# Healthcare.capstone

January 19, 2024

DATASCIENCE CAPSTONE PROJECT

HEALTHCARE BY SUJATA KINHEKAR

```
[1]: #IMPORT LIBRARIES
     import pandas as pd
     import numpy as np
     import matplotlib.pyplot as plt
     import seaborn as sns
```

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

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

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

        DiabetesPedigreeFunction  Age  Outcome
     0                     0.627   50        1
     1                     0.351   31        0
     2                     0.672   32        1
     3                     0.167   21        0
     4                     2.288   33        1
```

```
[4]: data.isnull().any()
```

```
[4]: Pregnancies                 False
     Glucose                     False
     BloodPressure               False
     SkinThickness               False
     Insulin                     False
     BMI                         False
     DiabetesPedigreeFunction    False
     Age                         False
     Outcome                     False
```

```
dtype: bool
```

```
[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
```

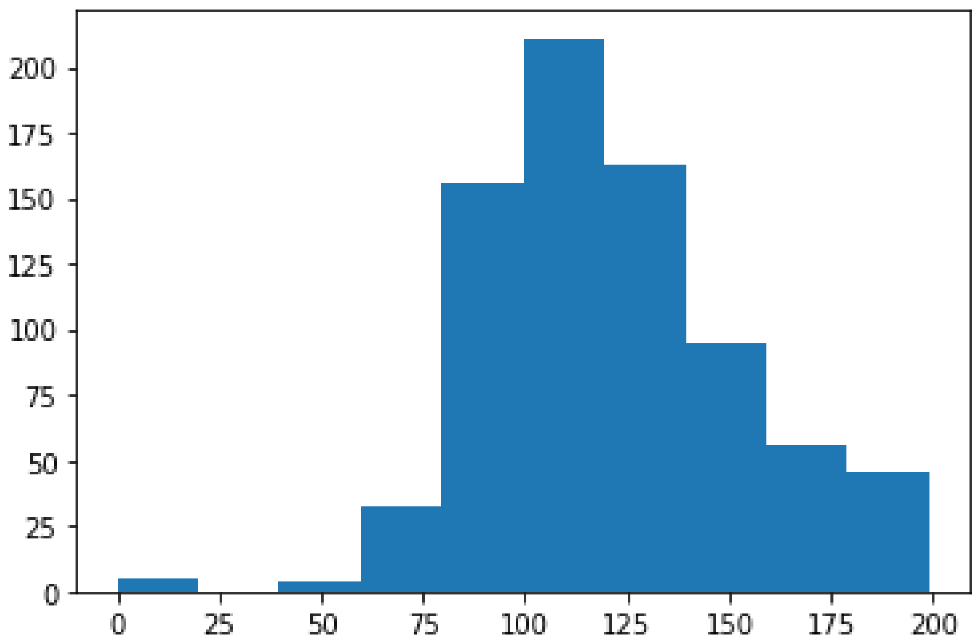
## 0.1 USING HISTOGRAMS

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

```
[6]: 100    17
     99     17
     129    14
     125    14
     111    14
     106    14
     95     13
     Name: Glucose, dtype: int64
```

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

```
[7]: (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>)
```

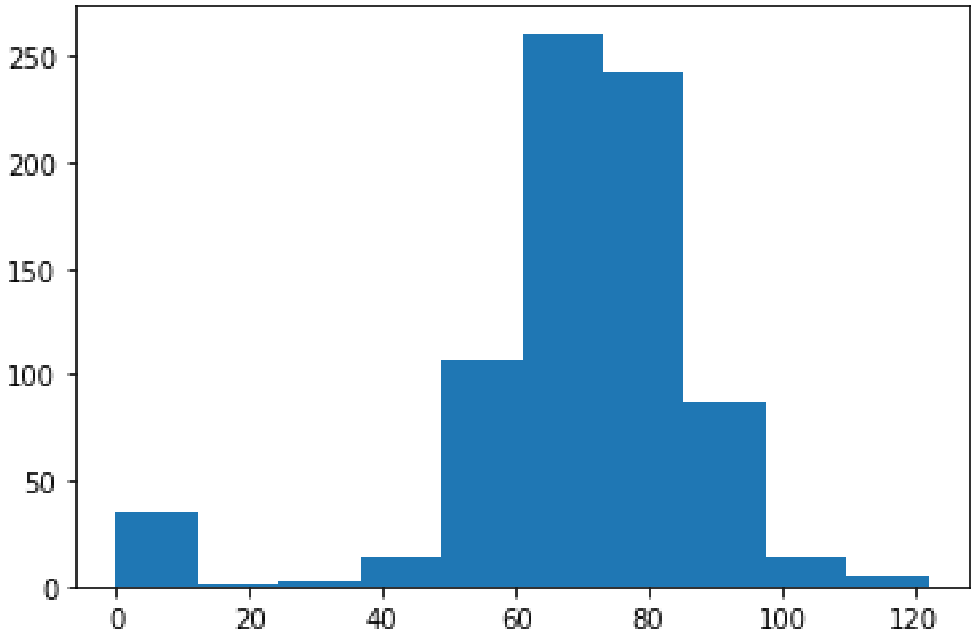


[8]:
```
data['BloodPressure'].value_counts().head(7)
```

[8]:
```
70    57
74    52
68    45
78    45
72    44
64    43
80    40
Name: BloodPressure, dtype: int64
```

[9]:
```
plt.hist(data['BloodPressure'])
```

[9]:
```
(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>)
```

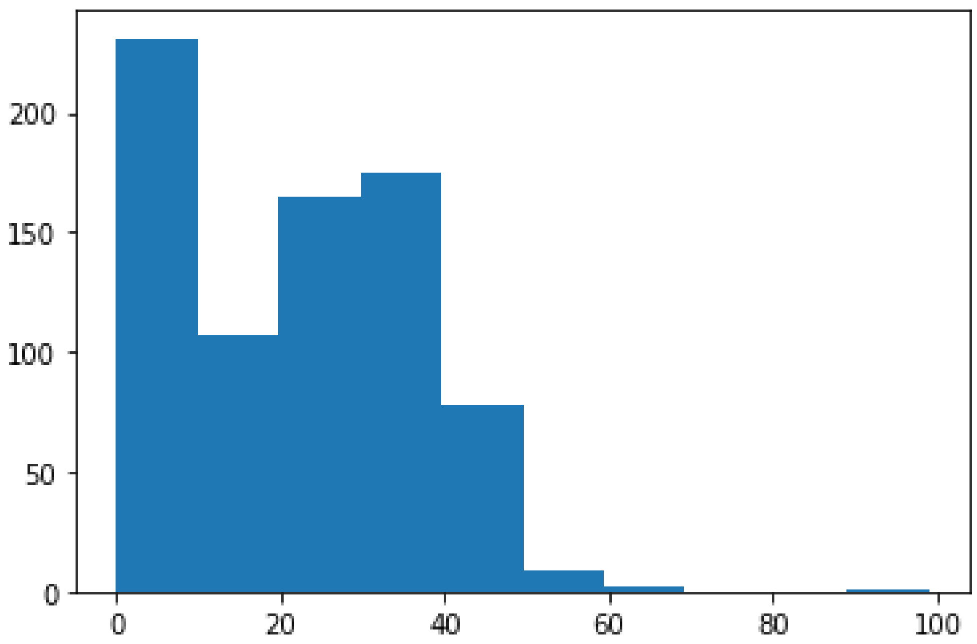


[10]:
```
data['SkinThickness'].value_counts().head(7)
```

[10]:
```
0     227
32     31
30     27
27     23
23     22
33     20
18     20
Name: SkinThickness, dtype: int64
```

[11]:
```
plt.hist(data['SkinThickness'])
```

[11]:
```
(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>)
```

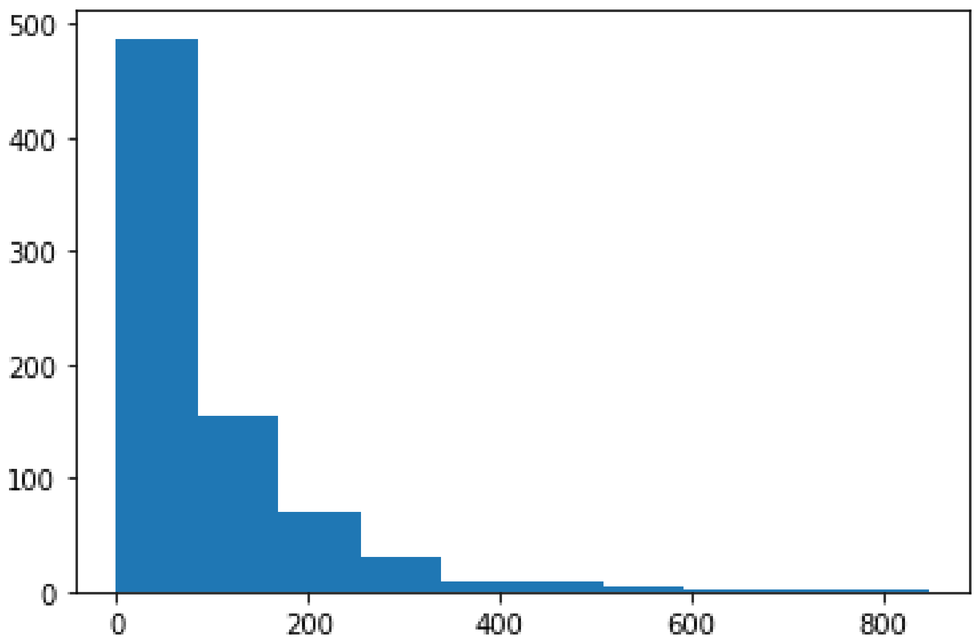


```
[12]: data['Insulin'].value_counts().head(7)
```

```
[12]: 0      374
      105     11
      140      9
      130      9
      120      8
      100      7
      94       7
      Name: Insulin, dtype: int64
```

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

```
[13]: (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>)
```

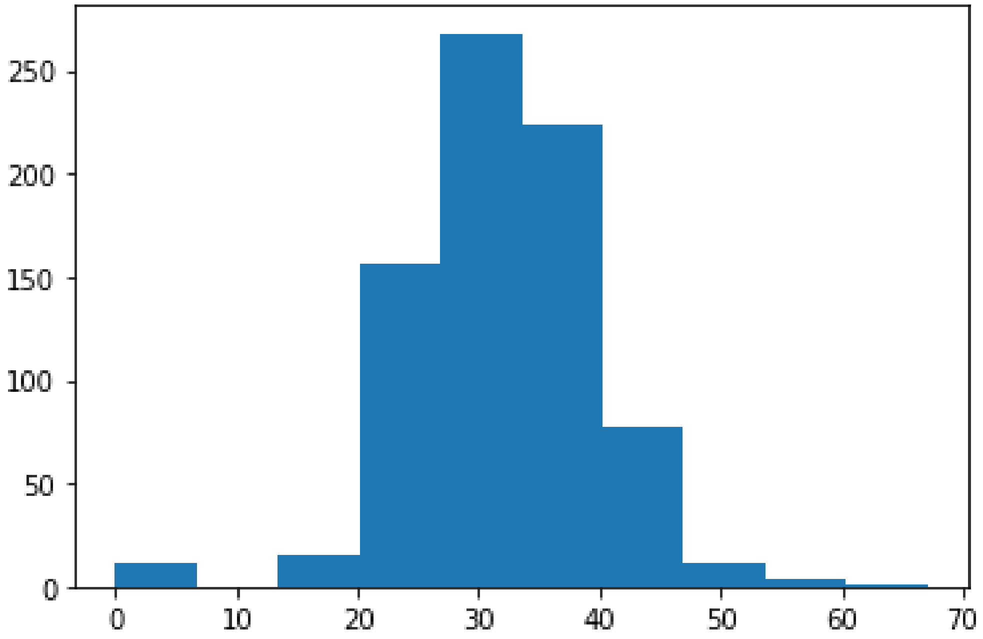


```
[14]: data['BMI'].value_counts().head(7)
```

```
[14]: 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
```

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

```
[15]: (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>)
```



```
[16]: data.describe().transpose()
```

```
[16]:                           count        mean         std     min       25%  \
      Pregnancies               768.0    3.845052    3.369578   0.000   1.00000
      Glucose                   768.0  120.894531   31.972618   0.000  99.00000
      BloodPressure             768.0   69.105469   19.355807   0.000  62.00000
      SkinThickness             768.0   20.536458   15.952218   0.000   0.00000
      Insulin                   768.0   79.799479  115.244002   0.000   0.00000
      BMI                       768.0   31.992578    7.884160   0.000  27.30000
      DiabetesPedigreeFunction  768.0    0.471876    0.331329   0.078   0.24375
      Age                       768.0   33.240885   11.760232  21.000  24.00000
      Outcome                   768.0    0.348958    0.476951   0.000   0.00000

                                     50%        75%     max
      Pregnancies                 3.0000    6.00000   17.00
      Glucose                   117.0000  140.25000  199.00
      BloodPressure              72.0000   80.00000  122.00
      SkinThickness              23.0000   32.00000   99.00
      Insulin                    30.5000  127.25000  846.00
      BMI                        32.0000   36.60000   67.10
      DiabetesPedigreeFunction    0.3725    0.62625    2.42
      Age                        29.0000   41.00000   81.00
      Outcome                     0.0000    1.00000    1.00
```

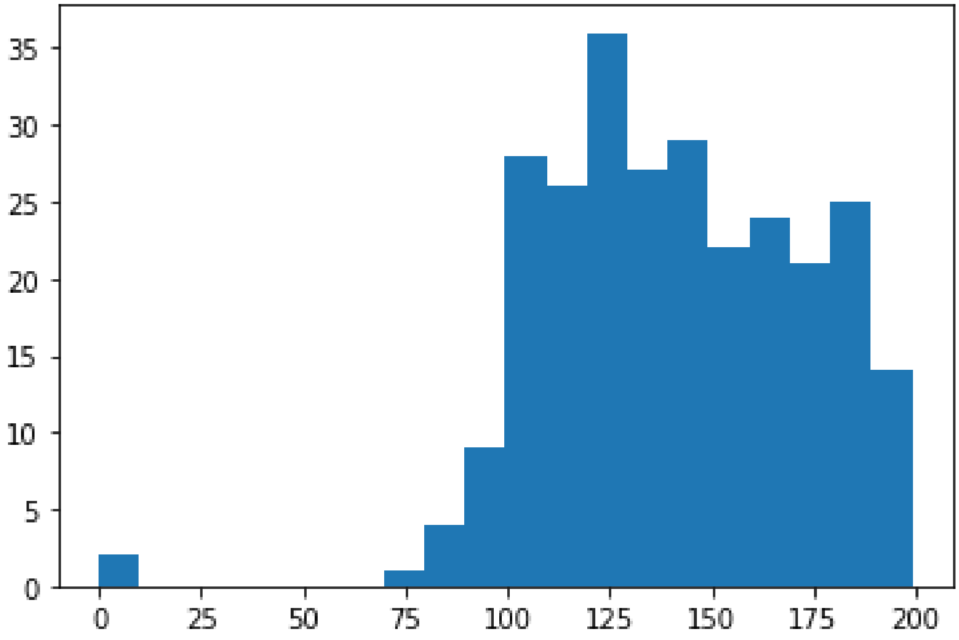
```
[17]: Positive=data[data['Outcome']==1]
      Positive.head(5)
```

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

         DiabetesPedigreeFunction  Age  Outcome
      0                     0.627   50        1
      2                     0.672   32        1
      4                     2.288   33        1
      6                     0.248   26        1
      8                     0.158   53        1
```

0.2 USING HISTOGRAM STREAT THE MISSING VALUES

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

```
[18]: (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 0x7f9c984aad90>])
```

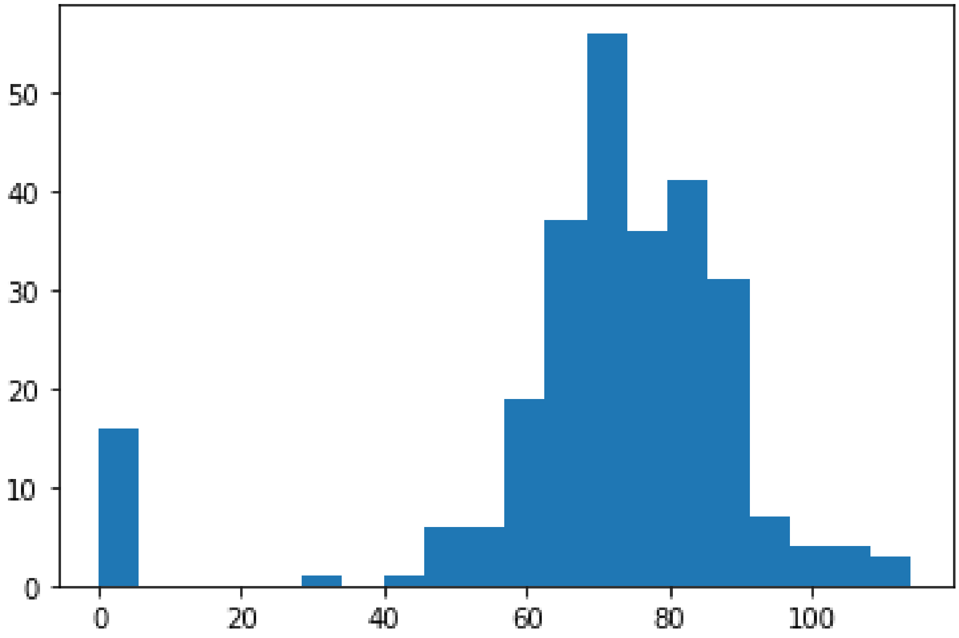


```
[20]: Positive['Glucose'].value_counts().head(7)
```

```
[20]: 125    7
      158    6
      128    6
      115    6
      129    6
      146    5
      162    5
      Name: Glucose, dtype: int64
```

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

```
[21]: (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 0x7f9c982b8fd0>])
```



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

```
[23]: 70     23
      76     18
      78     17
      74     17
      72     16
      0      16
```

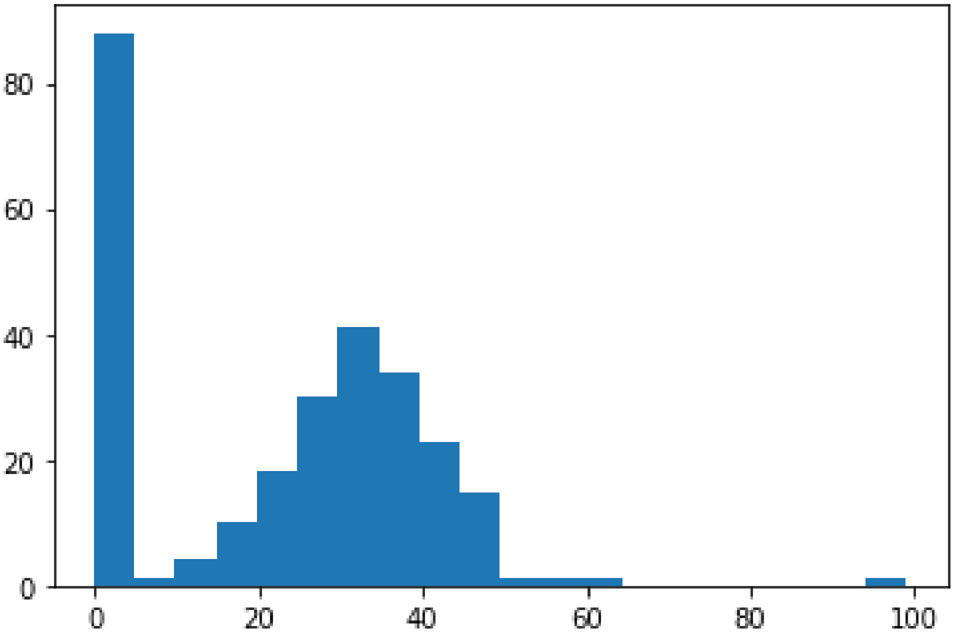
```
82    13
Name: BloodPressure, dtype: int64
```

[24]:

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

[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 0x7f9c98238a90>])
```



[26]:

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

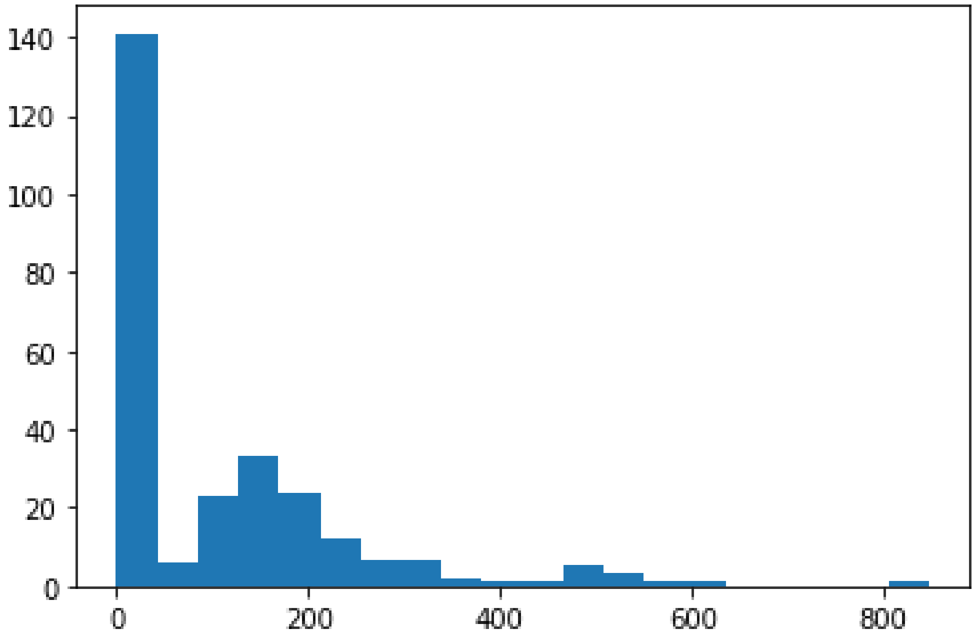
[26]:

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

[27]:

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

```
[27]: (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 0x7f9c981b4a50>])
```

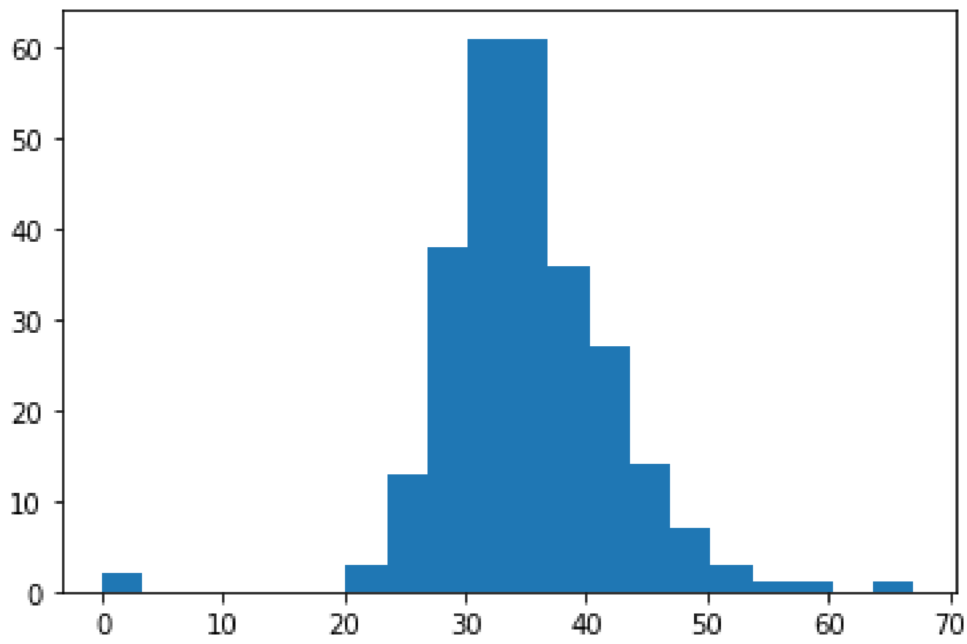


```
[28]: Positive['Insulin'].value_counts().head(7)
```

```
[28]: 0      138
      130      6
      180      4
      156      3
      175      3
      194      2
      125      2
      Name: Insulin, dtype: int64
```

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

```
[29]: (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 0x7f9c981256d0>])
```



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

```
[30]: 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
```

```
[31]: Positive.describe().transpose()
```

```
[31]:                           count        mean         std     min       25%  \
      Pregnancies               268.0    4.865672    3.741239   0.000    1.7500
      Glucose                   268.0  141.257463   31.939622   0.000  119.0000
      BloodPressure             268.0   70.824627   21.491812   0.000   66.0000
      SkinThickness             268.0   22.164179   17.679711   0.000    0.0000
      Insulin                   268.0  100.335821  138.689125   0.000    0.0000
      BMI                       268.0   35.142537    7.262967   0.000   30.8000
      DiabetesPedigreeFunction  268.0    0.550500    0.372354   0.088    0.2625
      Age                       268.0   37.067164   10.968254  21.000   28.0000
      Outcome                   268.0    1.000000    0.000000   1.000    1.0000

                                  50%      75%     max
      Pregnancies               4.000    8.000   17.00
```

```
Glucose                     140.000  167.000  199.00
BloodPressure                74.000   82.000  114.00
SkinThickness                27.000   36.000   99.00
Insulin                       0.000  167.250  846.00
BMI                          34.250   38.775   67.10
DiabetesPedigreeFunction      0.449    0.728    2.42
Age                          36.000   44.000   70.00
Outcome                       1.000    1.000    1.00
```

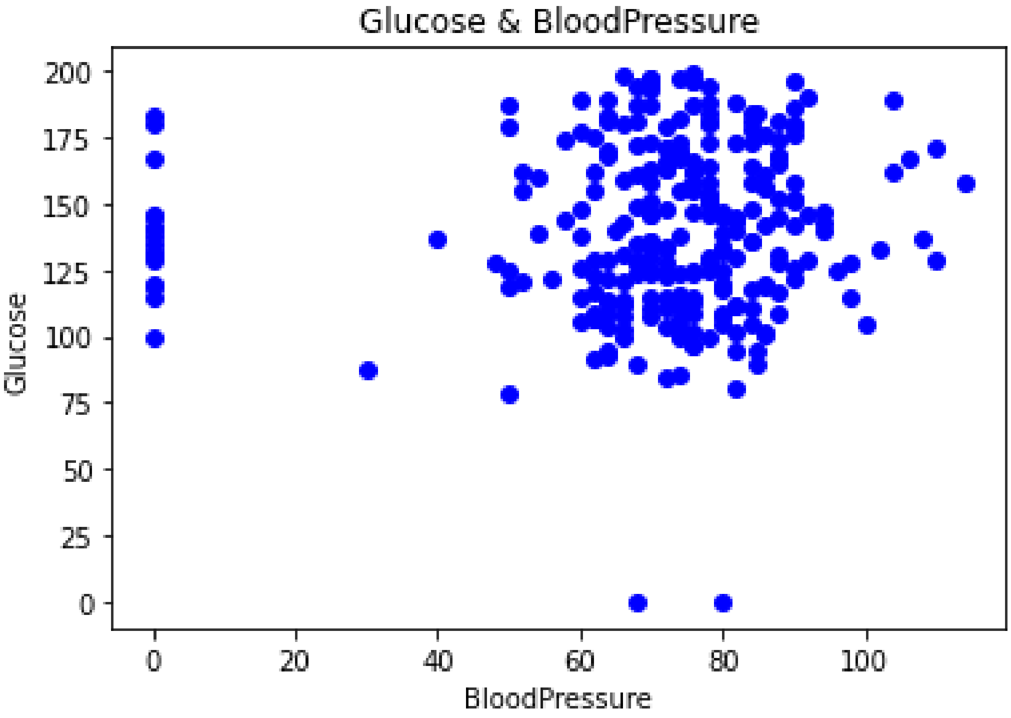
1 SCATTERPLOT

[32]:

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

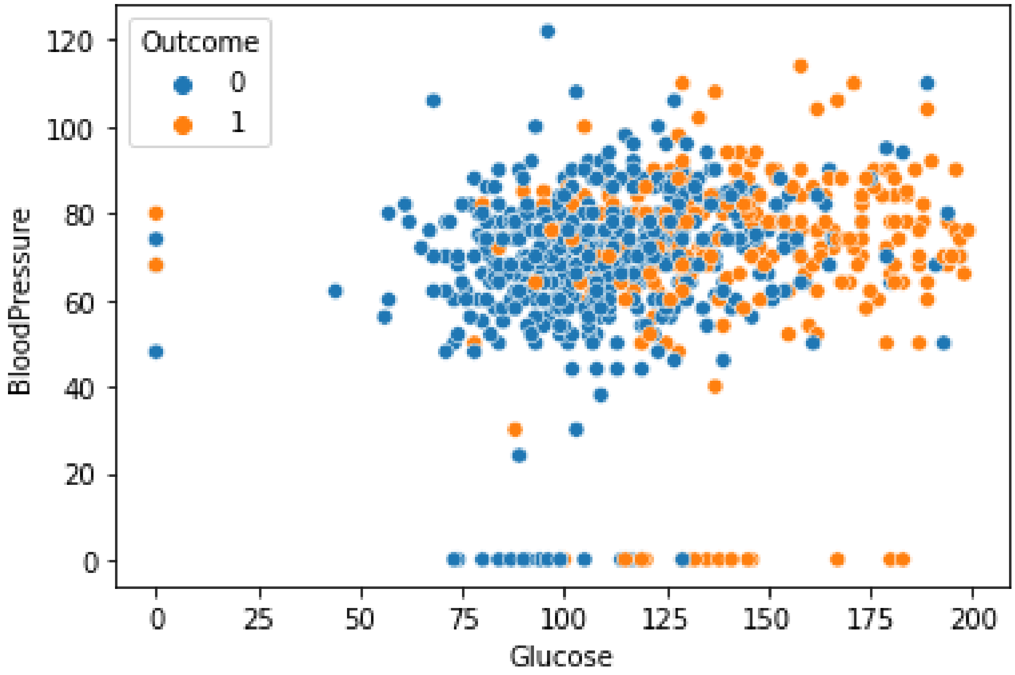
[33]:

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

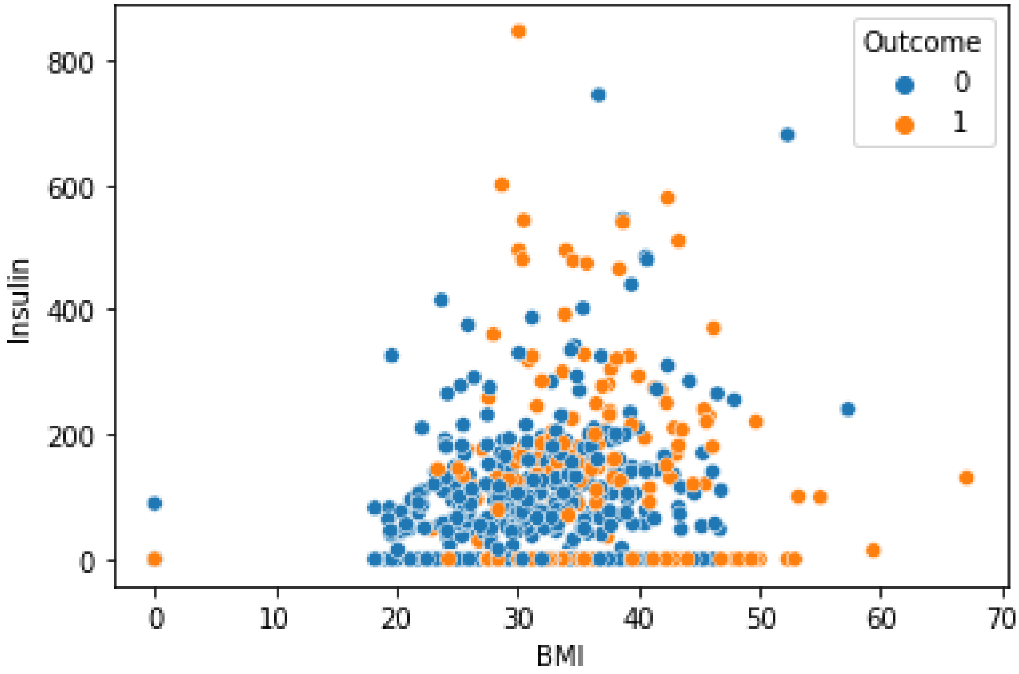


[34]:

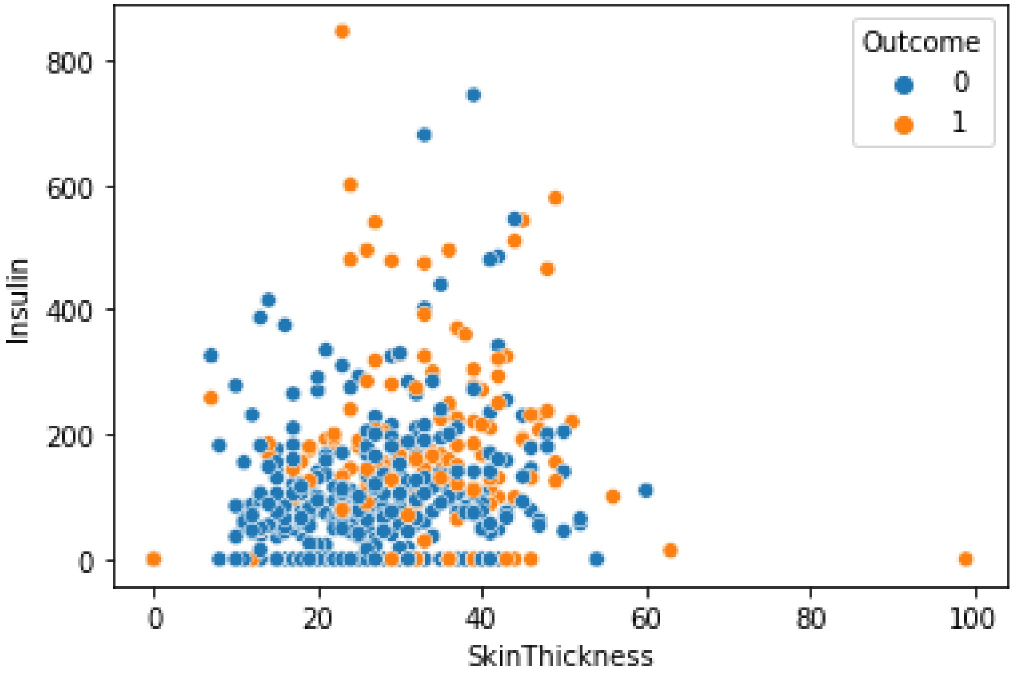
```
g=sns.scatterplot(x='Glucose',y='BloodPressure',hue='Outcome',data=data);
```



[35]:
```
B=sns.scatterplot(x='BMI', y='Insulin', hue='Outcome', data=data);
```



[36]:
```
g=sns.scatterplot(x='SkinThickness',y='Insulin',hue='Outcome', data=data);
```



1.1 CORRELATIONANALYSIS

[37]:
```
data.corr()
```

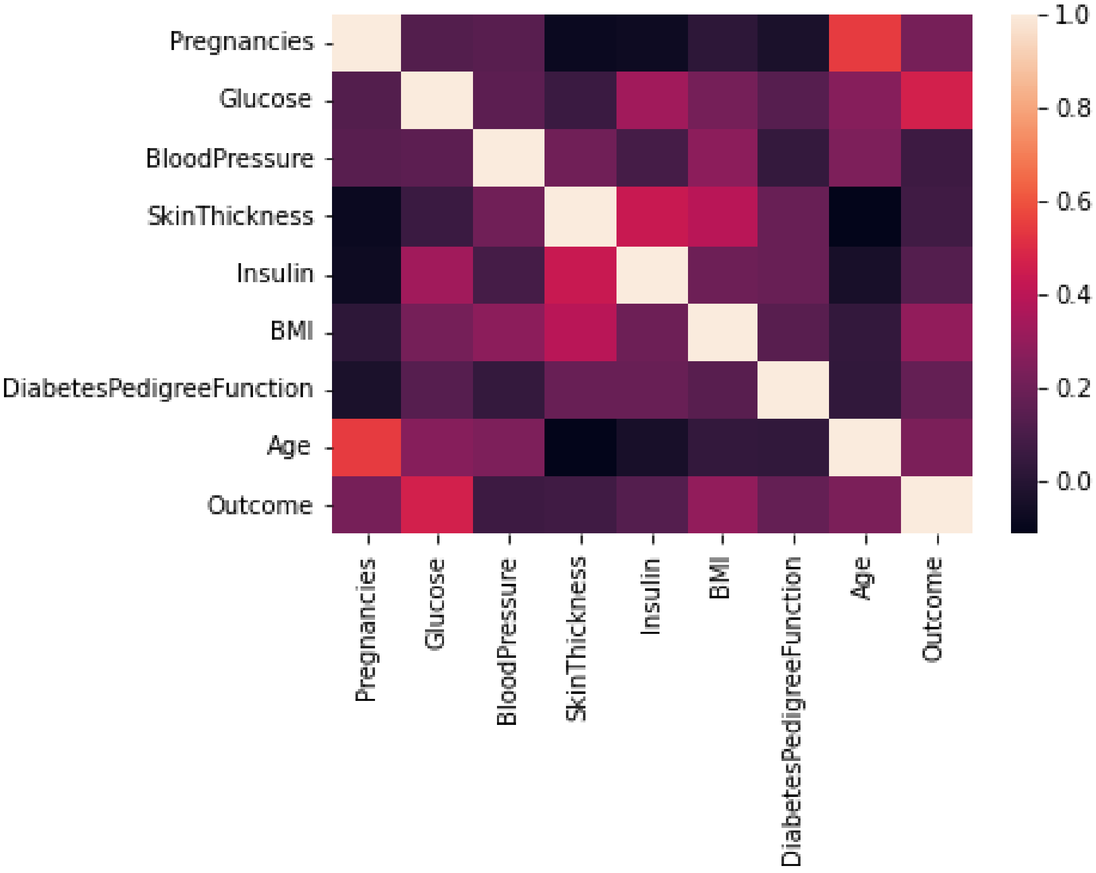
[37]:
```
                          Pregnancies   Glucose  BloodPressure  SkinThickness  \
Pregnancies                  1.000000  0.129459       0.141282      -0.081672
Glucose                      0.129459  1.000000       0.152590       0.057328
BloodPressure                0.141282  0.152590       1.000000       0.207371
SkinThickness               -0.081672  0.057328       0.207371       1.000000
Insulin                     -0.073535  0.331357       0.088933       0.436783
BMI                          0.017683  0.221071       0.281805       0.392573
DiabetesPedigreeFunction    -0.033523  0.137337       0.041265       0.183928
Age                          0.544341  0.263514       0.239528      -0.113970
Outcome                      0.221898  0.466581       0.065068       0.074752

                           Insulin       BMI  DiabetesPedigreeFunction  \
Pregnancies              -0.073535  0.017683                 -0.033523
Glucose                   0.331357  0.221071                  0.137337
BloodPressure             0.088933  0.281805                  0.041265
SkinThickness             0.436783  0.392573                  0.183928
Insulin                   1.000000  0.197859                  0.185071
BMI                       0.197859  1.000000                  0.140647
DiabetesPedigreeFunction  0.185071  0.140647                  1.000000
```

```
Age                      -0.042163  0.036242                  0.033561
Outcome                   0.130548  0.292695                  0.173844

                               Age   Outcome
Pregnancies               0.544341  0.221898
Glucose                   0.263514  0.466581
BloodPressure             0.239528  0.065068
SkinThickness            -0.113970  0.074752
Insulin                  -0.042163  0.130548
BMI                       0.036242  0.292695
DiabetesPedigreeFunction  0.033561  0.173844
Age                       1.000000  0.238356
Outcome                   0.238356  1.000000
```

## 2 HEATMAPS

[38]:
```
sns.heatmap(data.corr())
```

[38]:
```
<AxesSubplot:>
```

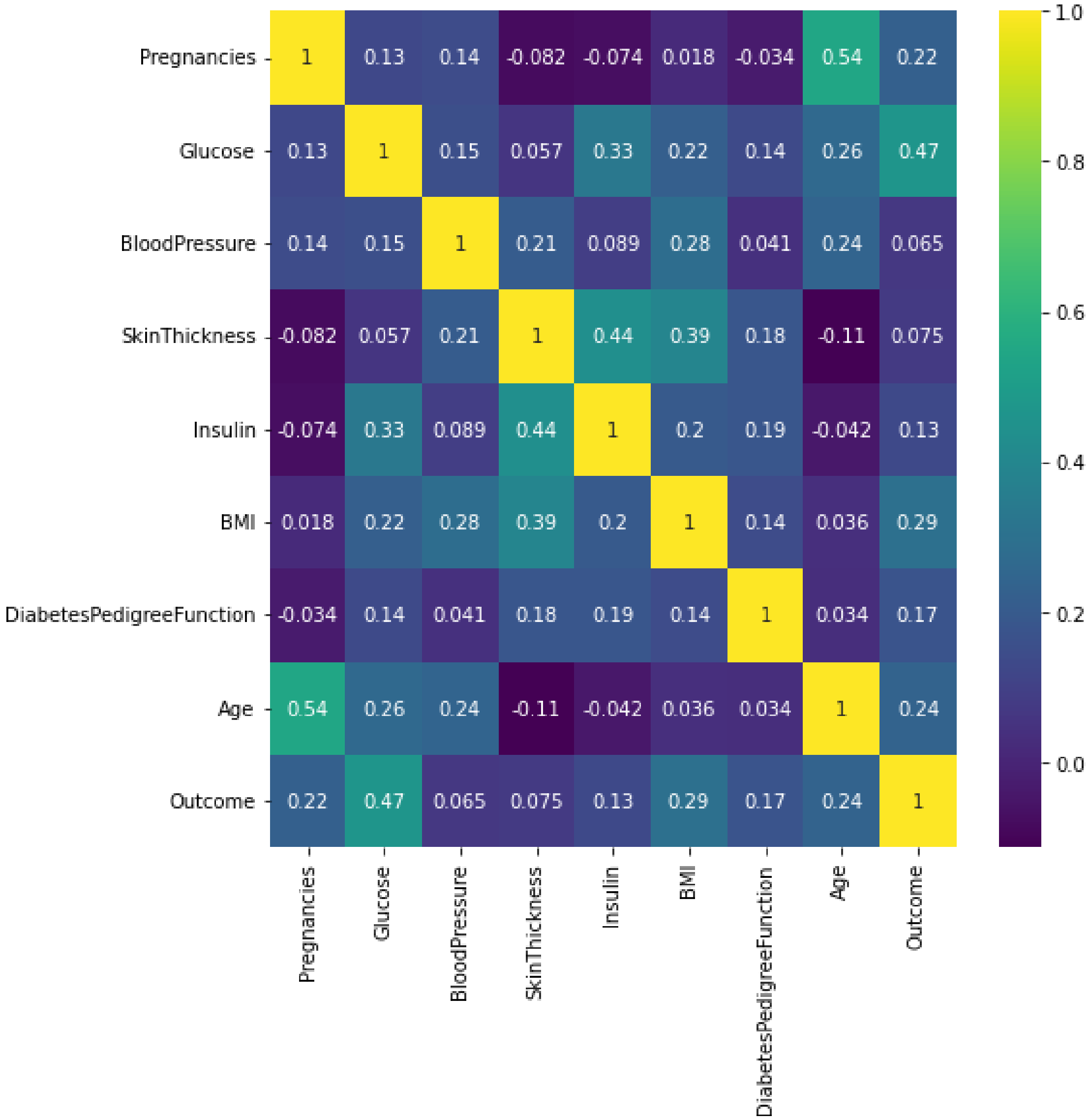


[43]:

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

[43]:

```
<AxesSubplot:>
```

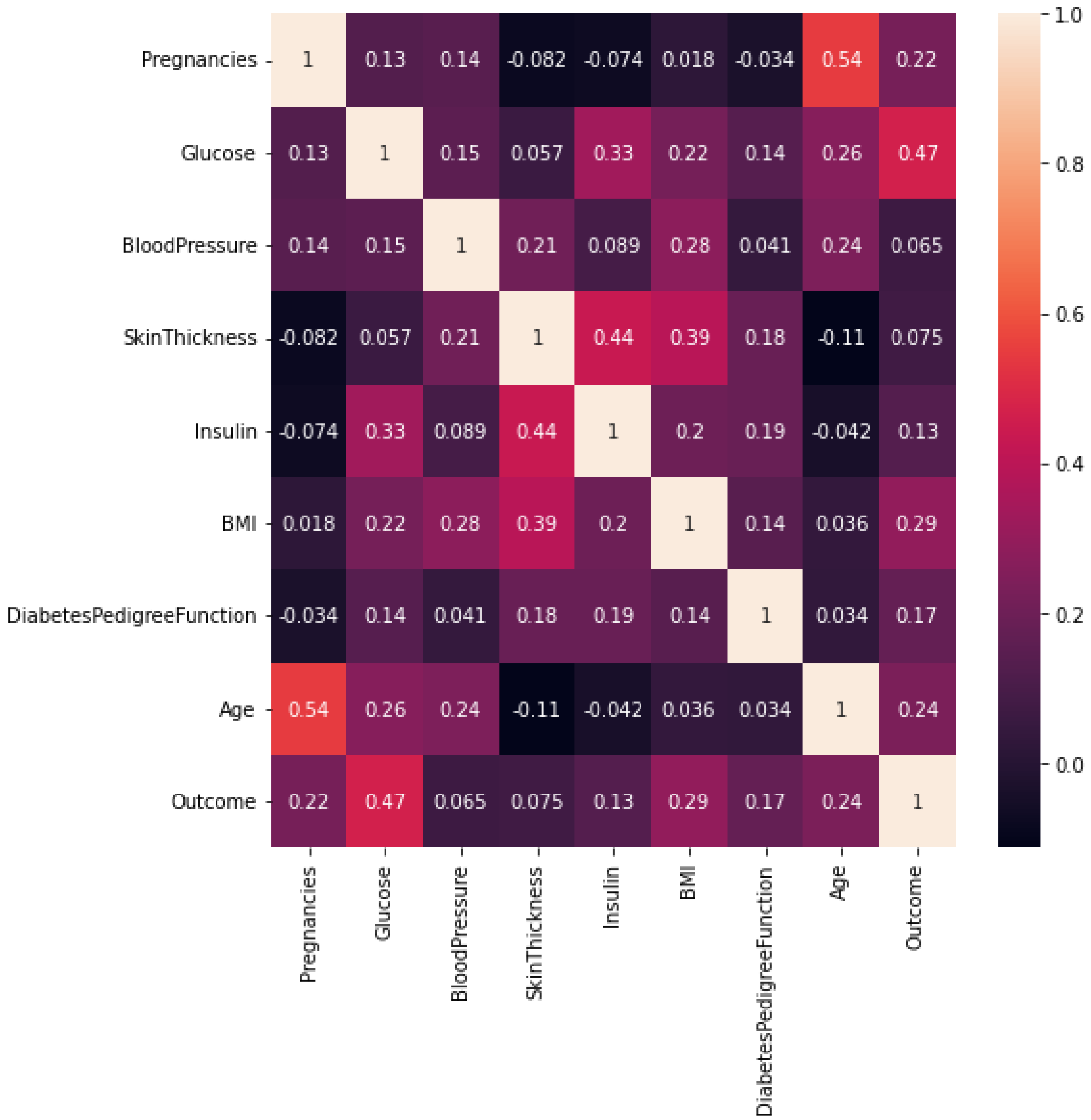


[45]:

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

[45]:

```
<AxesSubplot:>
```



WEEK 2: DATA MODELING

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

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

         DiabetesPedigreeFunction  Age  Outcome
```

```
0                      0.627   50         1
1                      0.351   31         0
2                      0.672   32         1
3                      0.167   21         0
4                      2.288   33         1
```

[47]:

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

[50]:

```
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)
```

[52]:

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

[52]:

```
LogisticRegression()
```

[53]:

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

```
0.7719869706840391
0.7662337662337663
```

[56]:

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

[56]:

```
array([[446,  54],
       [122, 146]])
```

[57]:

```
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
```

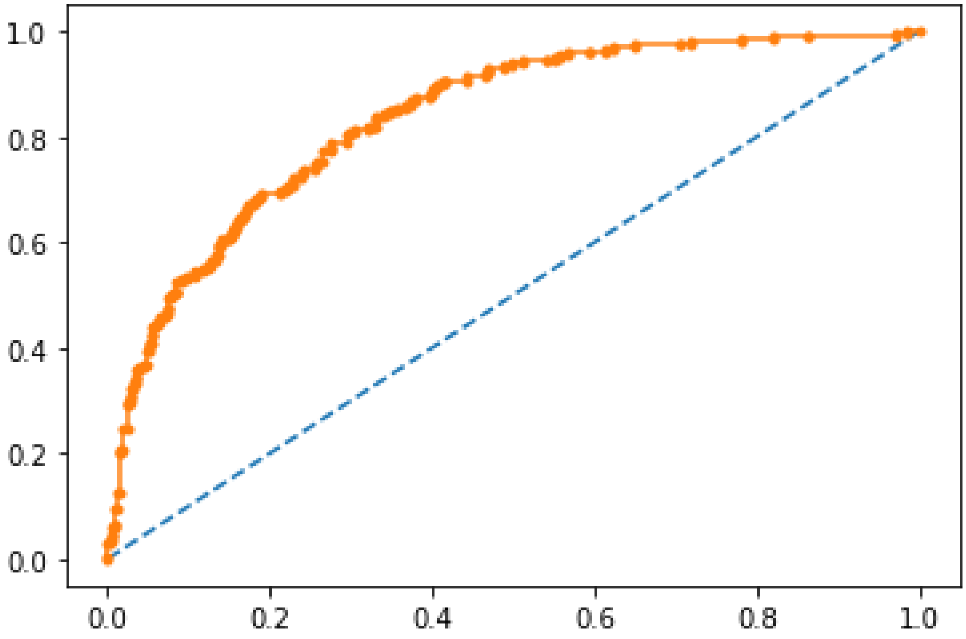
[61]:

```
#PREPARING ROC CURVE(RECEIVER OPERATING CHARACTERISTICS CURVE)
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score

#PredictProbabilities
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)
#plotno skill
plt.plot([0,1],[0,1],linestyle='--')
#plottheroccurveforthemodel
plt.plot(fpr, tpr, marker='.')
```

```
AUC: 0.837
```

[61]:

```
[<matplotlib.lines.Line2D at 0x7f9c949e7150>]
```



[63]:

```
#Applying decision tree classifier
from sklearn.tree import DecisionTreeClassifier
model3=DecisionTreeClassifier(max_depth=5)
```

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

```
[63]: DecisionTreeClassifier(max_depth=5)
```

```
[64]: model3.score(X_train,y_train)
```

```
[64]: 0.8289902280130294
```

```
[65]: model3.score(X_test,y_test)
```

```
[65]: 0.7662337662337663
```

```
[66]: #APPLYING RANDOM FOREST
      from sklearn.ensemble import RandomForestClassifier
      model4=RandomForestClassifier(n_estimators=1)
      model4.fit(X_train,y_train)
```

```
[66]: RandomForestClassifier(n_estimators=1)
```

```
[68]: model4.score(X_train,y_train)
```

```
[68]: 0.8648208469055375
```

```
[69]: model4.score(X_test,y_test)
```

```
[69]: 0.7077922077922078
```

```
[70]: #Support Vector Classifier
      from sklearn.svm import SVC
      model5=SVC(kernel='rbf',gamma='auto')
      model5.fit(X_train,y_train)
```

```
[70]: SVC(gamma='auto')
```

```
[73]: model5.score(X_test,y_test),model5.score(X_train,y_train)
```

```
[73]: (0.6168831168831169, 1.0)
```

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

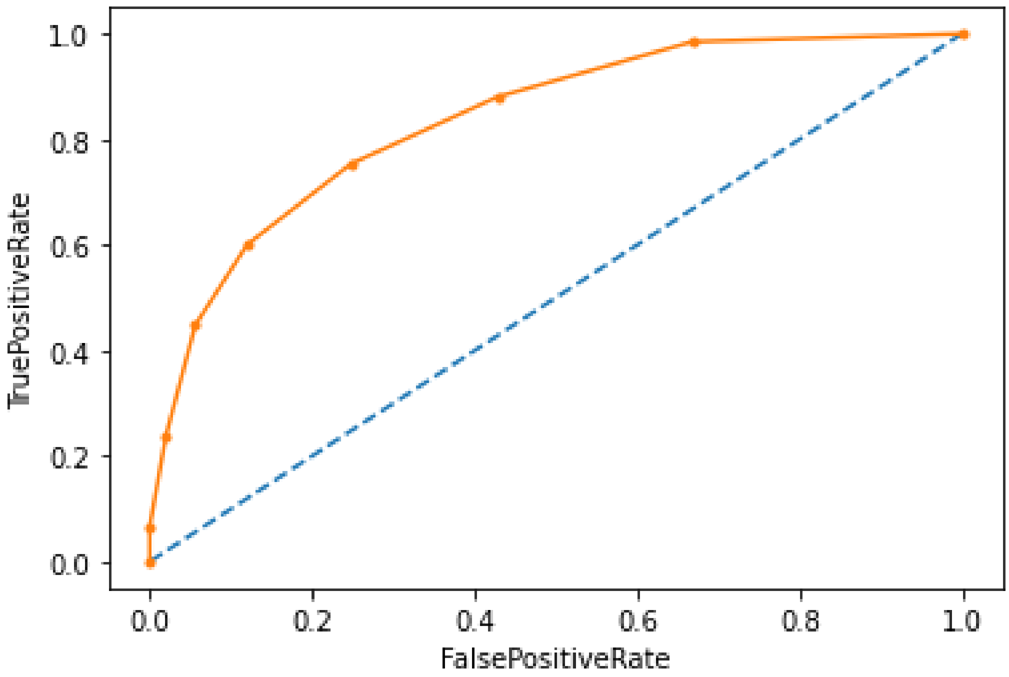
```
[74]: KNeighborsClassifier(n_neighbors=7)
```

```
[75]: #Preparing ROC Curve(Receiver Operating Characteristics Curve)
      from sklearn.metrics import roc_curve
```

```python
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("TruePositiveRate-{}, FalsePositiveRate-{}Threshold-{}".
      format(tpr, fpr, thresholds))
#plotno skill
plt.plot([0,1],[0,1],linestyle='--')
#plottheroccurveforthemodel
plt.plot(fpr, tpr, marker='.')
plt.xlabel("FalsePositiveRate")
plt.ylabel("TruePositiveRate")
```

```
AUC: 0.836
TruePositiveRate-[0.         0.06716418 0.23880597 0.44776119 0.60074627
0.75373134
 0.88059701 0.98507463 1.        ], FalsePositiveRate-[0.    0.    0.02  0.056
0.12  0.248 0.428 0.668 1.   ]Threshold-[2.         1.         0.85714286
0.71428571 0.57142857 0.42857143
 0.28571429 0.14285714 0.        ]
```

```
[75]: Text(0, 0.5, 'TruePositiveRate')
```



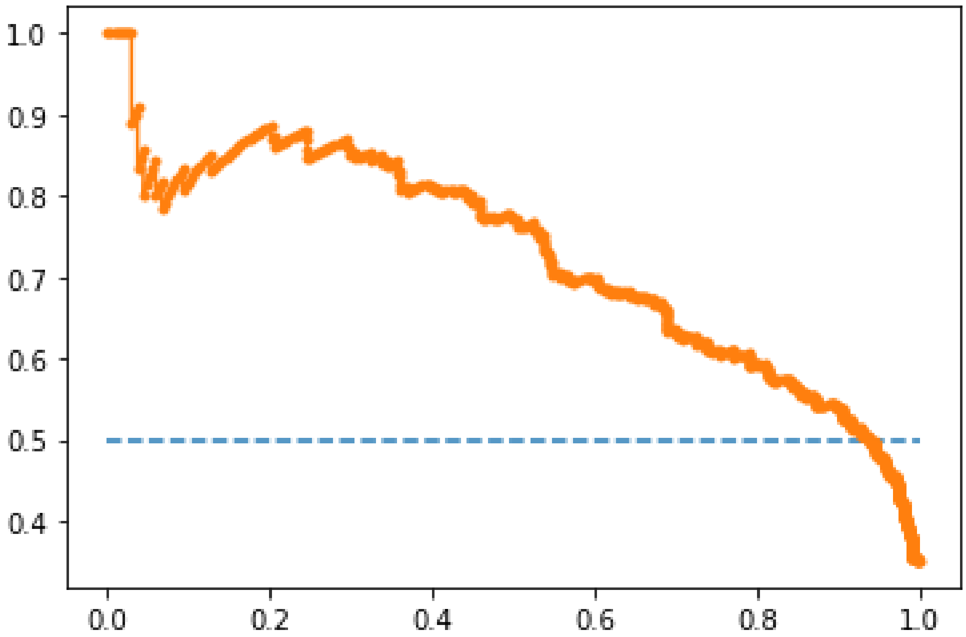
[80]:

```
#PrecisionRecallCurveforLogisticRegression

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=%.3fauc=%.3fap=%.3f'%(f1,auc,ap))#plotnoskill
plt.plot([0,1],[0.5,0.5],linestyle='--')
#plot the precision-recall curve for the model
plt.plot(recall,precision,marker='.')
```

```
f1=0.624auc=0.726ap=0.727
```

[80]:

```
[<matplotlib.lines.Line2D at 0x7f9c8fd1c8d0>]
```



[82]:

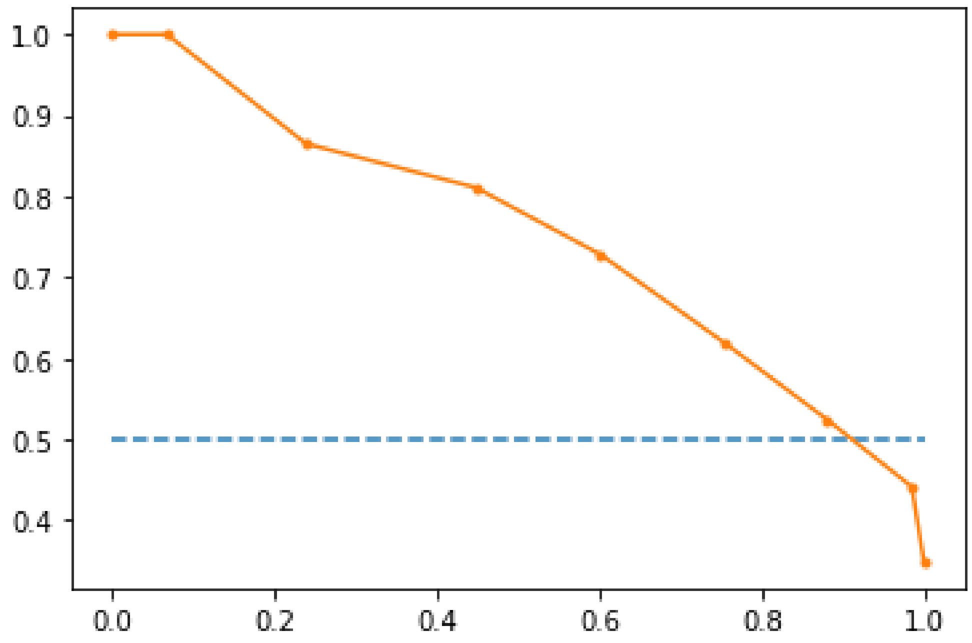
```
#PrecisionRecallCurveforKNNAlgorithms

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=%.3fauc=%.3fap=%.3f'%(f1,auc,ap))
#plotnoskill
```

```
plt.plot([0,1],[0.5,0.5],linestyle='--')
#plotthe precision-recall curve for the model
plt.plot(recall,precision,marker='.')
```

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

[82]:

```
[<matplotlib.lines.Line2D at 0x7f9c97cf4d50>]
```



[83]:

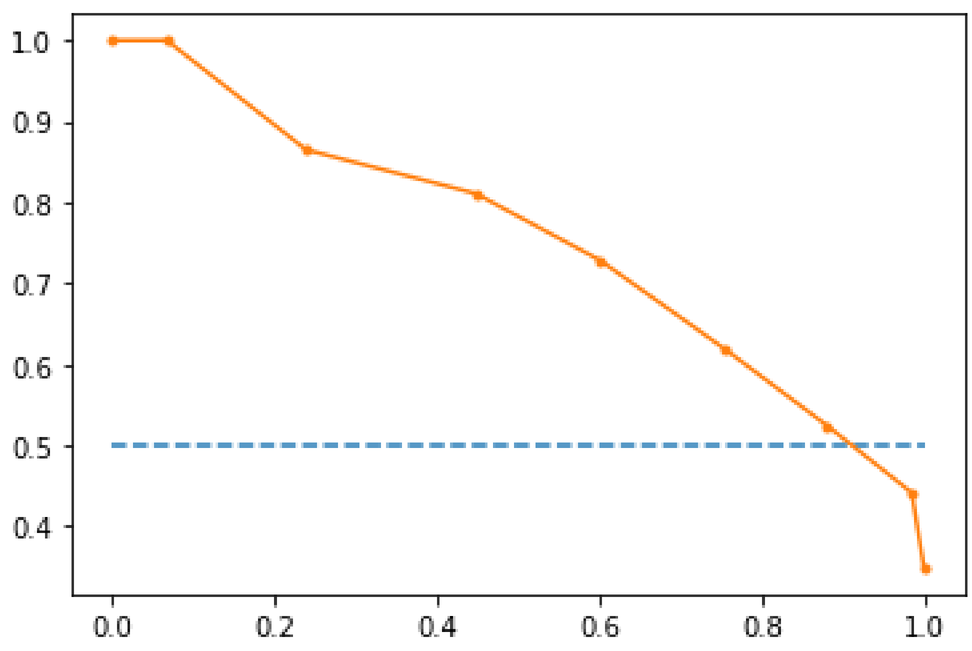
```
#PrecisionRecallCurveforDecissionTreeClassifier

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)
```

```
#calculateF1 score
f1=f1_score(label,yhat)
# calculate  precision-recall  AUC
auc=auc(recall,precision)

#calculateaverage precision score
ap = average_precision_score(label, probs)
print('f1=%.3fauc=%.3fap=%.3f'%(f1,auc,ap))

#plotnoskill
plt.plot([0,1],[0.5,0.5],linestyle='--')

#plotthe precision-recall curve for the model
plt.plot(recall,precision,marker='.')
```

```
f1=0.658auc=0.752ap=0.765
```

[83]:

```
[<matplotlib.lines.Line2D at 0x7f9c97c3ee10>]
```



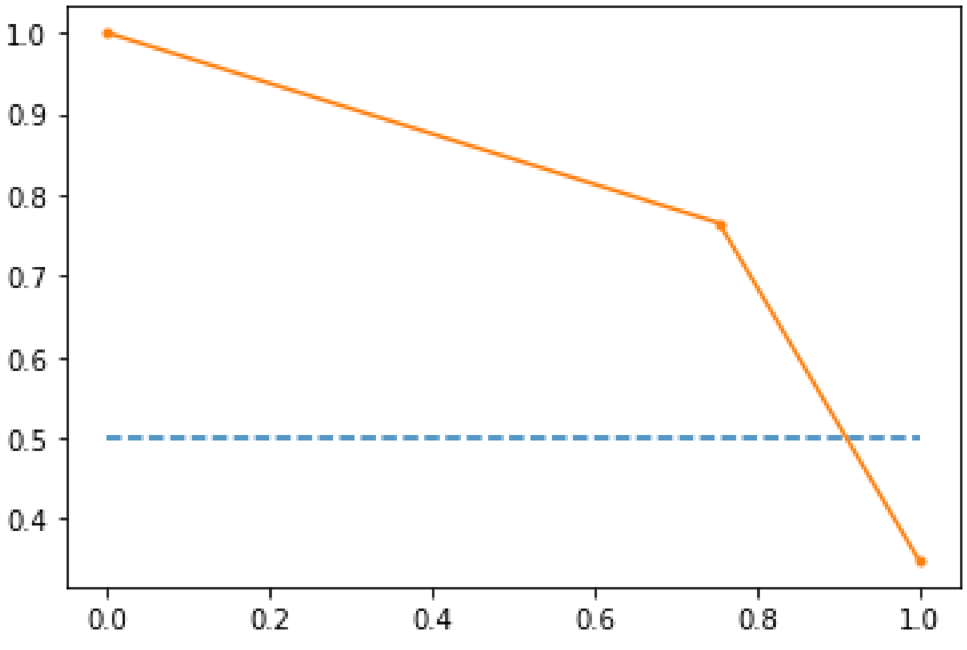
[84]:

```
#PrecisionRecallCurveforRandomForest

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)
#keepprobabilities 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)
#calculateF1 score
f1=f1_score(label,yhat)
# calculate  precision-recall  AUC
auc=auc(recall,precision)
#calculateaverage precision score
ap = average_precision_score(label, probs)
print('f1=%.3fauc=%.3fap=%.3f'%(f1,auc,ap))#plotnoskill
plt.plot([0,1],[0.5,0.5],linestyle='--')
#plotthe precision-recall curve for the model
plt.plot(recall,precision,marker='.')
```

```
f1=0.759auc=0.802ap=0.663
```

```
[84]: [<matplotlib.lines.Line2D at 0x7f9c8fc98150>]
```



### 3.0.1 THANKYOU

```
[ ]:
```