In [1]:
```
%matplotlib inline
### import libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from matplotlib import style
import seaborn as sns
```

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

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

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

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):
 #   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 [6]:
```
Positive = data[data['Outcome']==1]
Positive.head(5)
```

Out[6]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
2	8	183	64	0	0	23.3	0.672	32	1
4	0	137	40	35	168	43.1	2.288	33	1
6	3	78	50	32	88	31.0	0.248	26	1
8	2	197	70	45	543	30.5	0.158	53	1

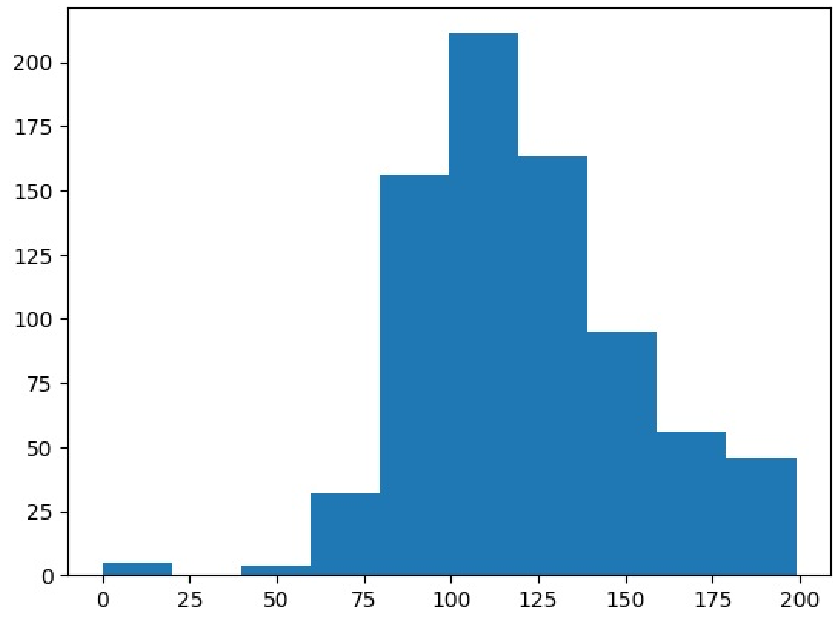
In [7]:
```
data['Glucose'].value_counts().head(7)
```

Out[7]:
```
Glucose
99     17
100    17
111    14
129    14
125    14
106    14
112    13
Name: count, dtype: int64
```

In [8]:
```
plt.hist(data['Glucose'])
```

```
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. ]),
         <BarContainer object of 10 artists>)
```

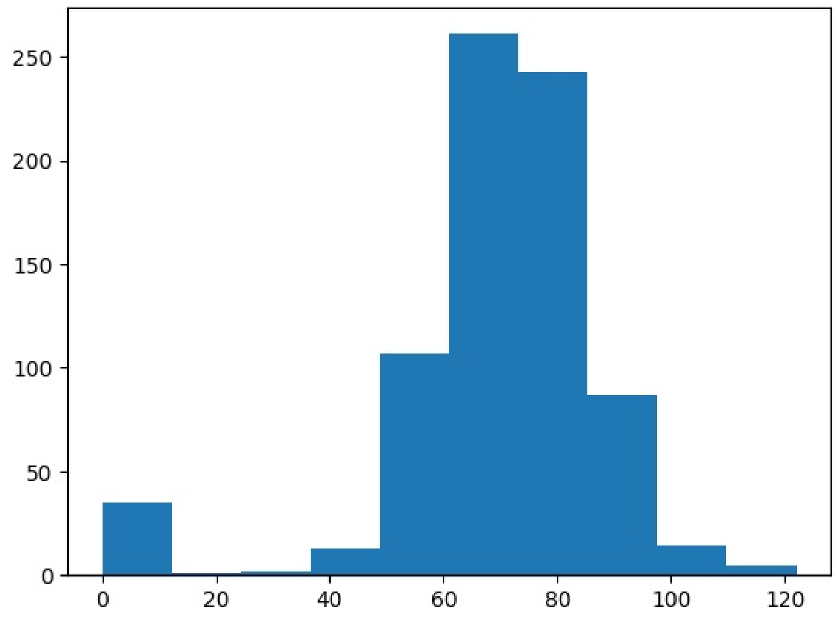


```
In [9]: data['BloodPressure'].value_counts().head(7)
```

```
Out[9]: BloodPressure
        70    57
        74    52
        78    45
        68    45
        72    44
        64    43
        80    40
        Name: count, 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. ]),
          <BarContainer object of 10 artists>)
```

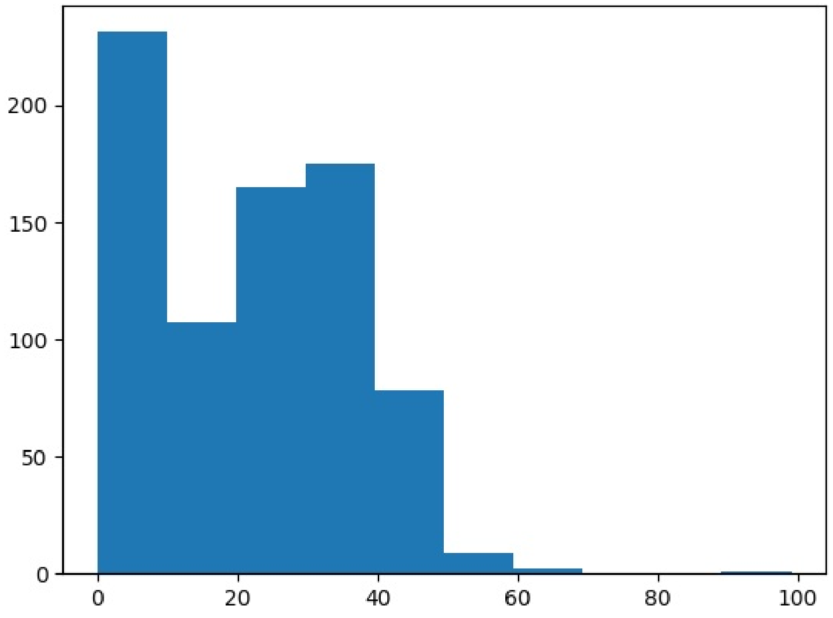


```
In [11]: data['SkinThickness'].value_counts().head(7)
```

```
Out[11]: SkinThickness
         0     227
         32     31
         30     27
         27     23
         23     22
         33     20
         28     20
         Name: count, 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. ]),
          <BarContainer object of 10 artists>)
```

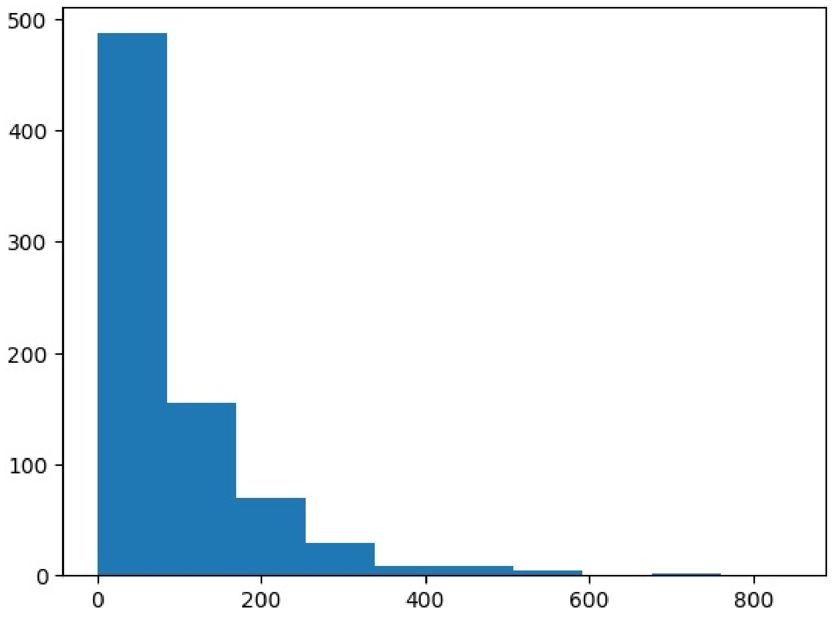


```
In [13]: data['Insulin'].value_counts().head(7)
```

```
Out[13]: Insulin
         0      374
         105     11
         130      9
         140      9
         120      8
         94       7
         180      7
         Name: count, 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. ]),
          <BarContainer object of 10 artists>)
```

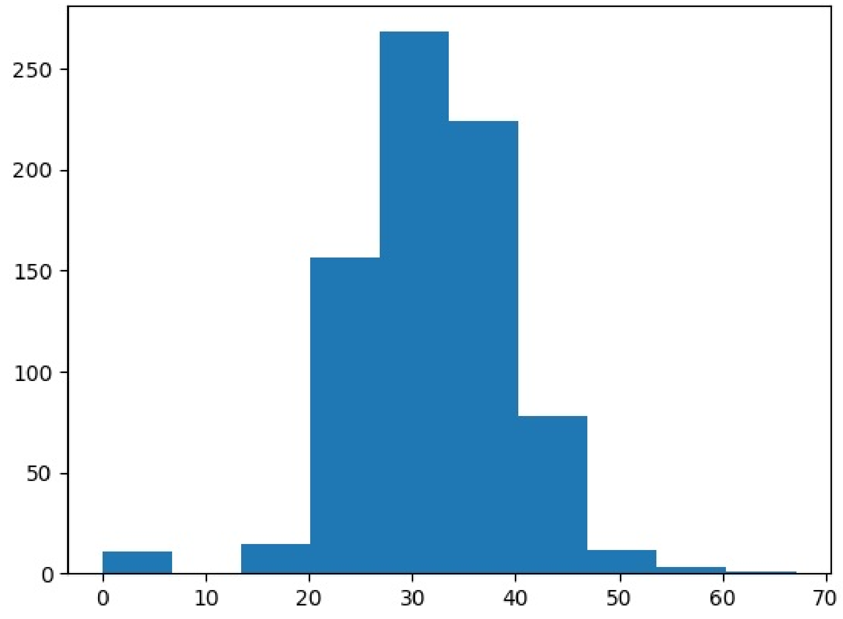


In [15]:
```
data['BMI'].value_counts().head(7)
```

Out[15]:
```
BMI
32.0    13
31.6    12
31.2    12
0.0     11
32.4    10
33.3    10
30.1     9
Name: count, 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 ]),
 <BarContainer object of 10 artists>)
```



In [17]:
```
data.describe().transpose()
```

Out[17]:

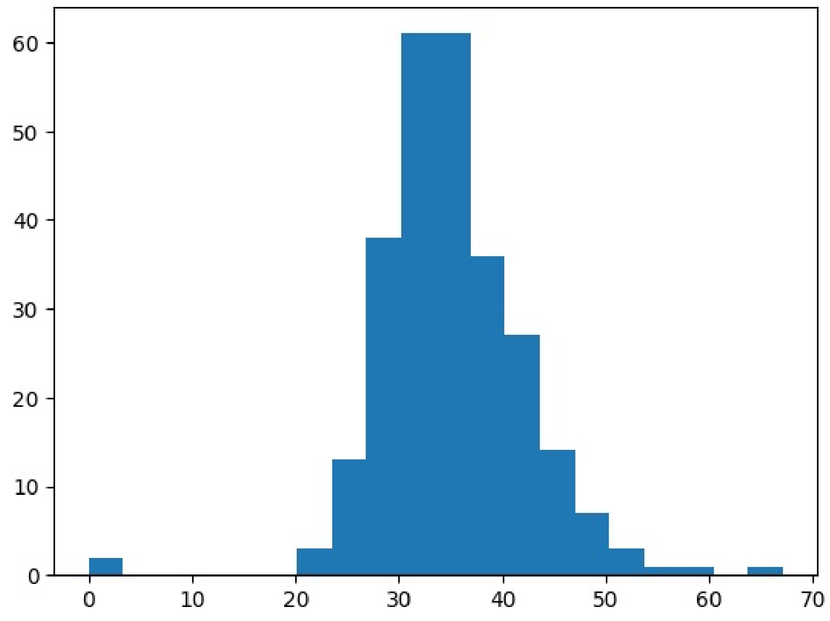
	count	mean	std	min	25%	50%	75%	max
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
SkinThickness	768.0	20.536458	15.952218	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

In [ ]:

Week 2

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  ]),
 [<matplotlib.patches.Polygon at 0x1f3cd35d650>])
```

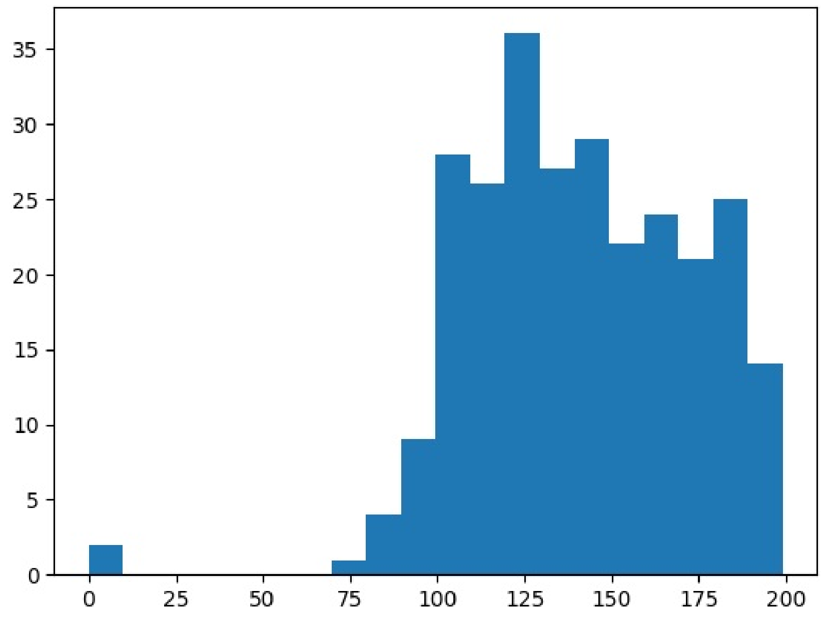


```
In [19]: Positive['BMI'].value_counts().head(7)
```

```
Out[19]: BMI
         32.9    8
         31.6    7
         33.3    6
         31.2    5
         30.5    5
         32.0    5
         34.3    4
         Name: count, 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.  ]),
          [<matplotlib.patches.Polygon at 0x1f3cf58ac10>])
```

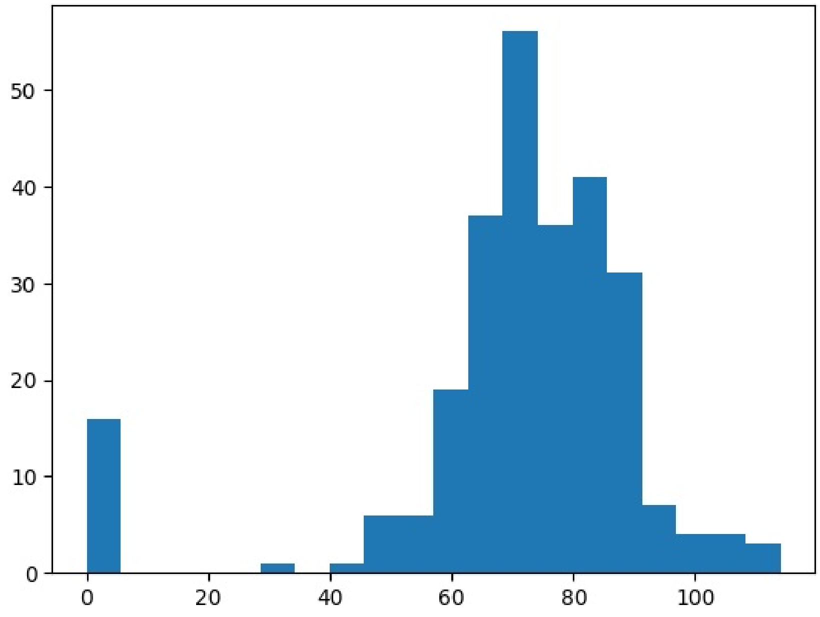


```
In [21]: Positive['Glucose'].value_counts().head(7)
```

```
Out[21]: Glucose
         125    7
         128    6
         129    6
         115    6
         158    6
         146    5
         124    5
         Name: count, 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. ]),
          [<matplotlib.patches.Polygon at 0x1f3cf6bac10>])
```

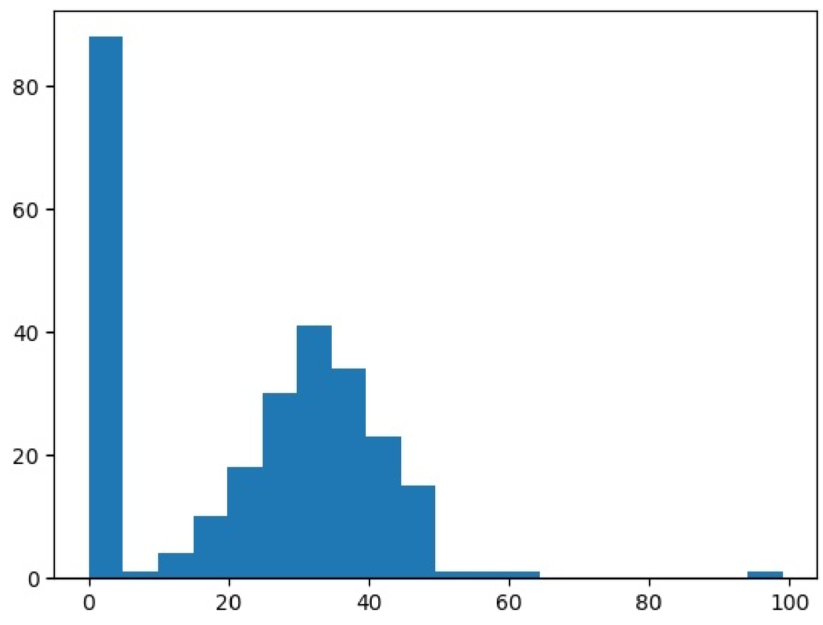


```
In [23]: Positive['BloodPressure'].value_counts().head(7)
```

```
Out[23]: BloodPressure
         70    23
         76    18
         78    17
         74    17
         72    16
         0     16
         80    13
         Name: count, 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.  ]),
          [<matplotlib.patches.Polygon at 0x1f3cf89ef50>])
```

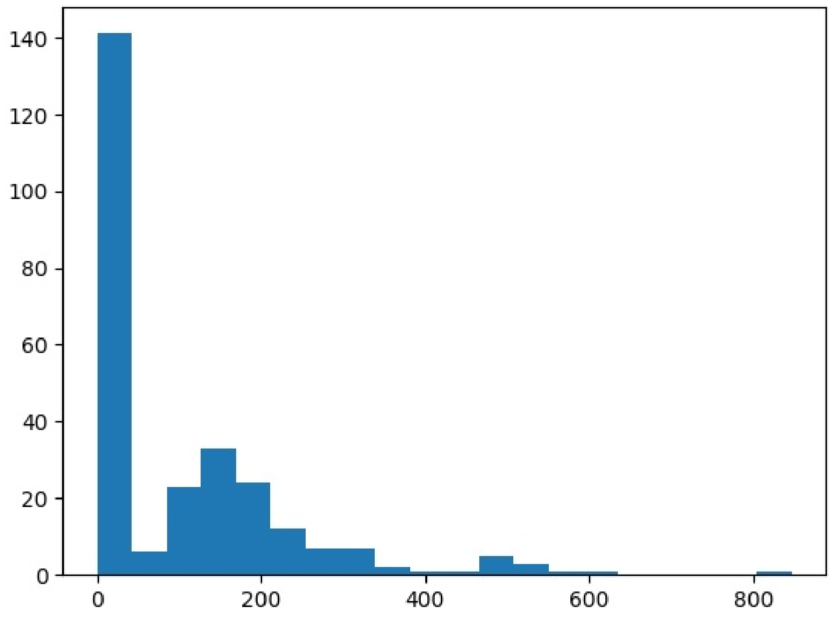


```
In [25]: Positive['SkinThickness'].value_counts().head(7)
```

```
Out[25]: SkinThickness
0     88
32    14
30     9
33     9
39     8
37     8
36     8
Name: count, 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. ]),
 [<matplotlib.patches.Polygon at 0x1f3cf91f9d0>])
```



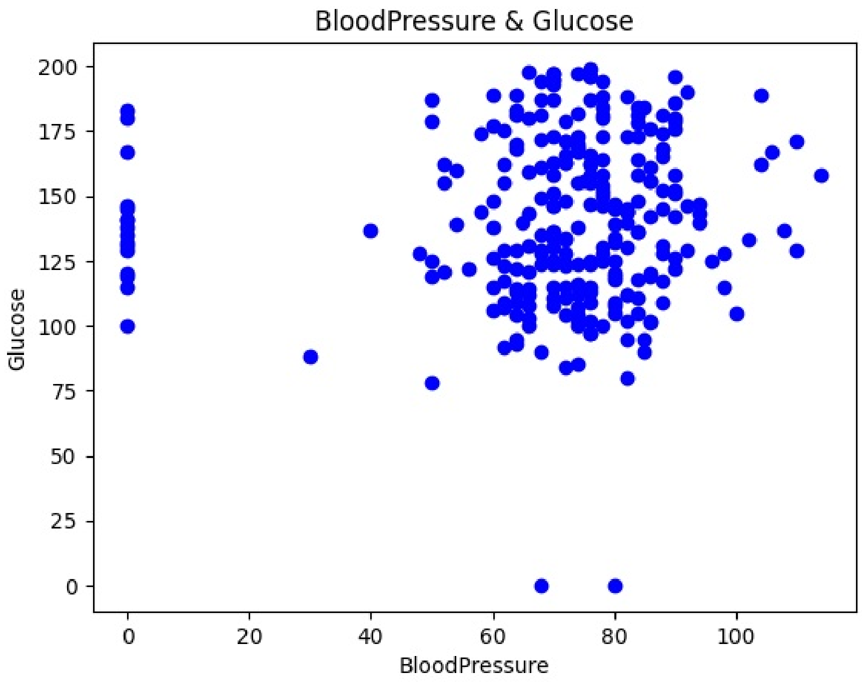
In [27]:
```
Positive['Insulin'].value_counts().head(7)
```

Out[27]:
```
Insulin
0      138
130      6
180      4
175      3
156      3
185      2
194      2
Name: count, dtype: int64
```

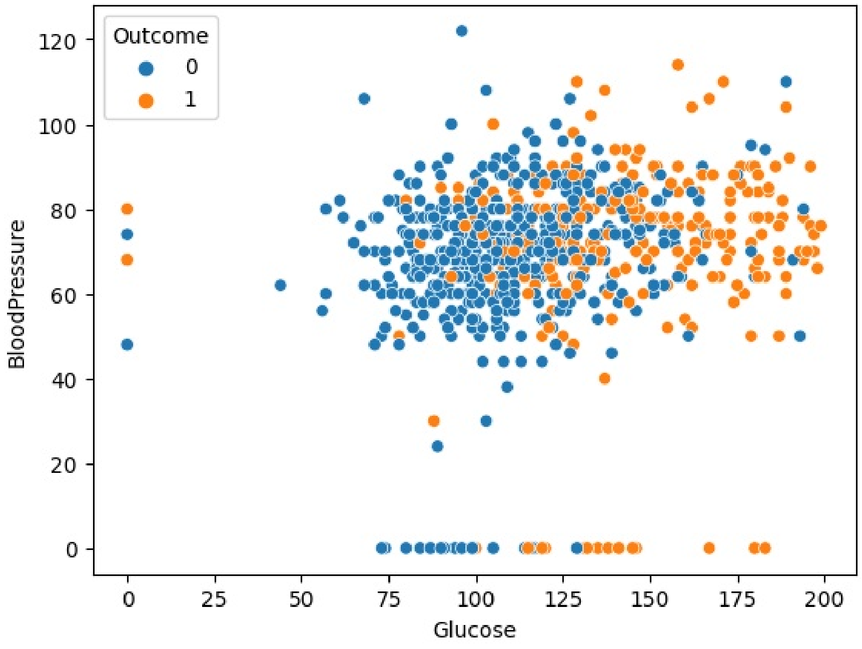
In [28]:
```
#Scatter plot
```

In [29]:
```
BloodPressure = Positive['BloodPressure']
Glucose = Positive['Glucose']
SkinThickness = Positive['SkinThickness']
Insulin = Positive['Insulin']
BMI = Positive['BMI']
```

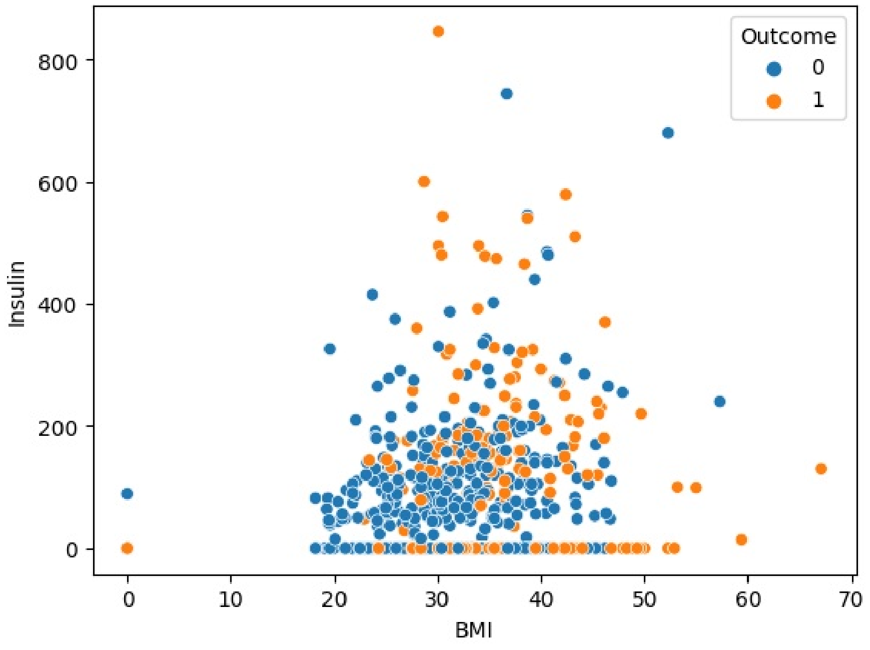
In [30]:
```
plt.scatter(BloodPressure, Glucose, color=['b'])
plt.xlabel('BloodPressure')
plt.ylabel('Glucose')
plt.title('BloodPressure & Glucose')
plt.show()
```



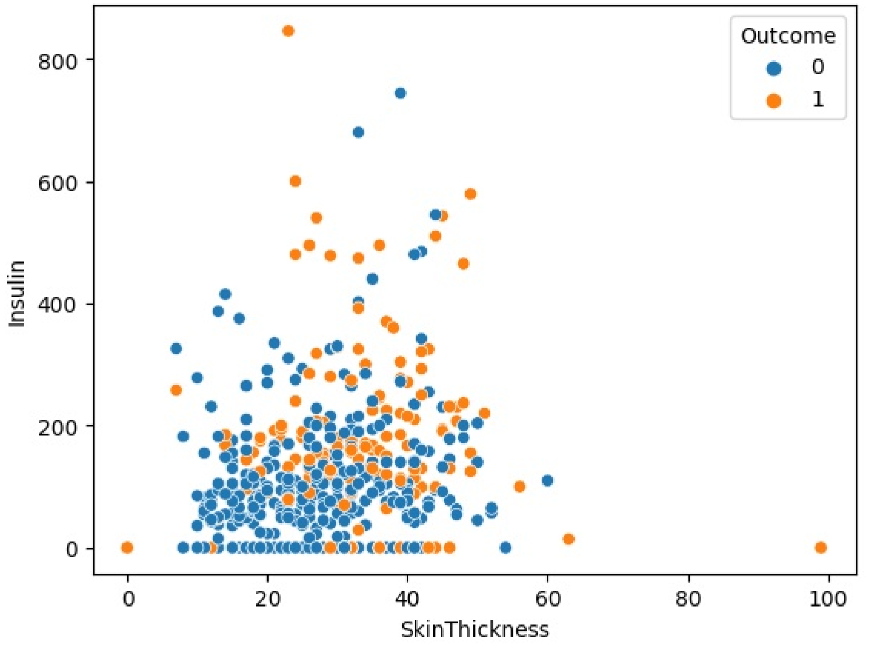
```
In [31]: g =sns.scatterplot(x= "Glucose" ,y= "BloodPressure",
                        hue="Outcome",
                        data=data);
```



```
In [32]: B =sns.scatterplot(x= "BMI" ,y= "Insulin",
                        hue="Outcome",
                        data=data);
```



In [33]:
```python
S =sns.scatterplot(x= "SkinThickness" ,y= "Insulin",
              hue="Outcome",
              data=data);
```



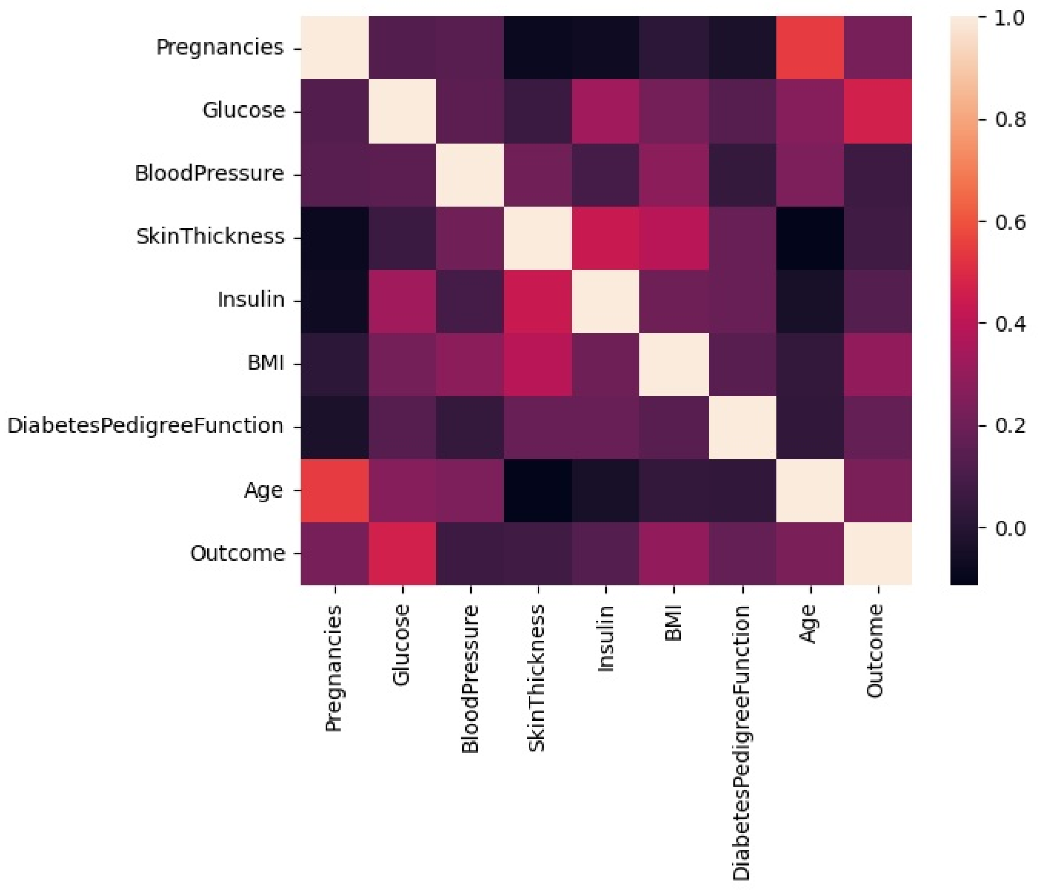
In [34]:
```python
### correlation matrix
data.corr()
```

Out[34]:

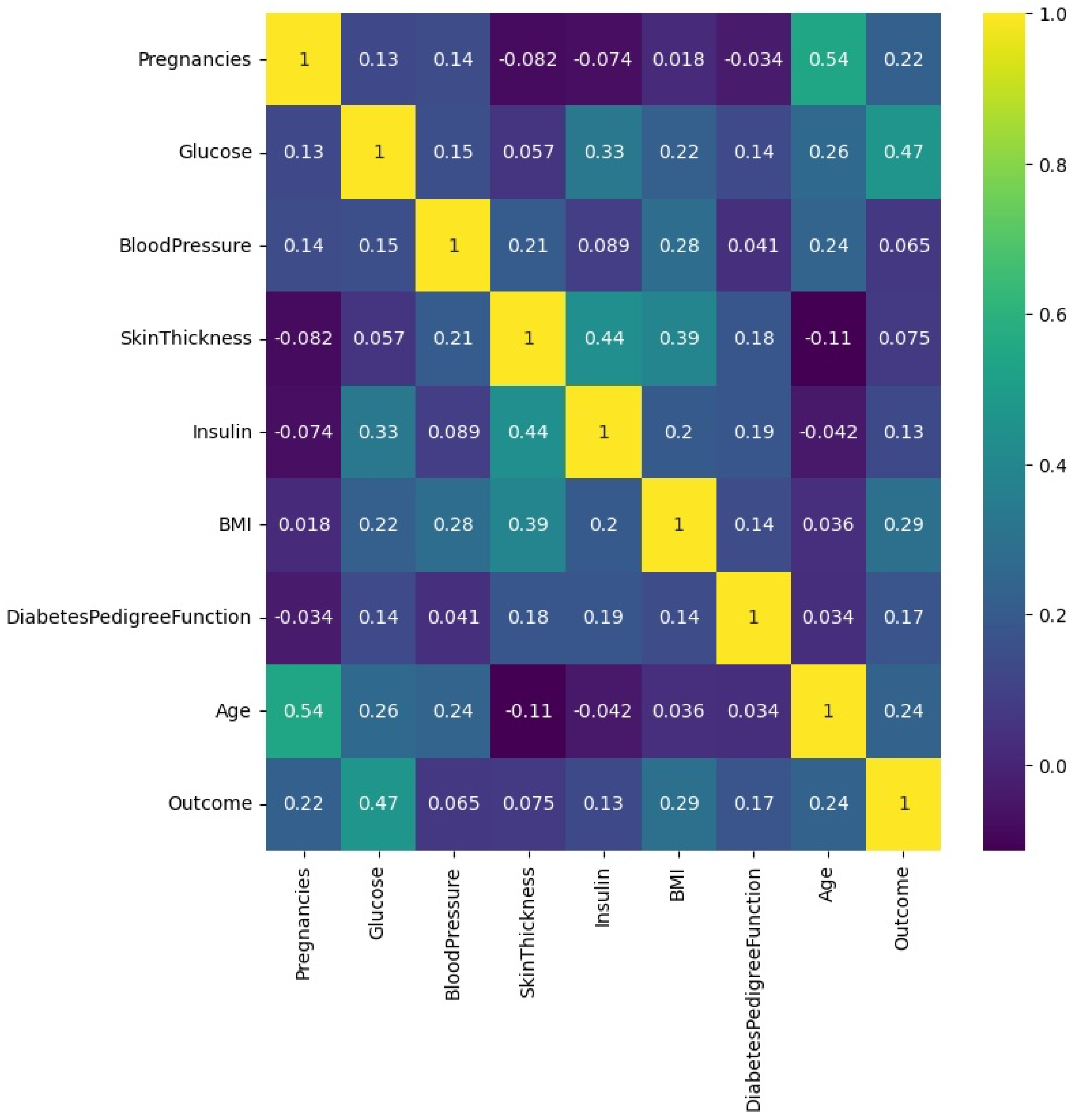
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.017683	-0.033523	0
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.221071	0.137337	0
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.281805	0.041265	0
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.392573	0.183928	-0
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.197859	0.185071	-0
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.000000	0.140647	0
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.140647	1.000000	0
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.036242	0.033561	1
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.292695	0.173844	0

In [35]:
```python
### create correlation heat map
sns.heatmap(data.corr())
```

Out[35]:
```
<Axes: >
```

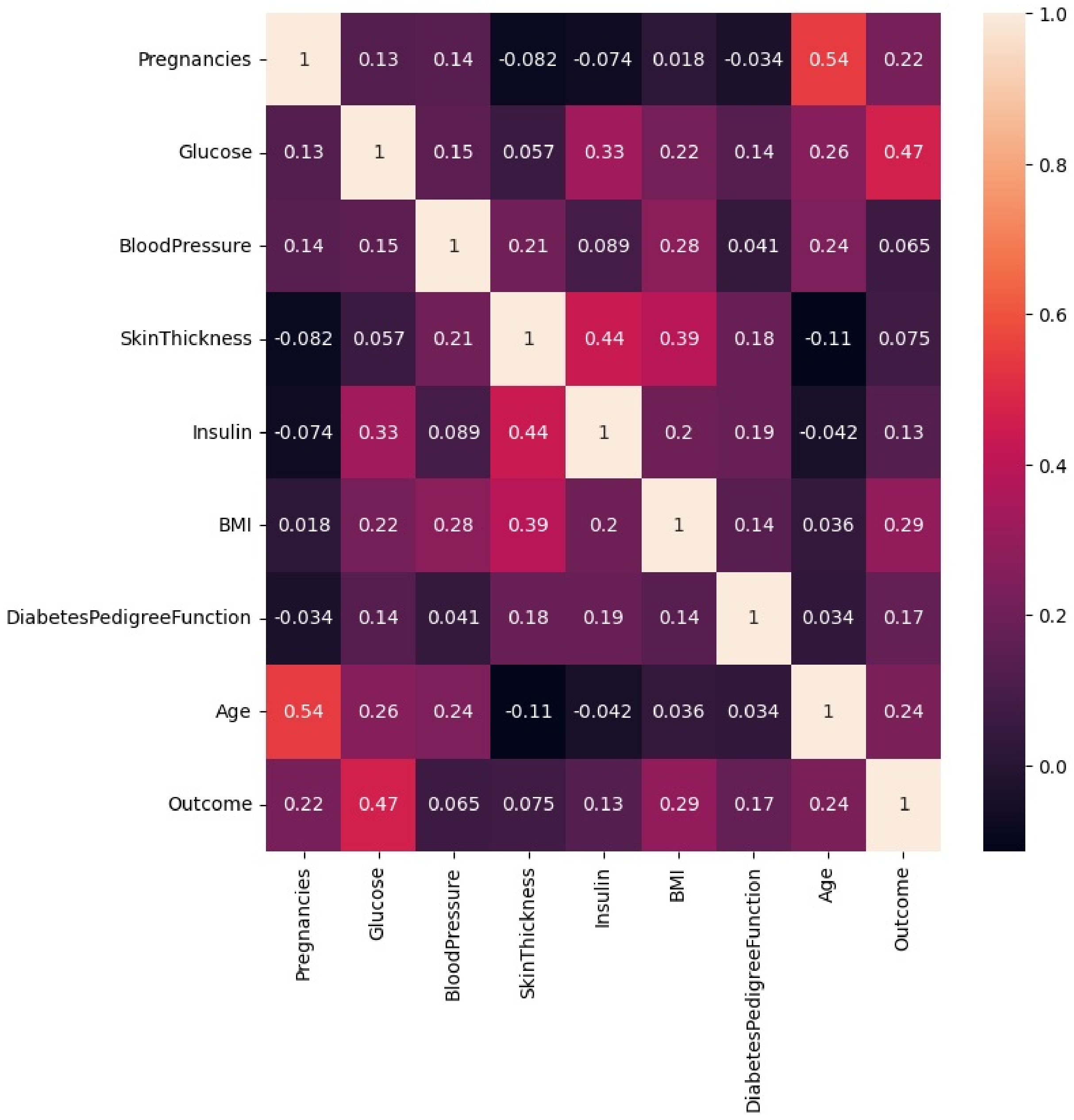


```
In [36]: plt.subplots(figsize=(8,8))
         sns.heatmap(data.corr(),annot=True,cmap='viridis')  ### gives correlation value

Out[36]: <Axes: >
```



	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]: <Axes: >
```



	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 [38]:
```
# Logistic Regreation and model building
```

In [39]:
```
data.head(5)
```

Out[39]:

	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 [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)
```

Out[42]:
```
▾ LogisticRegression
LogisticRegression()
```

In [43]:
```
print(model.score(X_train,y_train))
print(model.score(X_test,y_test))
```

```
0.7719869706840391
0.7662337662337663
```

In [44]:
```
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(label,model.predict(features))
cm
```

Out[44]:
```
array([[446,  54],
       [122, 146]], dtype=int64)
```

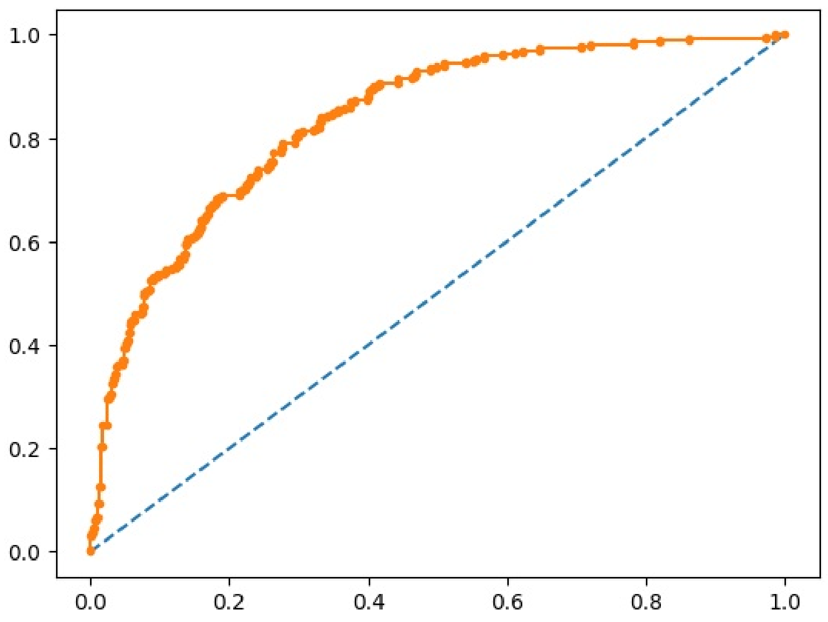
In [45]:
```
from sklearn.metrics import classification_report
print(classification_report(label,model.predict(features)))
```

```
              precision    recall  f1-score   support

           0       0.79      0.89      0.84       500
           1       0.73      0.54      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='.')
```

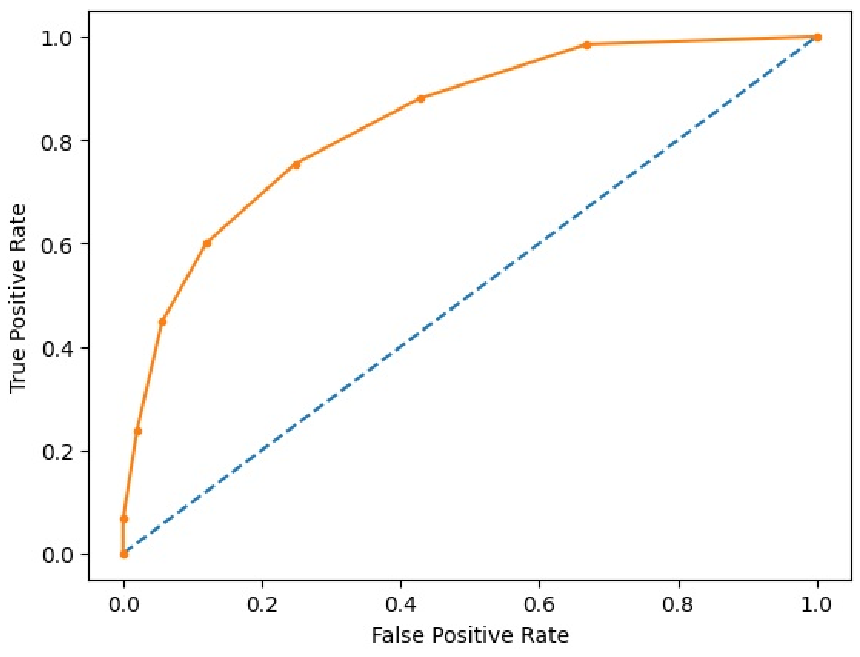
```
AUC: 0.837
```

Out[46]:
```
[<matplotlib.lines.Line2D at 0x1f3d21d97d0>]
```



```
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
         DecisionTreeClassifier(max_depth=5)

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
         RandomForestClassifier(n_estimators=11)

In [51]: model4.score(X_train,y_train)

Out[51]: 0.993485342019544

In [52]: model4.score(X_test,y_test)

Out[52]: 0.7207792207792207

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
         SVC(gamma='auto')

In [57]: model5.score(X_train,y_train)
```

```
Out[57]: 1.0

In [58]: model5.score(X_test,y_test)

Out[58]: 0.6168831168831169

In [59]: #Applying K-NN
         from sklearn.neighbors import KNeighborsClassifier
         model2 = KNeighborsClassifier(n_neighbors=7,
                                       metric='minkowski',
                                       p = 2)
         model2.fit(X_train,y_train)

Out[59]: ▾         KNeighborsClassifier
         KNeighborsClassifier(n_neighbors=7)

In [60]: #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,fpr,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 0.60074627 0.75373134
         0.88059701 0.98507463 1.        ], False Positive Rate - [0.    0.    0.02  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[60]: Text(0, 0.5, 'True Positive Rate')
```

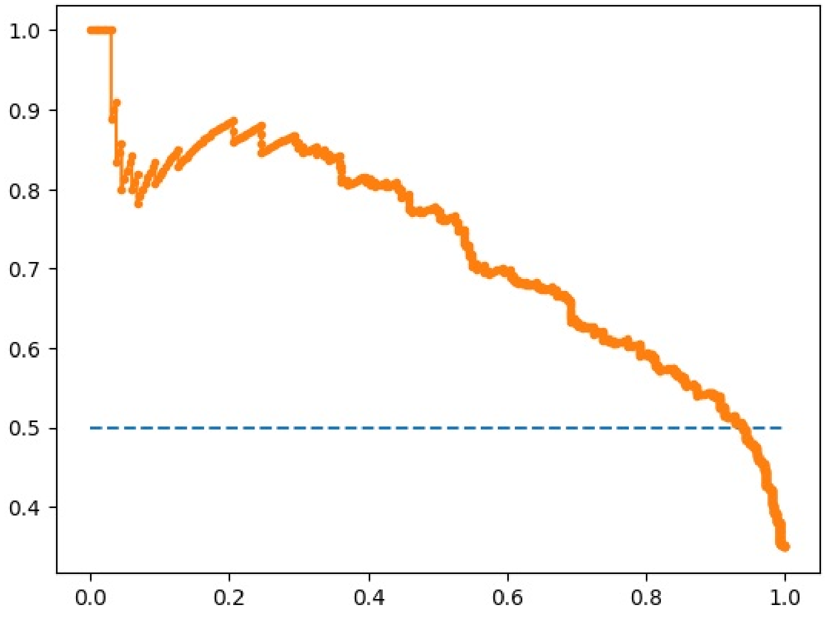


```
In [61]: #Precision Recall Curve for Logistic Regression

         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=0.624 auc=0.726 ap=0.727
```

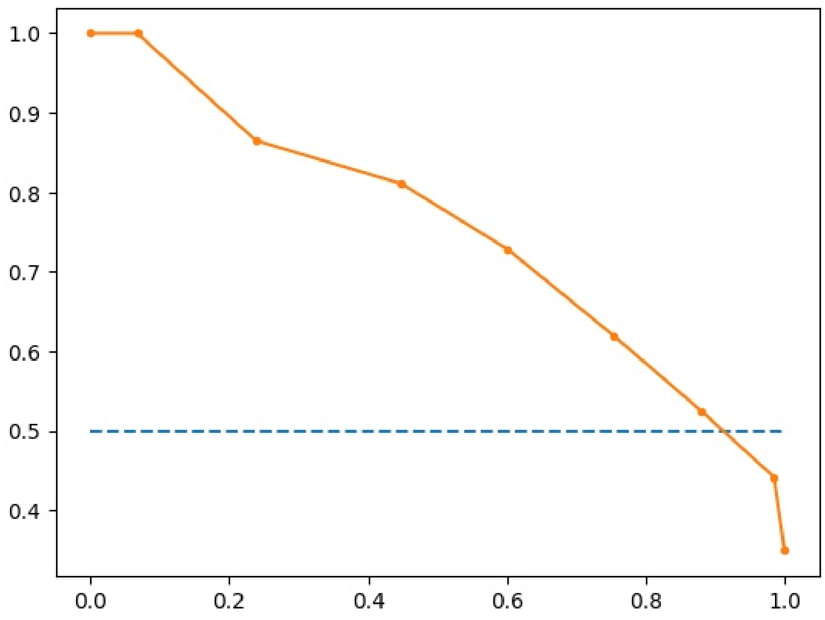
Out[61]: `[<matplotlib.lines.Line2D at 0x1f3d3b07350>]`



In [62]:
```
#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='.')
```

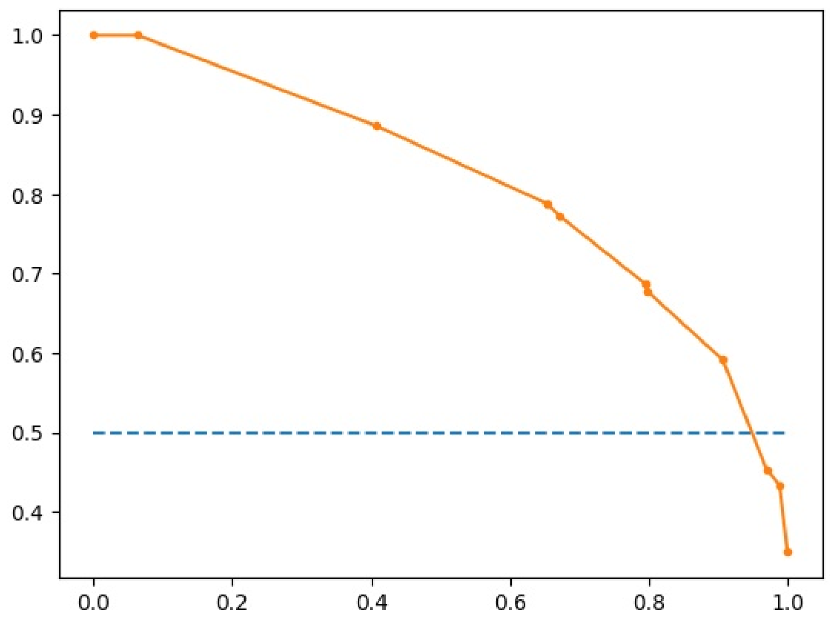
```
f1=0.658 auc=0.752 ap=0.709
```

Out[62]: `[<matplotlib.lines.Line2D at 0x1f3d3d47a90>]`



```
In [63]: #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='.')
```

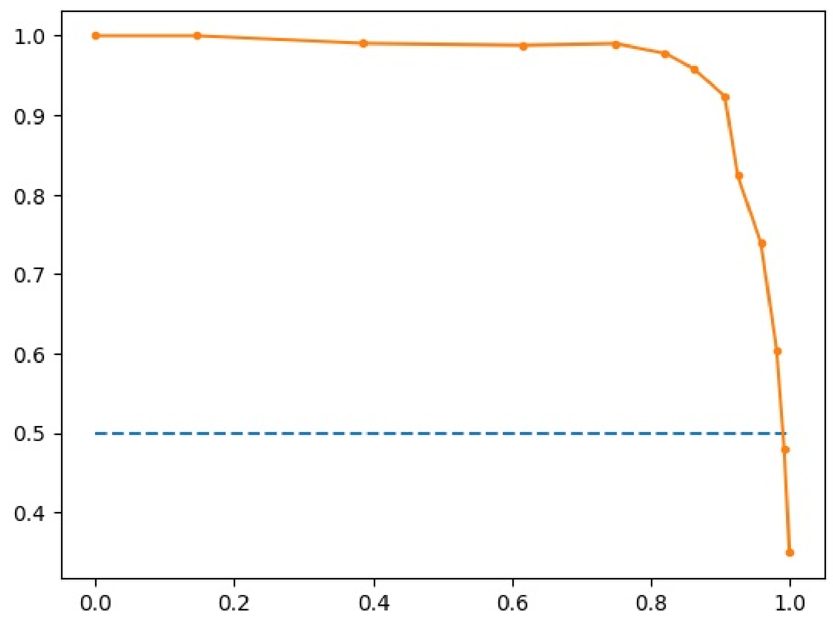
```
        f1=0.714 auc=0.815 ap=0.768
Out[63]: [<matplotlib.lines.Line2D at 0x1f3d3dbd9d0>]
```



```
In [64]: #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=0.908 auc=0.963 ap=0.955
```

```
Out[64]: [<matplotlib.lines.Line2D at 0x1f3d3ad80d0>]
```


1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.0
0.2
0.4
0.6
0.8
1.0