Data___Science_Capstone_HealthCare_Project_By_Keshav

October 1, 2022

[77]:
```
#import the library
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

[2]:
```
#Load the dataset
from google.colab import files
uploaded = files.upload()
```

```
<IPython.core.display.HTML object>


Saving health care diabetes.csv to health care diabetes.csv
```

[3]:
```
data = pd.read_csv('health care diabetes.csv')
```

[4]:
```
data.head()
```

[4]:

	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

[5]:
```
data.shape
```

[5]:
```
(768, 9)
```

[6]:
```
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
```

[7]:
```
data.describe()
```

[7]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	\
count	768.000000	768.000000	768.000000	768.000000	768.000000	
mean	3.845052	120.894531	69.105469	20.536458	79.799479	
std	3.369578	31.972618	19.355807	15.952218	115.244002	
min	0.000000	0.000000	0.000000	0.000000	0.000000	
25%	1.000000	99.000000	62.000000	0.000000	0.000000	
50%	3.000000	117.000000	72.000000	23.000000	30.500000	
75%	6.000000	140.250000	80.000000	32.000000	127.250000	
max	17.000000	199.000000	122.000000	99.000000	846.000000	

	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000
mean	31.992578	0.471876	33.240885	0.348958
std	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.078000	21.000000	0.000000
25%	27.300000	0.243750	24.000000	0.000000
50%	32.000000	0.372500	29.000000	0.000000
75%	36.600000	0.626250	41.000000	1.000000
max	67.100000	2.420000	81.000000	1.000000

[8]:
```
data.head()
```

[8]:

	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
```

[9]:
```
data.tail()
```

[9]:
```
     Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
763           10      101             76             48      180  32.9
764            2      122             70             27        0  36.8
765            5      121             72             23      112  26.2
766            1      126             60              0        0  30.1
767            1       93             70             31        0  30.4

     DiabetesPedigreeFunction  Age  Outcome
763                     0.171   63        0
764                     0.340   27        0
765                     0.245   30        0
766                     0.349   47        1
767                     0.315   23        0
```

[10]:
```
data.isnull().any()
```

[10]:
```
Pregnancies                 False
Glucose                     False
BloodPressure               False
SkinThickness               False
Insulin                     False
BMI                         False
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

[11]:
```
Positive = data[data['Outcome']==1]
Positive.head(5)
```

[11]:
```
   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
```

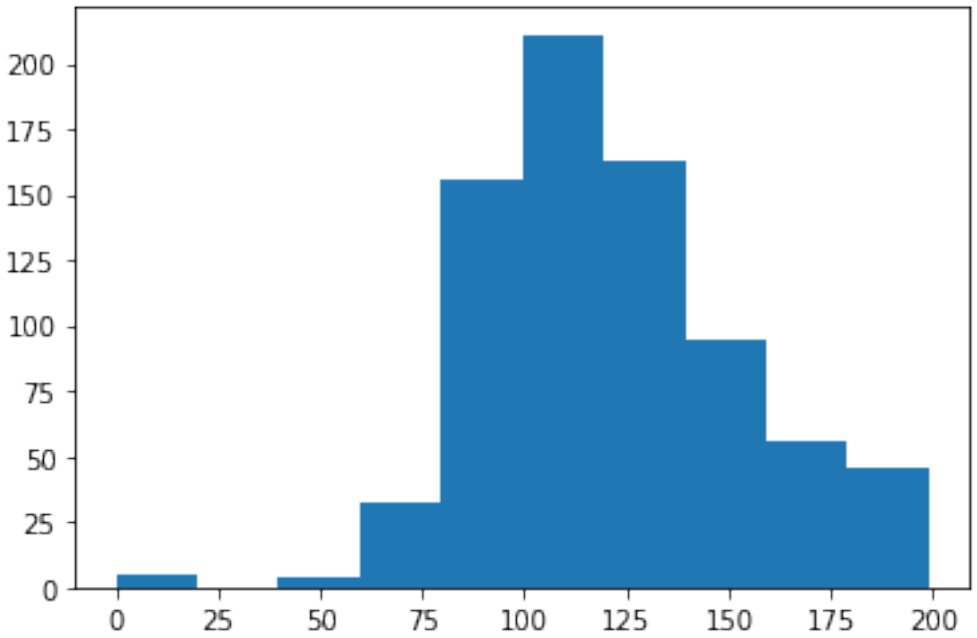
```
   DiabetesPedigreeFunction  Age  Outcome
0                     0.627   50        1
2                     0.672   32        1
4                     2.288   33        1
6                     0.248   26        1
8                     0.158   53        1
```

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

[12]:
```
99     17
100    17
111    14
129    14
125    14
106    14
112    13
Name: Glucose, dtype: int64
```

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

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

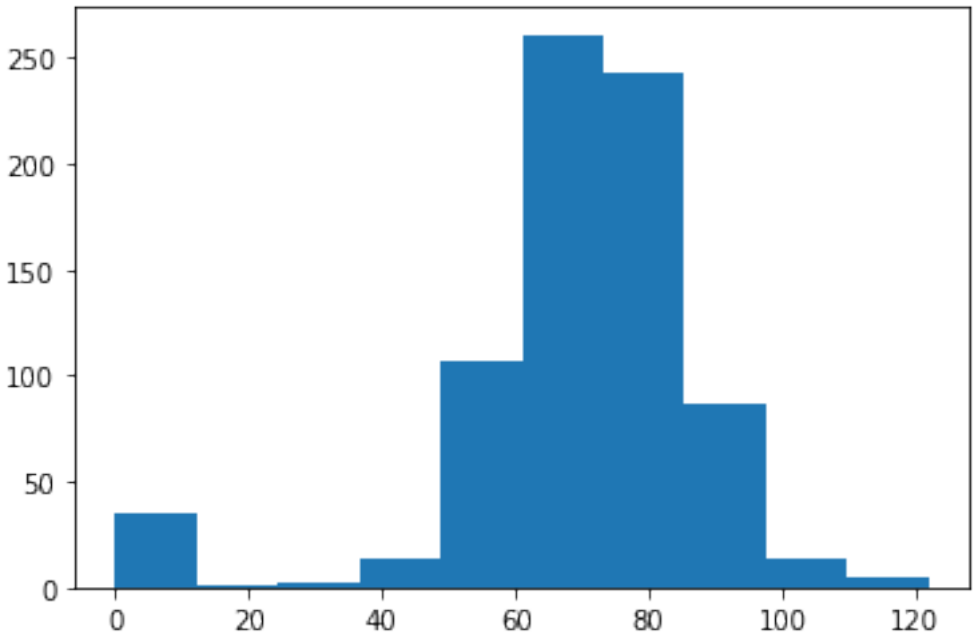


[14]:
```
data['BloodPressure'].value_counts().head(7)
```

[14]:
```
70    57
74    52
78    45
68    45
72    44
64    43
80    40
Name: BloodPressure, dtype: int64
```

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

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

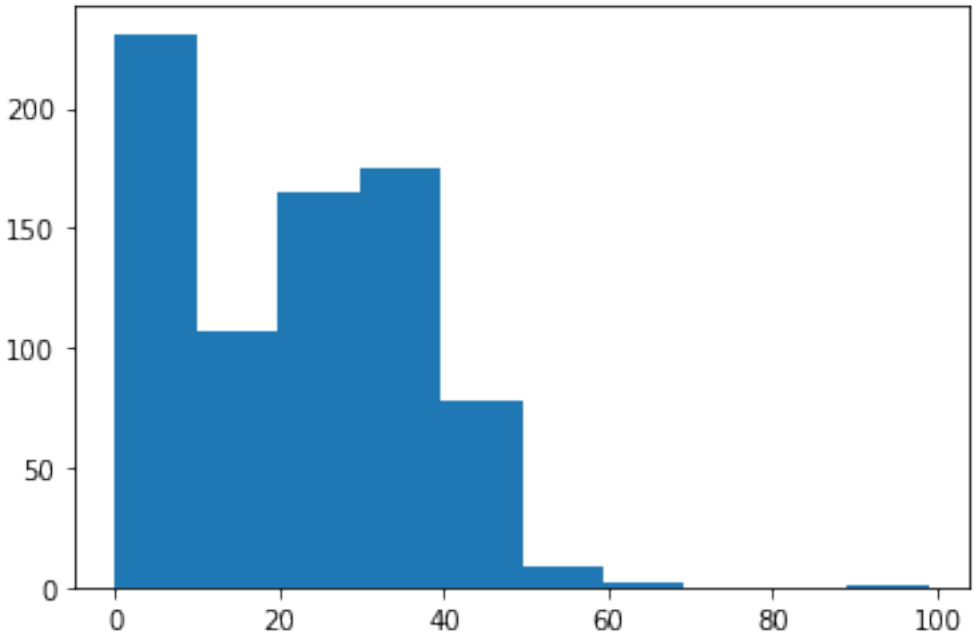


[16]:
```
data['SkinThickness'].value_counts().head(7)
```

[16]:
```
0     227
32     31
30     27
27     23
23     22
33     20
28     20
Name: SkinThickness, dtype: int64
```

[17]:
```
plt.hist(data['SkinThickness'])
```

[17]:
```
(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>)
```

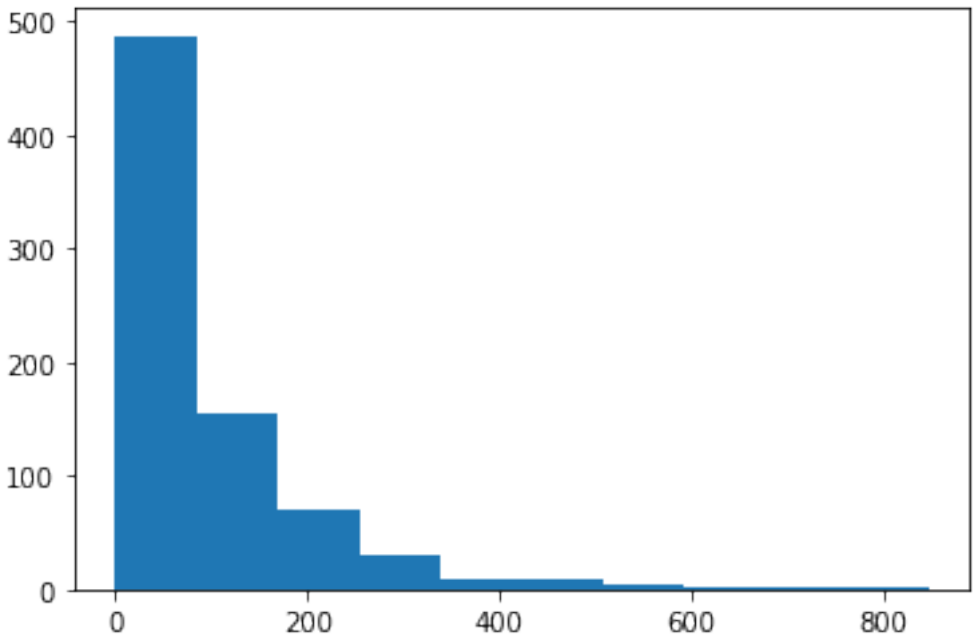


[18]:
```
data['Insulin'].value_counts().head(7)
```

[18]:
```
0      374
105     11
130      9
140      9
120      8
94       7
180      7
Name: Insulin, dtype: int64
```

[19]:
```
plt.hist(data['Insulin'])
```

[19]:
```
(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>)
```

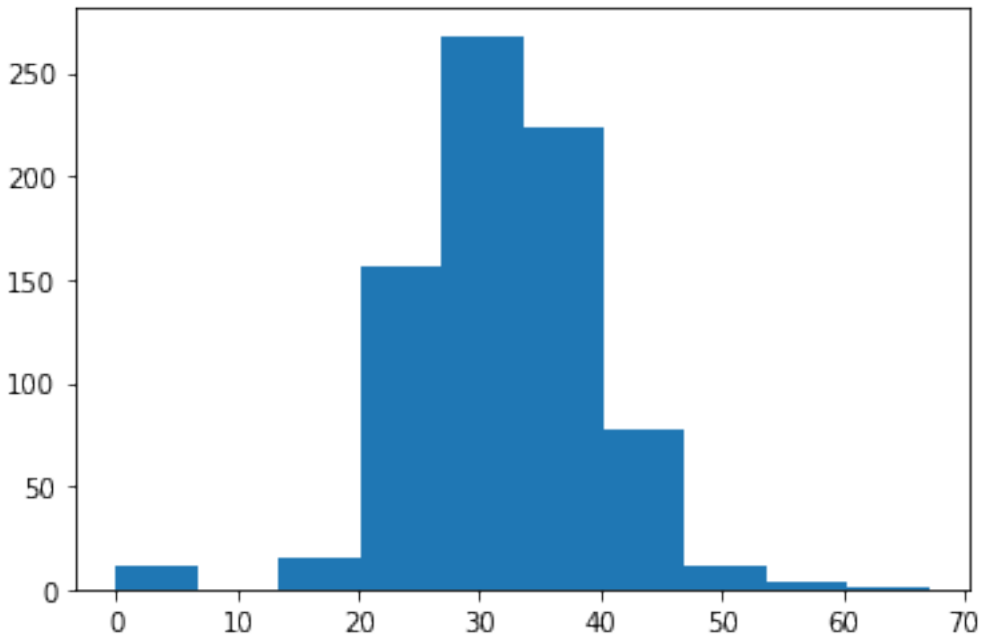


[20]:
```
data['BMI'].value_counts().head(7)
```

[20]:
```
32.0    13
31.6    12
31.2    12
0.0     11
32.4    10
33.3    10
30.1     9
Name: BMI, dtype: int64
```

[21]:
```
plt.hist(data['BMI'])
```

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



[22]:
```
data.describe().transpose()
```

[22]:

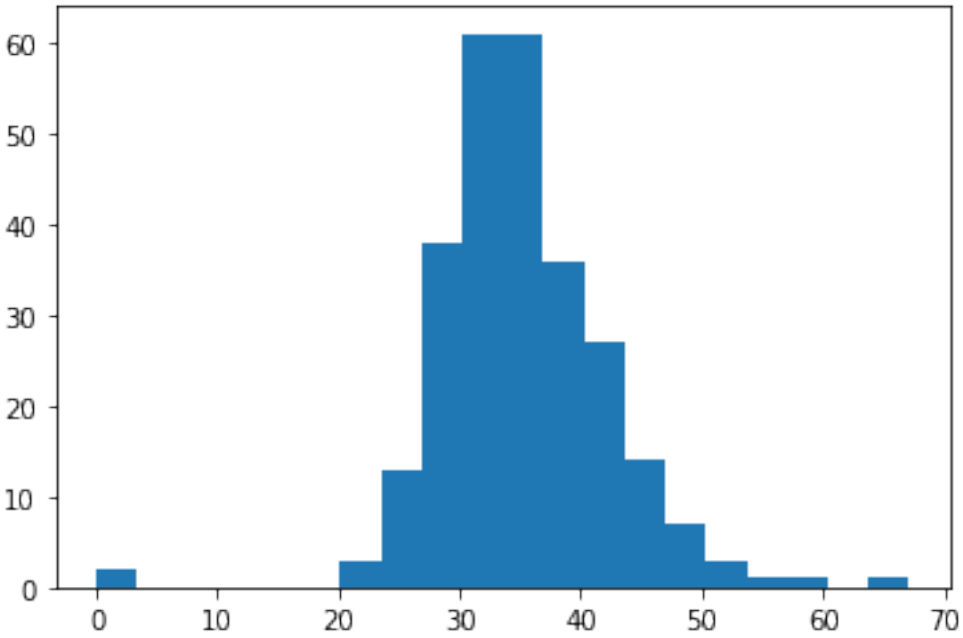
	count	mean	std	min	25%	\
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	
Glucose	768.0	120.894531	31.972618	0.000	99.00000	
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	
Insulin	768.0	79.799479	115.244002	0.000	0.00000	
BMI	768.0	31.992578	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

1 Week:-2

[23]:
```
plt.hist(Positive['BMI'],histtype='stepfilled',bins=20)
```

[23]:
```
(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>)
```

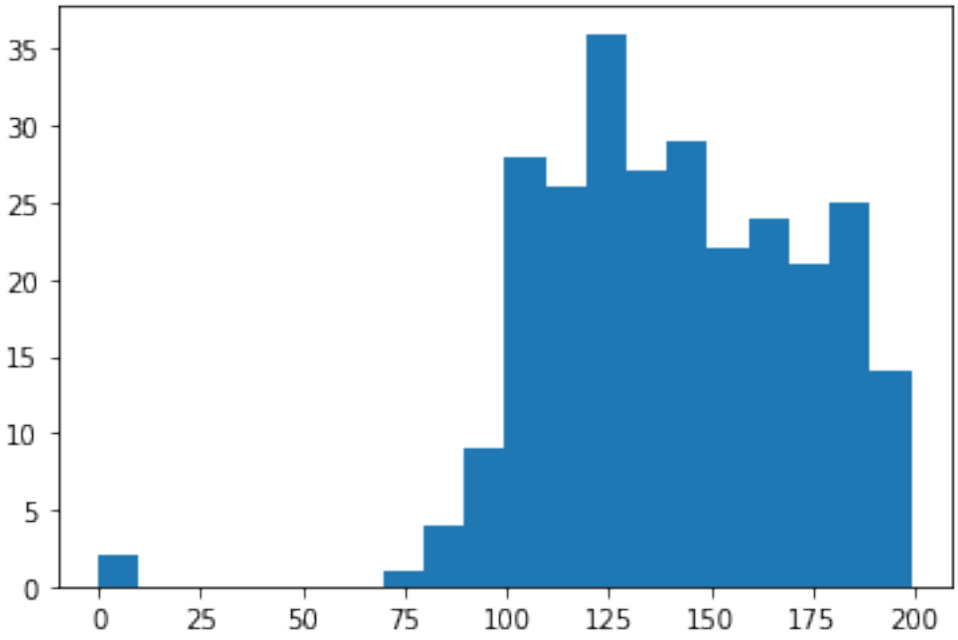


[24]:
```
Positive['BMI'].value_counts().head(7)
```

[24]:
```
32.9    8
31.6    7
33.3    6
31.2    5
30.5    5
32.0    5
34.3    4
Name: BMI, dtype: int64
```

[25]:
```
plt.hist(Positive['Glucose'],histtype='stepfilled',bins=20)
```

[25]:
```
(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>)
```

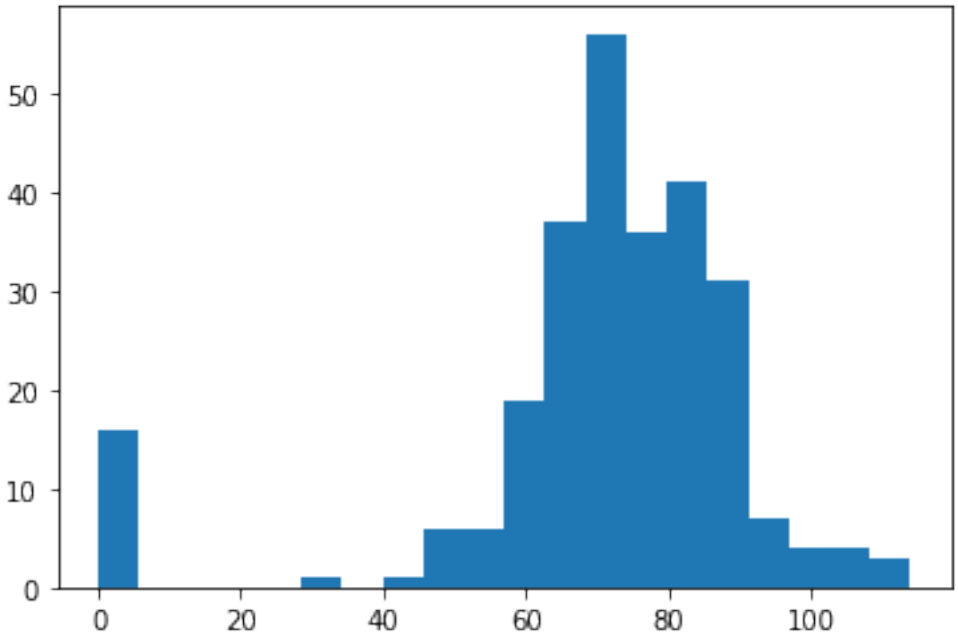


[26]:
```
Positive['Glucose'].value_counts().head(7)
```

[26]:
```
125    7
128    6
129    6
115    6
158    6
146    5
124    5
Name: Glucose, dtype: int64
```

[27]:
```
plt.hist(Positive['BloodPressure'],histtype='stepfilled',bins=20)
```

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

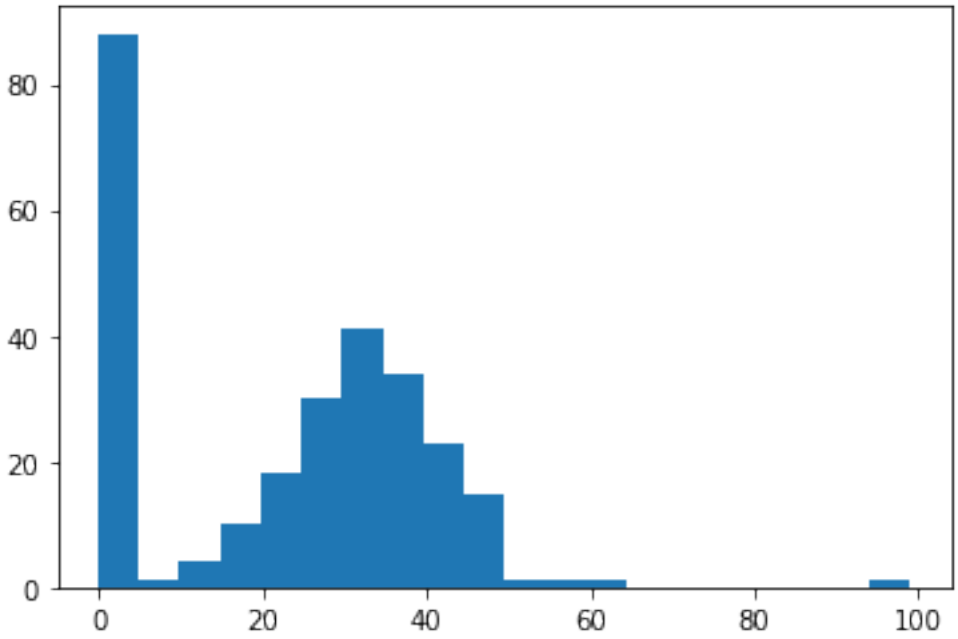


[28]:
```
Positive['BloodPressure'].value_counts().head(7)
```

[28]:
```
70    23
76    18
78    17
74    17
72    16
0     16
80    13
Name: BloodPressure, dtype: int64
```

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

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

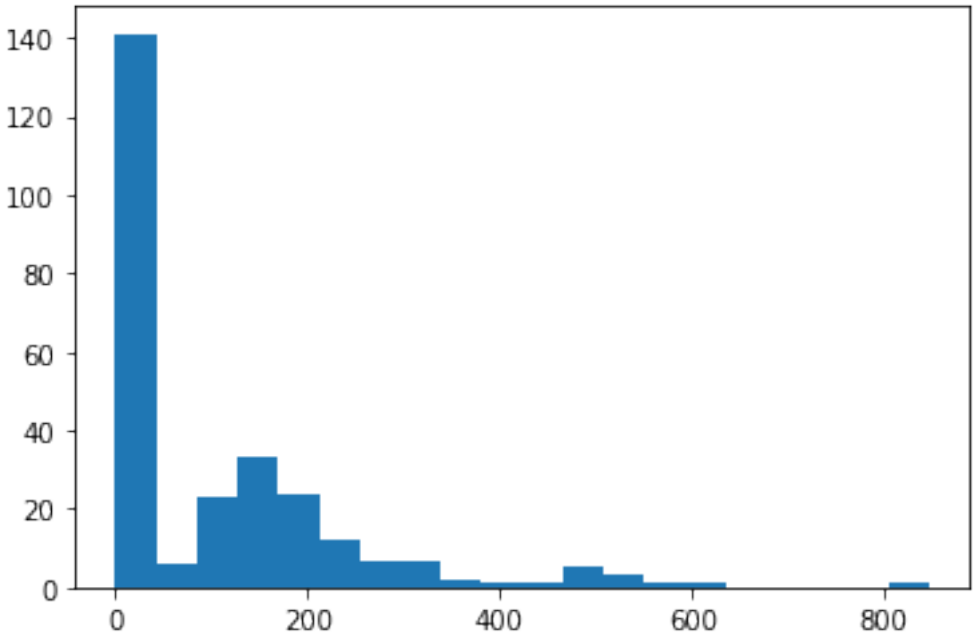


[30]:
```
Positive['SkinThickness'].value_counts().head(7)
```

[30]:
```
0     88
32    14
30     9
33     9
39     8
37     8
36     8
Name: SkinThickness, dtype: int64
```

[31]:
```
plt.hist(Positive['Insulin'],histtype='stepfilled',bins=20)
```

[31]:
```
(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>)
```



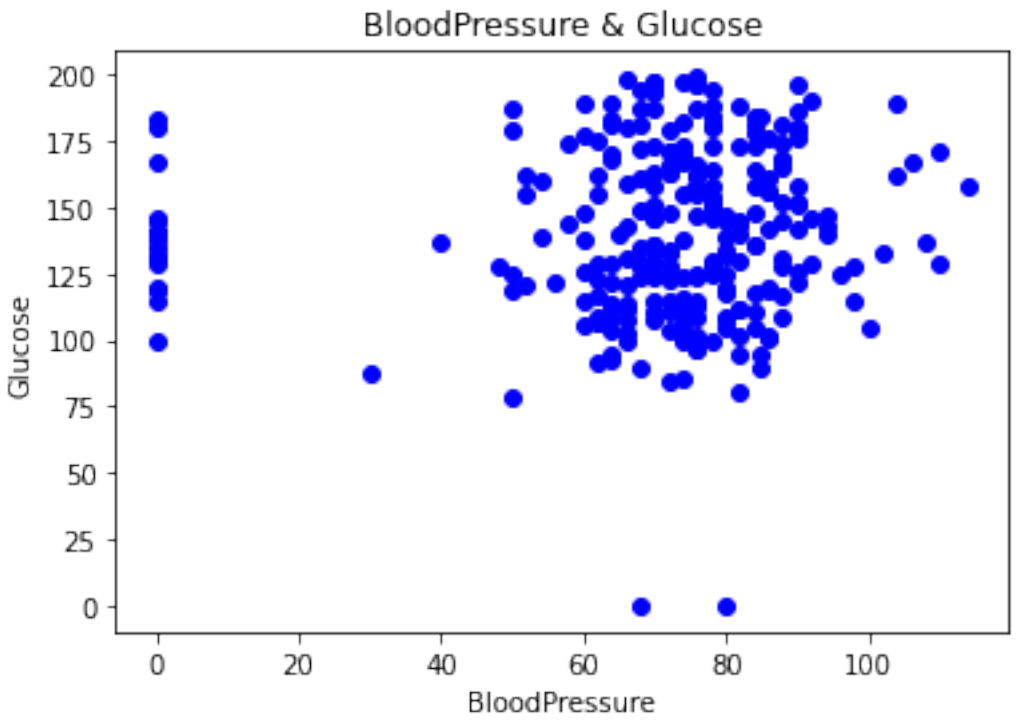
[32]:
```
Positive['Insulin'].value_counts().head(7)
```

[32]:
```
0      138
130      6
180      4
175      3
156      3
185      2
194      2
Name: Insulin, dtype: int64
```

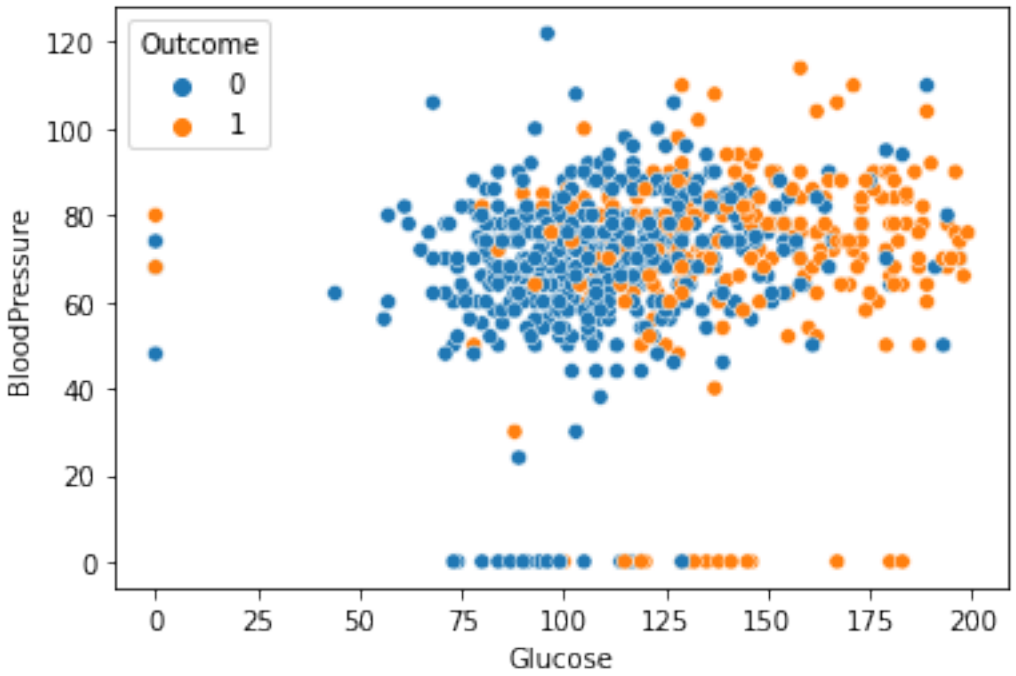
2 Scatter plot

[33]:
```
BloodPressure = Positive['BloodPressure']
Glucose = Positive['Glucose']
SkinThickness = Positive['SkinThickness']
Insulin = Positive['Insulin']
BMI = Positive['BMI']
```

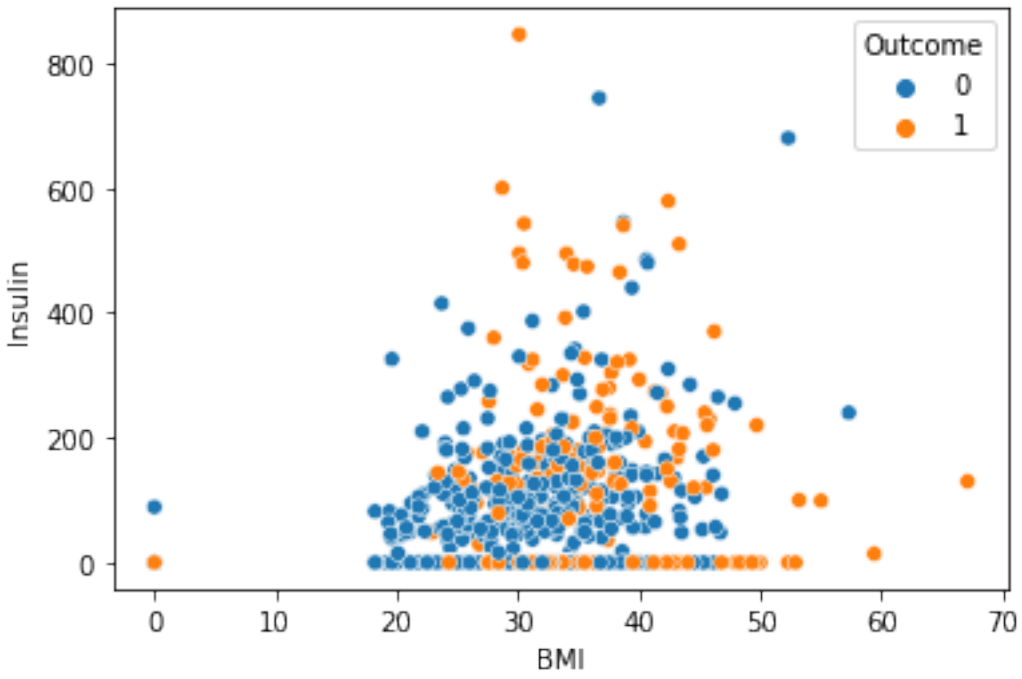
[34]:
```
plt.scatter(BloodPressure, Glucose, color=['b'])
plt.xlabel('BloodPressure')
plt.ylabel('Glucose')
plt.title('BloodPressure & Glucose')
plt.show()
```



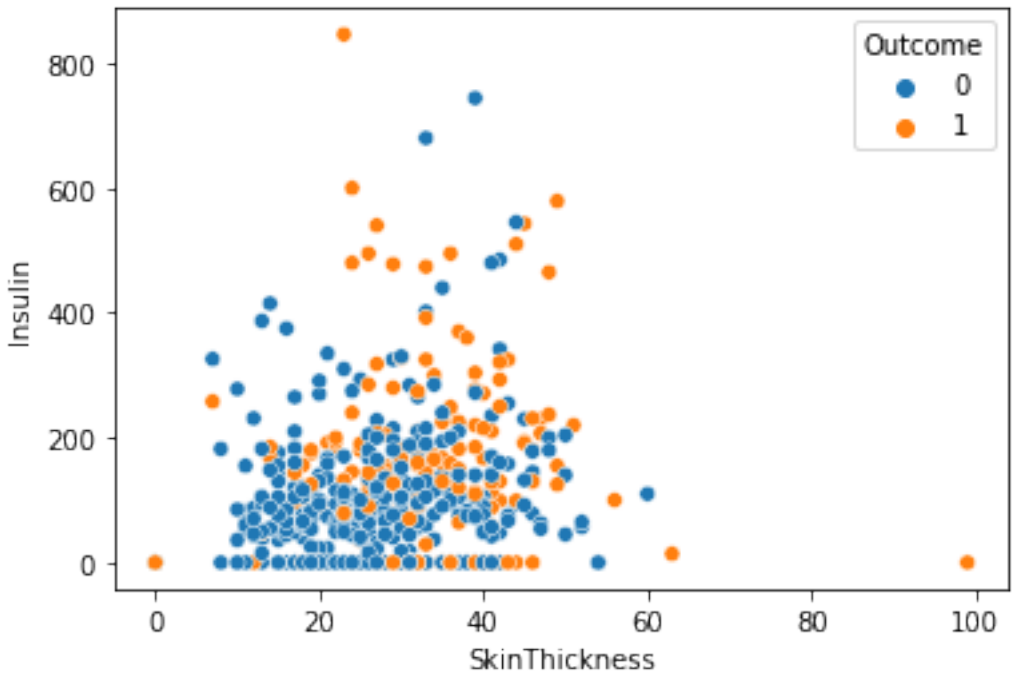
[37]:
```
g =sns.scatterplot(x= "Glucose" ,y= "BloodPressure",
                   hue="Outcome",
                   data=data);
```



[38]:
```
B =sns.scatterplot(x= "BMI" ,y= "Insulin",
                   hue="Outcome",
                   data=data);
```



[39]:
```
S =sns.scatterplot(x= "SkinThickness" ,y= "Insulin",
                   hue="Outcome",
                   data=data);
```



Correlation Matrix

[40]:
```
data.corr()
```

[40]:

	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

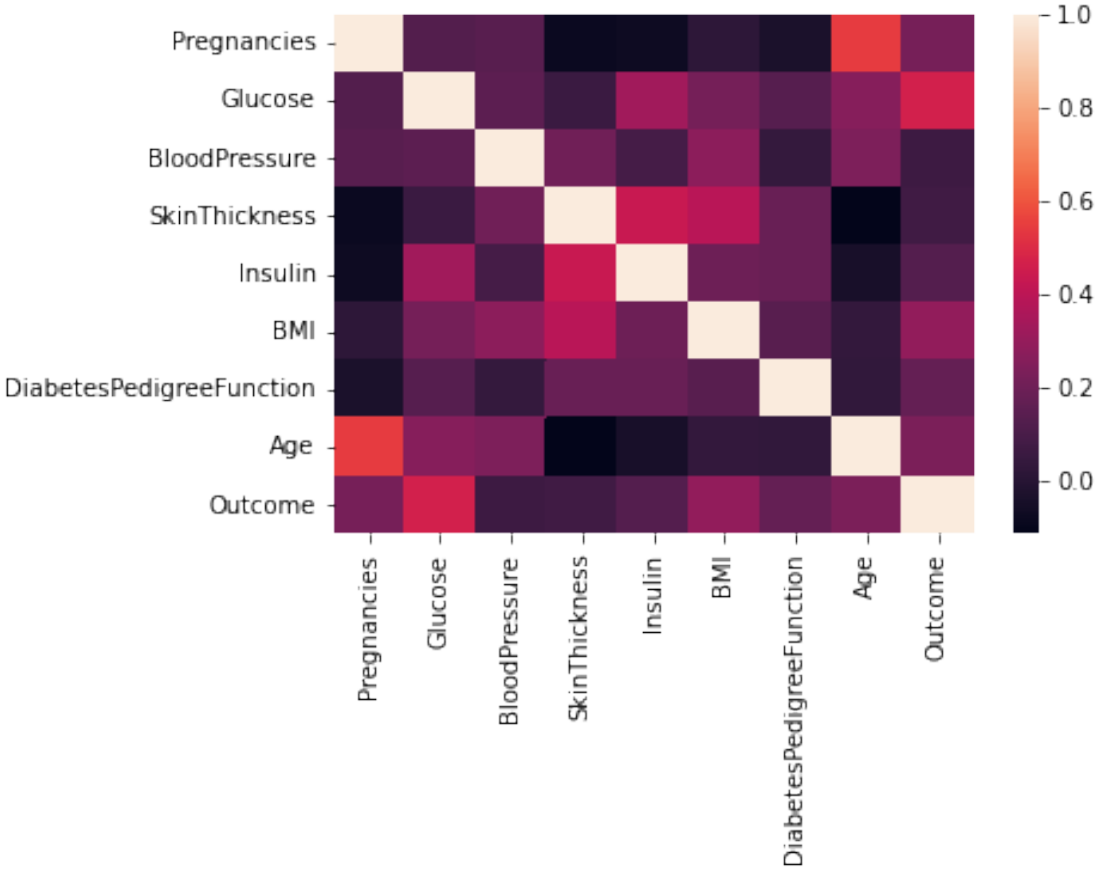
	Insulin	BMI	DiabetesPedigreeFunction
Pregnancies	-0.073535	0.017683	-0.033523
Glucose	0.331357	0.221071	0.137337
BloodPressure	0.088933	0.281805	0.041265
SkinThickness	0.436783	0.392573	0.183928
Insulin	1.000000	0.197859	0.185071
BMI	0.197859	1.000000	0.140647
DiabetesPedigreeFunction	0.185071	0.140647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

create correlation heat map

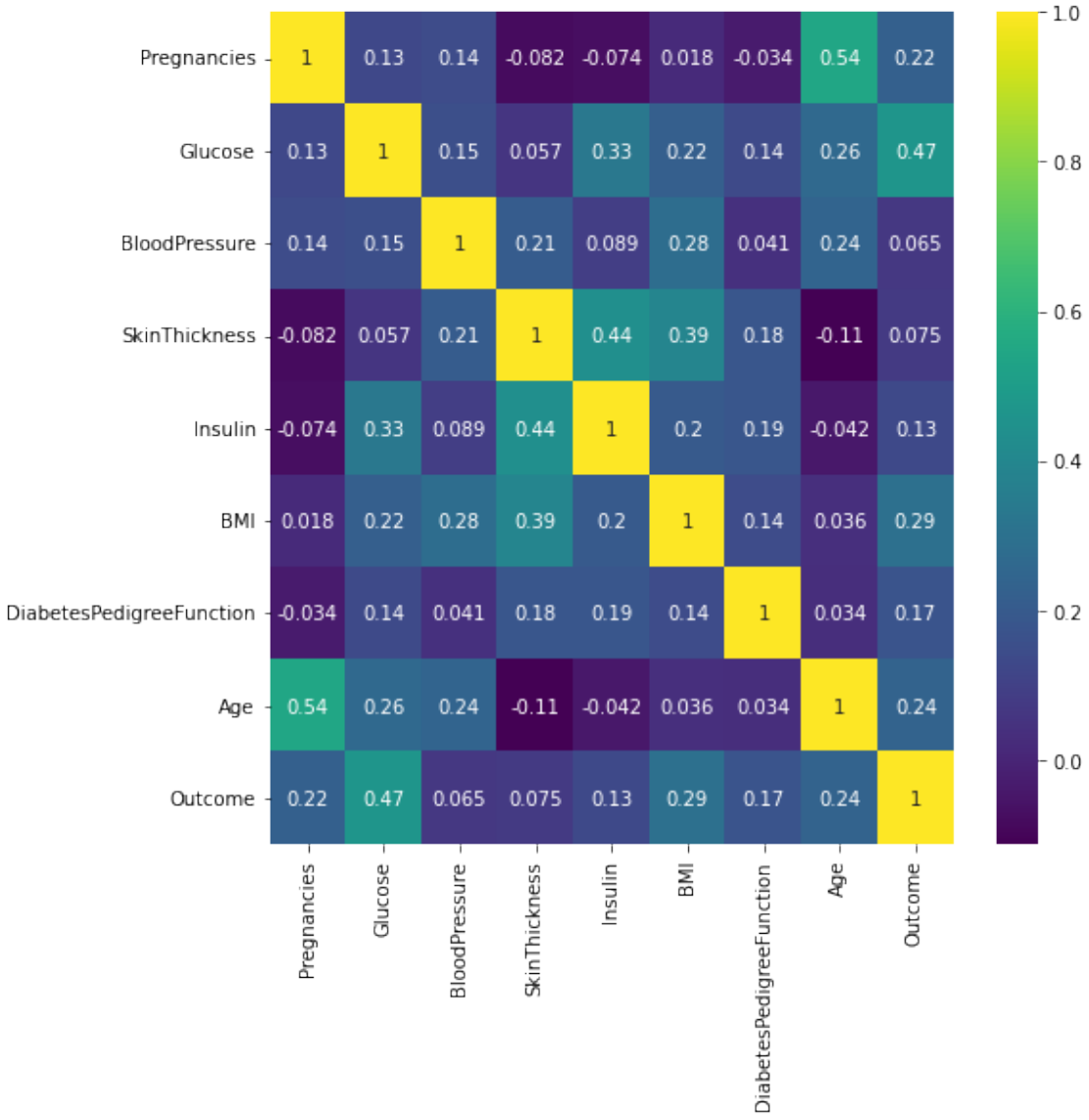
[41]:
```
sns.heatmap(data.corr())
```

[41]: <matplotlib.axes._subplots.AxesSubplot at 0x7f48a7d528d0>



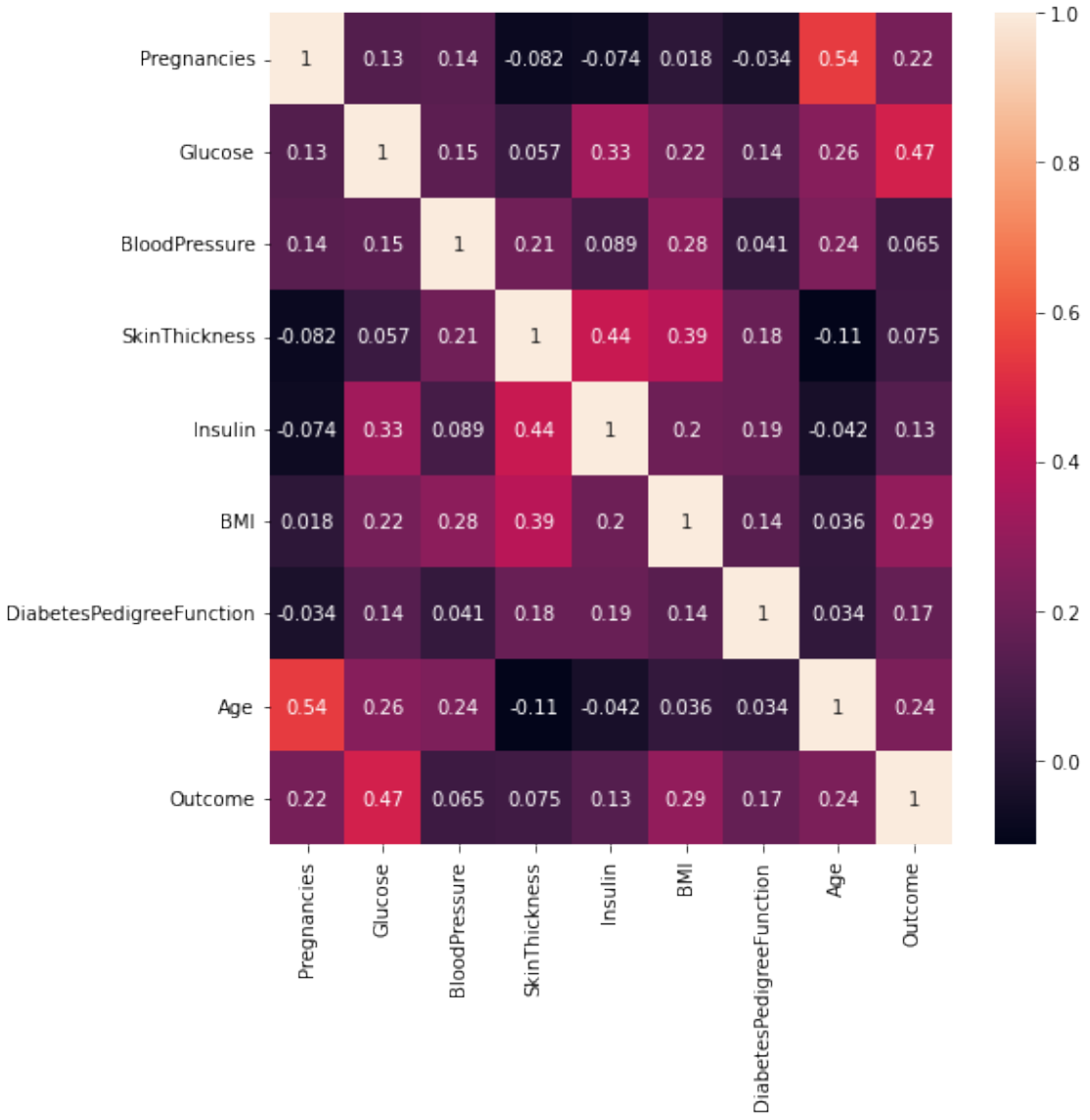
[42]:
```
plt.subplots(figsize=(8,8))
sns.heatmap(data.corr(),annot=True,cmap='viridis')
```

[42]: <matplotlib.axes._subplots.AxesSubplot at 0x7f48a7cf0ed0>



[43]:
```
plt.subplots(figsize=(8,8))
sns.heatmap(data.corr(),annot=True)
```

[43]: <matplotlib.axes._subplots.AxesSubplot at 0x7f48a5496850>



[44]:
```
# Logistic Regreation and model building
```

[45]:
```
data.head(5)
```

[45]:

	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
```

[78]:
```
features = data.iloc[:,[0,1,2,3,4,5,6,7]].values
label = data.iloc[:,8].values
```

[79]:
```
#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)
```

[82]:
```
#Create model
from sklearn.linear_model import LogisticRegression
model = LogisticRegression()
model.fit(X_train,y_train)
```

[82]:
```
LogisticRegression()
```

[83]:
```
y_predict=model.predict(X_test)
```

[53]:
```
y_predict
```

[53]:
```
array([1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 1, 0, 0,
       0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0,
       1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 1, 0, 1,
       0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0,
       1, 0, 0, 0, 0, 1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 1, 1, 0, 0, 0, 1, 0])
```

[84]:
```
print(model.score(X_train,y_train))
print(model.score(X_test,y_test))
```

```
0.7719869706840391
0.7662337662337663
```

[85]:
```
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(label,model.predict(features))
cm
```

[85]:
```
array([[446,  54],
       [122, 146]])
```

[86]:
```
from sklearn.metrics import classification_report
print(classification_report(label,model.predict(features)))
```

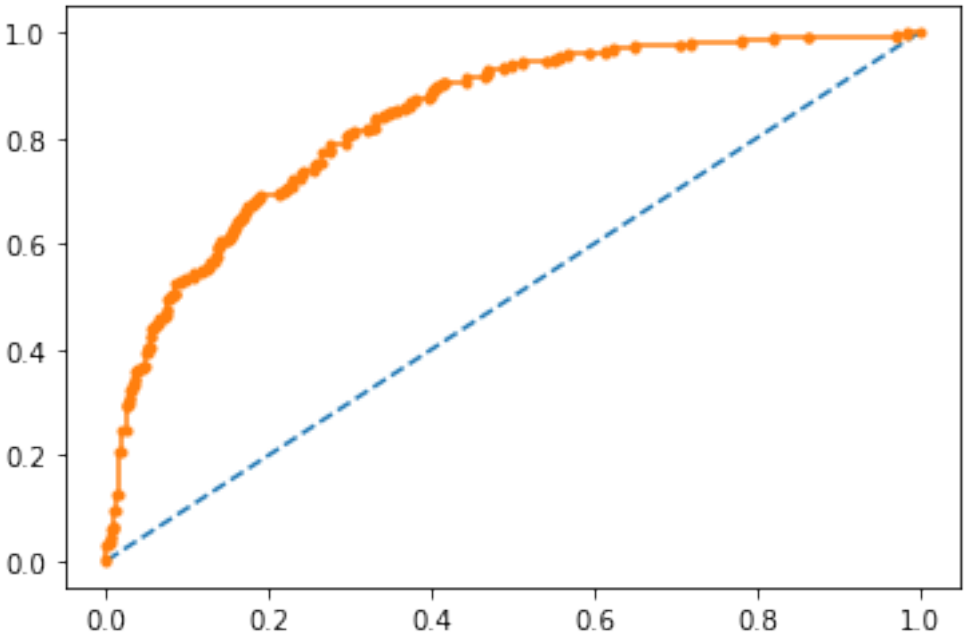
```
              precision    recall  f1-score   support

           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
```

[87]:
```
#Preparing ROC Curve (Receiver Operating Characteristics Curve)
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score
```

[88]:
```
# 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
```

[88]:
```
[<matplotlib.lines.Line2D at 0x7f4842f5d910>]
```



[89]:
```
#Applying Decission Tree Classifier
from sklearn.tree import DecisionTreeClassifier
model3 = DecisionTreeClassifier(max_depth=5)
model3.fit(X_train,y_train)
```

[89]: DecisionTreeClassifier(max_depth=5)

[90]:
```
model3.score(X_train,y_train)
```

[90]: 0.8289902280130294

[91]:
```
model3.score(X_test,y_test)
```

[91]: 0.7662337662337663

[92]:
```
#Applying Random Forest
from sklearn.ensemble import RandomForestClassifier
model4 = RandomForestClassifier(n_estimators=11)
model4.fit(X_train,y_train)
```

[92]: RandomForestClassifier(n_estimators=11)

[93]:
```
model4.score(X_train,y_train)
```

[93]: 0.99185667752443

[94]:
```
model4.score(X_test,y_test)
```

[94]:
```
0.7467532467532467
```

[95]:
```
#Support Vector Classifier

from sklearn.svm import SVC
```

[96]:
```
model5 = SVC(kernel='rbf',
             gamma='auto')
model5.fit(X_train,y_train)
```

[96]:
```
SVC(gamma='auto')
```

[99]:
```
model5.score(X_test,y_test)
```

[99]:
```
0.6168831168831169
```

[100]:
```
#Applying K-NN
from sklearn.neighbors import KNeighborsClassifier
model2 = KNeighborsClassifier(n_neighbors=7,
                              metric='minkowski',
                              p = 2)
model2.fit(X_train,y_train)
```

[100]:
```
KNeighborsClassifier(n_neighbors=7)
```

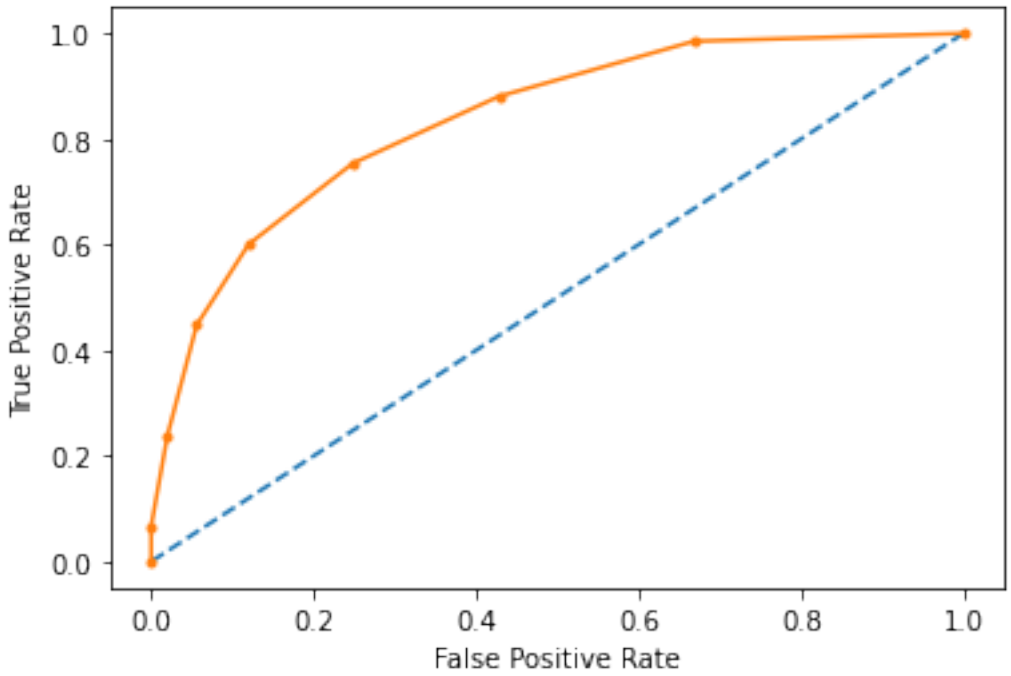
[101]:
```
#Preparing ROC Curve (Receiver Operating Characteristics Curve)
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score
```

[102]:
```
# 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.        ]
```

[102]:
```
Text(0, 0.5, 'True Positive Rate')
```



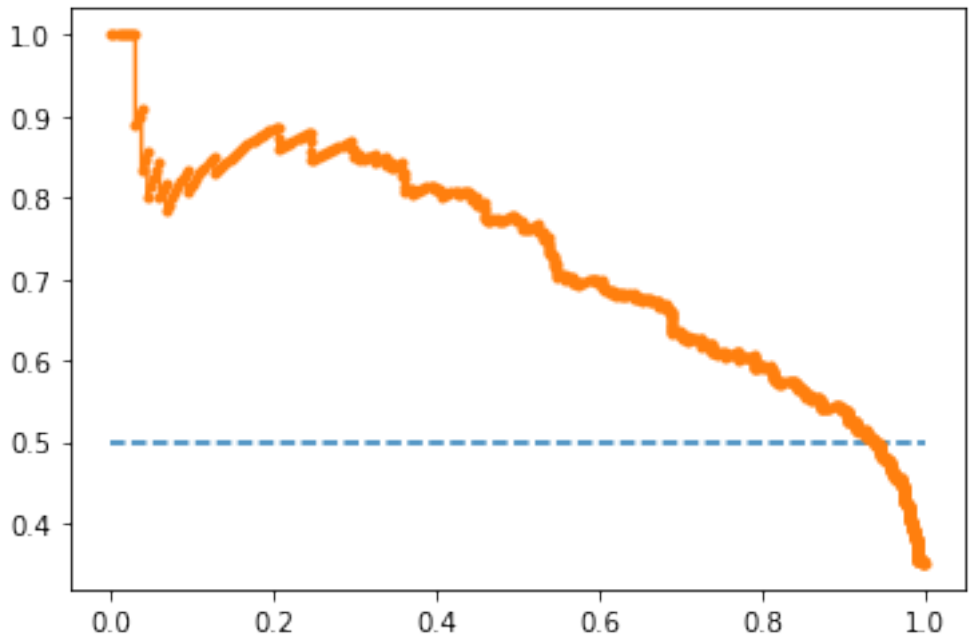
[103]:
```
#Precision Recall Curve for Logistic Regression

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
```

[104]:
```
# 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
```

[104]: [<matplotlib.lines.Line2D at 0x7f4842e99090>]

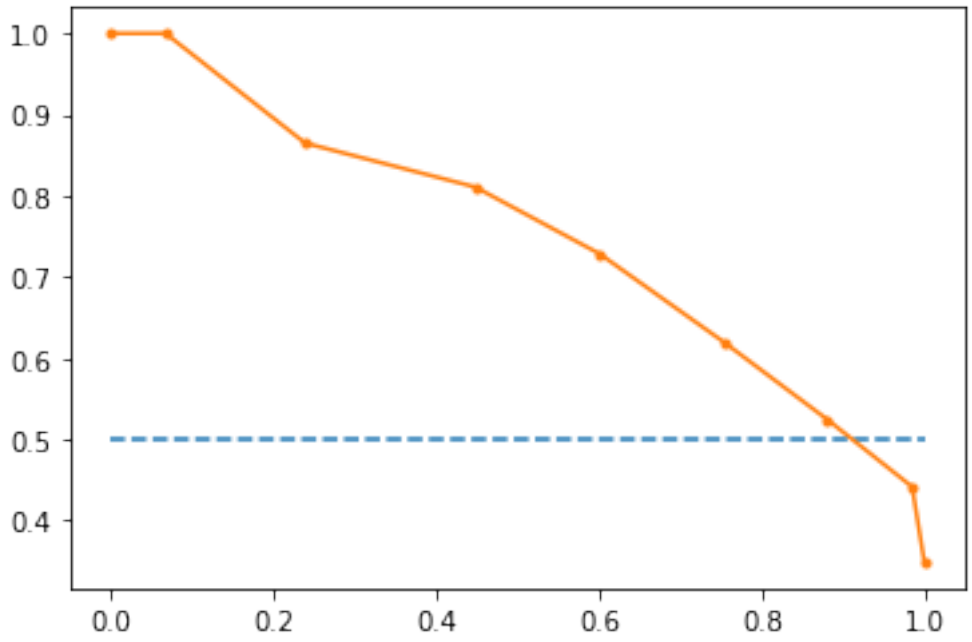


[105]:
```
#Precision Recall Curve for KNN

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
```

[106]:
```
# 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
```

[106]:
```
[<matplotlib.lines.Line2D at 0x7f4842d40f50>]
```



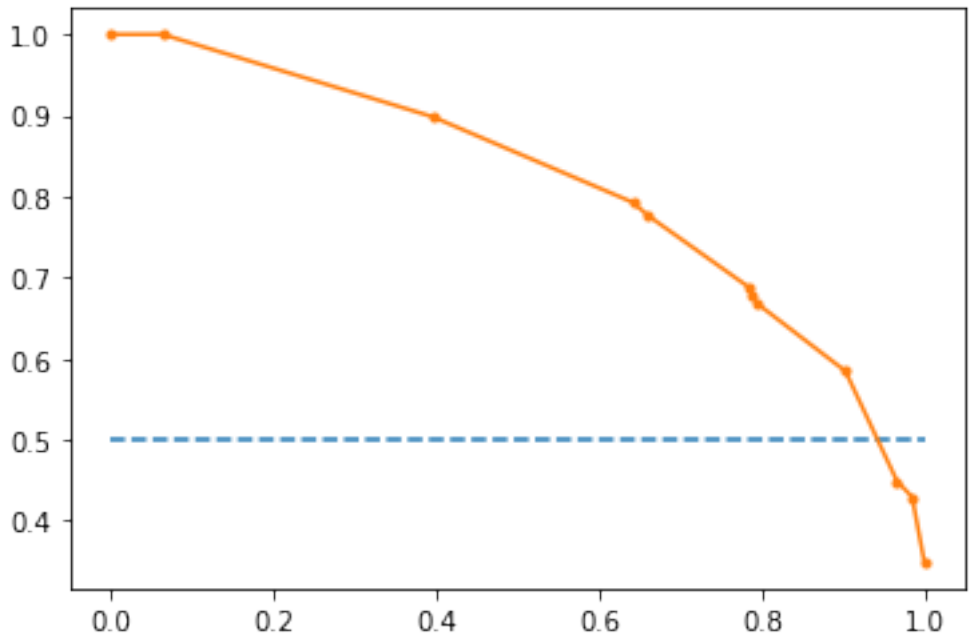
[107]:
```
#Precision Recall Curve for Decission Tree Classifier
```

```
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
```

[108]:
```
# 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=0.709 auc=0.814 ap=0.769
```

[108]:
```
[<matplotlib.lines.Line2D at 0x7f4842cb57d0>]
```

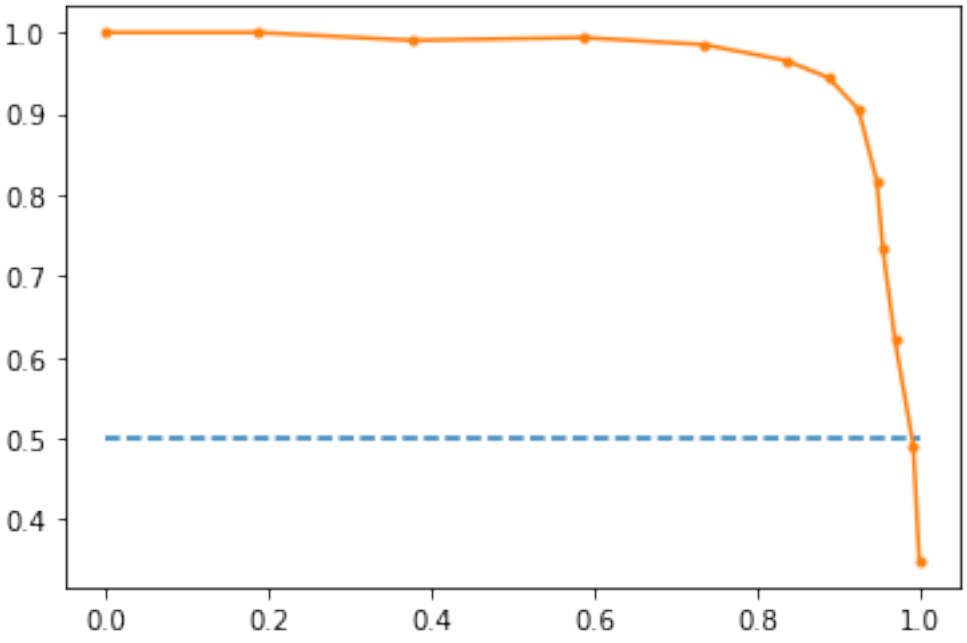


[109]:
```
#Precision Recall Curve for Random Forest

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
```

[110]:
```
# 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=0.915 auc=0.964 ap=0.957
```

[110]:
```
[<matplotlib.lines.Line2D at 0x7f4842c2c050>]
```


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