           gamma='auto')
model5.fit(X_train,y_train)
```

Out[53]:

```
SVC(C=1.0, cache_size=200, class_weight=None, coef0=0.0,
    decision_function_shape='ovr', degree=3, gamma='auto', kernel='rbf',
    max_iter=-1, probability=False, random_state=None, shrinking=True,
    tol=0.001, verbose=False)
```

In [56]:

```
model5.score(X_test,y_test)
```

Out[56]:

```
0.6168831168831169
```

In [57]:

```
#Applying K-NN
from sklearn.neighbors import KNeighborsClassifier
model2 = KNeighborsClassifier(n_neighbors=7,
                             metric='minkowski',
                             p = 2)
model2.fit(X_train,y_train)
```

Out[57]:

```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=7, p=2,
                     weights='uniform')
```

In [58]:

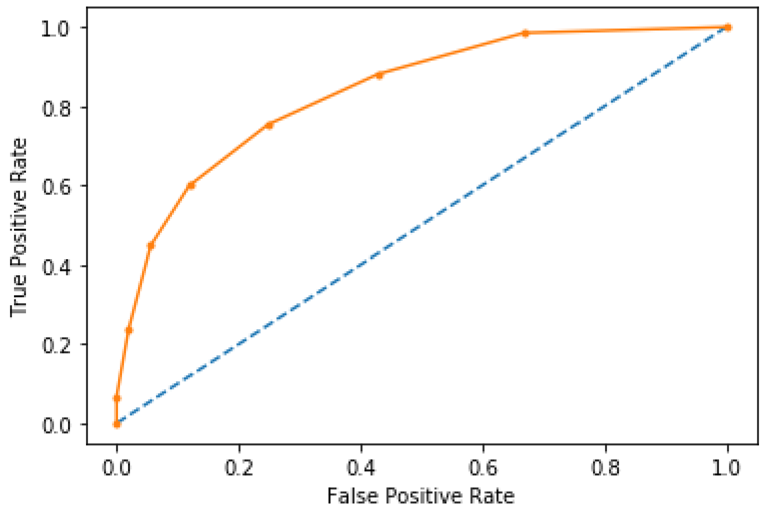
```
#Preparing ROC Curve (Receiver Operating Characteristics Curve)
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score

# predict probabilities
probs = model2.predict_proba(features)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# calculate AUC
auc = roc_auc_score(label, probs)
print('AUC: %.3f' % auc)
# calculate roc curve
fpr, tpr, thresholds = roc_curve(label, probs)
print("True Positive Rate - {}, False Positive Rate - {} Thresholds - {}".format(tpr,fp
r,thresholds))
# plot no skill
plt.plot([0, 1], [0, 1], linestyle='--')
# plot the roc curve for the model
plt.plot(fpr, tpr, marker='.')
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
```

```
AUC: 0.836
True Positive Rate - [0.         0.06716418 0.23880597 0.44776119 0.600746
27 0.75373134
 0.88059701 0.98507463 1.        ], False Positive Rate - [0.    0.    0.0
2  0.056 0.12  0.248 0.428 0.668 1.   ] Thresholds - [2.         1.
0.85714286 0.71428571 0.57142857 0.42857143
 0.28571429 0.14285714 0.        ]
```

Out[58]:

```
Text(0, 0.5, 'True Positive Rate')
```



In [59]:

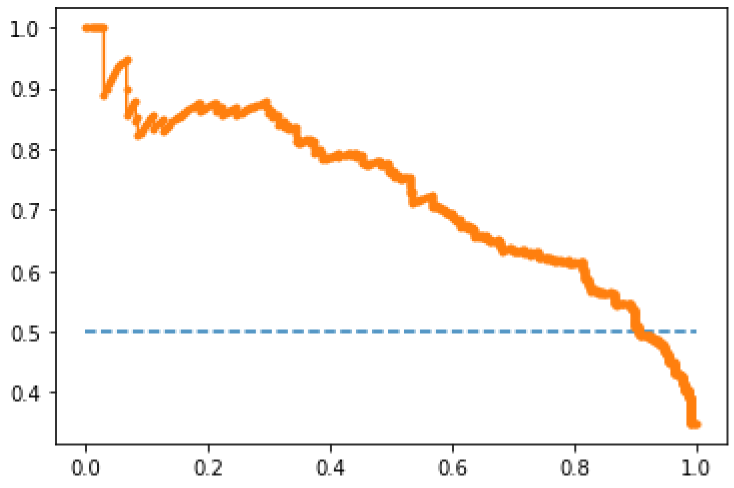
```
#Precision Recall Curve for Logistic Regression

from sklearn.metrics import precision_recall_curve
from sklearn.metrics import f1_score
from sklearn.metrics import auc
from sklearn.metrics import average_precision_score
# predict probabilities
probs = model.predict_proba(features)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# predict class values
yhat = model.predict(features)
# calculate precision-recall curve
precision, recall, thresholds = precision_recall_curve(label, probs)
# calculate F1 score
f1 = f1_score(label, yhat)
# calculate precision-recall AUC
auc = auc(recall, precision)
# calculate average precision score
ap = average_precision_score(label, probs)
print('f1=%.3f auc=%.3f ap=%.3f' % (f1, auc, ap))
# plot no skill
plt.plot([0, 1], [0.5, 0.5], linestyle='--')
# plot the precision-recall curve for the model
plt.plot(recall, precision, marker='.')
```

```
f1=0.620 auc=0.728 ap=0.728
```

Out[59]:

```
[<matplotlib.lines.Line2D at 0x1b86c87e588>]
```



In [60]:

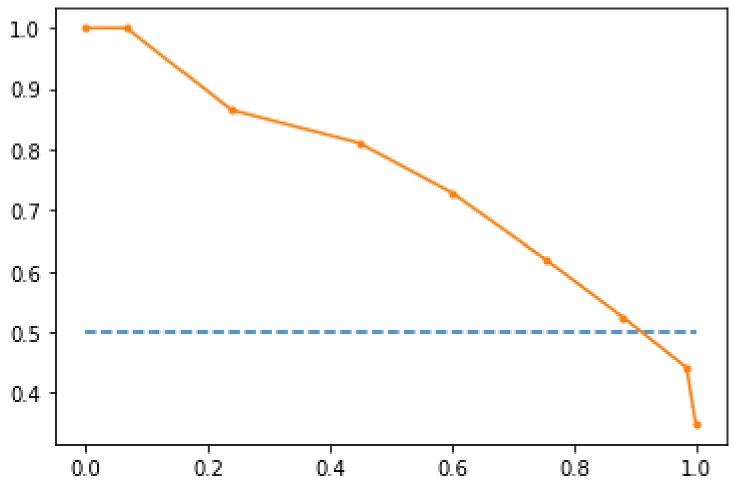
```
#Precision Recall Curve for KNN

from sklearn.metrics import precision_recall_curve
from sklearn.metrics import f1_score
from sklearn.metrics import auc
from sklearn.metrics import average_precision_score
# predict probabilities
probs = model2.predict_proba(features)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# predict class values
yhat = model2.predict(features)
# calculate precision-recall curve
precision, recall, thresholds = precision_recall_curve(label, probs)
# calculate F1 score
f1 = f1_score(label, yhat)
# calculate precision-recall AUC
auc = auc(recall, precision)
# calculate average precision score
ap = average_precision_score(label, probs)
print('f1=%.3f auc=%.3f ap=%.3f' % (f1, auc, ap))
# plot no skill
plt.plot([0, 1], [0.5, 0.5], linestyle='--')
# plot the precision-recall curve for the model
plt.plot(recall, precision, marker='.')
```

```
f1=0.658 auc=0.752 ap=0.709
```

Out[60]:

```
[<matplotlib.lines.Line2D at 0x1b86c966f08>]
```



In [61]:

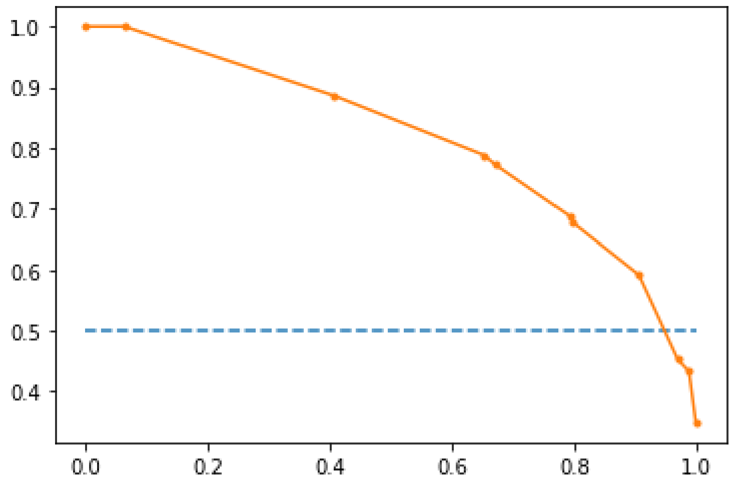
```
#Precision Recall Curve for Decission Tree Classifier

from sklearn.metrics import precision_recall_curve
from sklearn.metrics import f1_score
from sklearn.metrics import auc
from sklearn.metrics import average_precision_score
# predict probabilities
probs = model3.predict_proba(features)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# predict class values
yhat = model3.predict(features)
# calculate precision-recall curve
precision, recall, thresholds = precision_recall_curve(label, probs)
# calculate F1 score
f1 = f1_score(label, yhat)
# calculate precision-recall AUC
auc = auc(recall, precision)
# calculate average precision score
ap = average_precision_score(label, probs)
print('f1=%.3f auc=%.3f ap=%.3f' % (f1, auc, ap))
# plot no skill
plt.plot([0, 1], [0.5, 0.5], linestyle='--')
# plot the precision-recall curve for the model
plt.plot(recall, precision, marker='.')
```

```
f1=0.714 auc=0.815 ap=0.768
```

Out[61]:

```
[<matplotlib.lines.Line2D at 0x1b86c935388>]
```



In [62]:

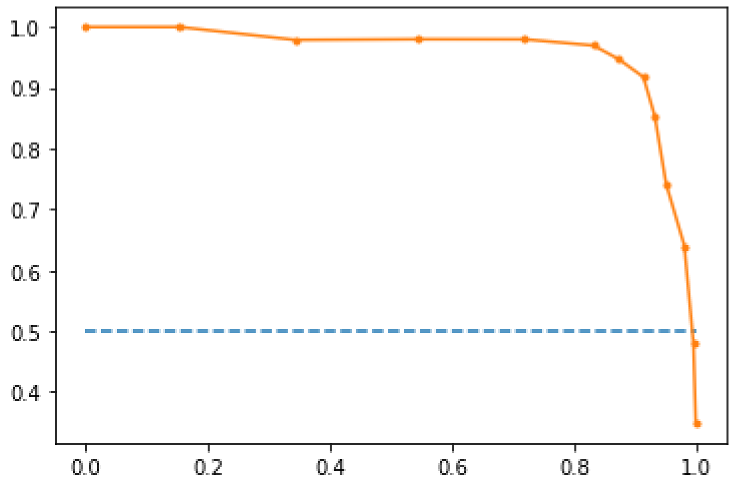
```
#Precision Recall Curve for Random Forest

from sklearn.metrics import precision_recall_curve
from sklearn.metrics import f1_score
from sklearn.metrics import auc
from sklearn.metrics import average_precision_score
# predict probabilities
probs = model4.predict_proba(features)
# keep probabilities for the positive outcome only
probs = probs[:, 1]
# predict class values
yhat = model4.predict(features)
# calculate precision-recall curve
precision, recall, thresholds = precision_recall_curve(label, probs)
# calculate F1 score
f1 = f1_score(label, yhat)
# calculate precision-recall AUC
auc = auc(recall, precision)
# calculate average precision score
ap = average_precision_score(label, probs)
print('f1=%.3f auc=%.3f ap=%.3f' % (f1, auc, ap))
# plot no skill
plt.plot([0, 1], [0.5, 0.5], linestyle='--')
# plot the precision-recall curve for the model
plt.plot(recall, precision, marker='.')
```

```
f1=0.909 auc=0.959 ap=0.951
```

Out[62]:

```
[<matplotlib.lines.Line2D at 0x1b86ca016c8>]
```



In [ ]: