In [1]:
```python
import numpy as np
import pandas as pd


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

%matplotlib inline
```

In [7]:
```python
data = pd.read_csv('health care diabetes.csv')
```

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

Out[8]:

	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 [9]:
```python
data.isnull().any()
```

Out[9]:
```
Pregnancies                 False
Glucose                     False
BloodPressure               False
SkinThickness               False
Insulin                     False
BMI                         False
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

In [10]:
```python
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 [11]:
```python
Positive = data[data['Outcome']==1]
Positive.head(5)
```

Out[11]:

	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 [12]:

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

Out[12]:

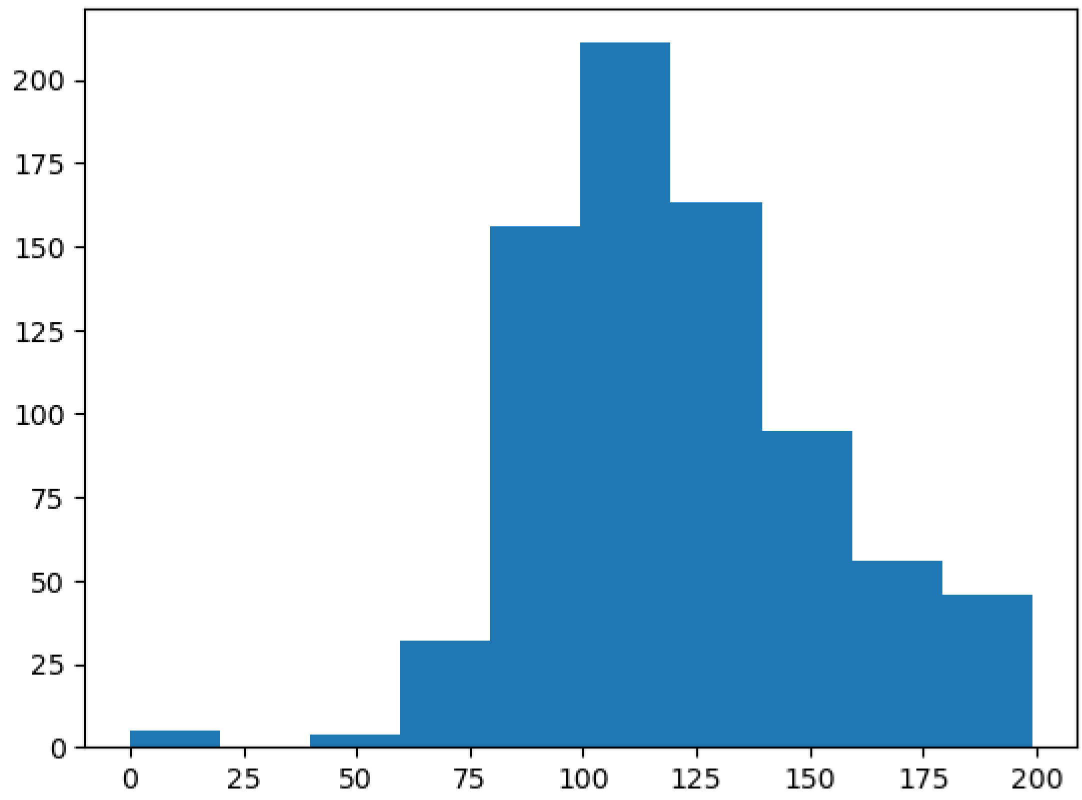
```
99     17
100    17
111    14
129    14
125    14
106    14
112    13
Name: Glucose, dtype: int64
```

In [13]:

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

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



In [14]:

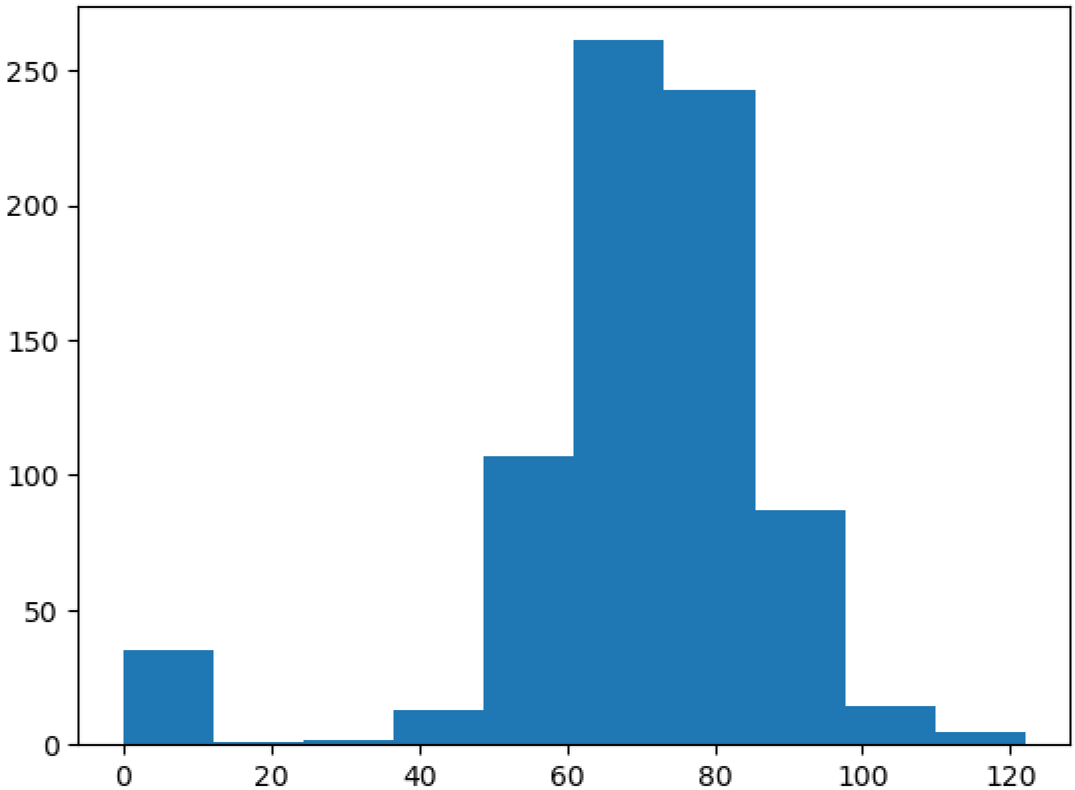
```
data['BloodPressure'].value_counts().head(7)
```

Out[14]:

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

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

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



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

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

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

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

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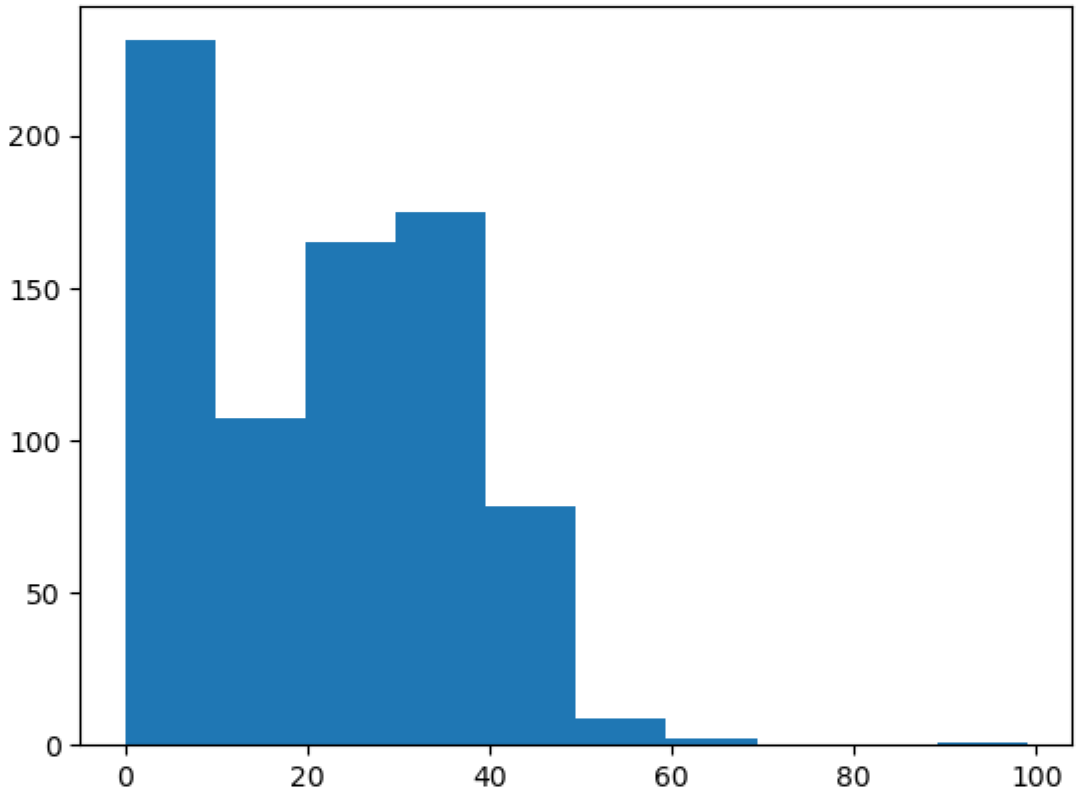

In [18]:
```
data['Insulin'].value_counts().head(7)
```

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

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

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

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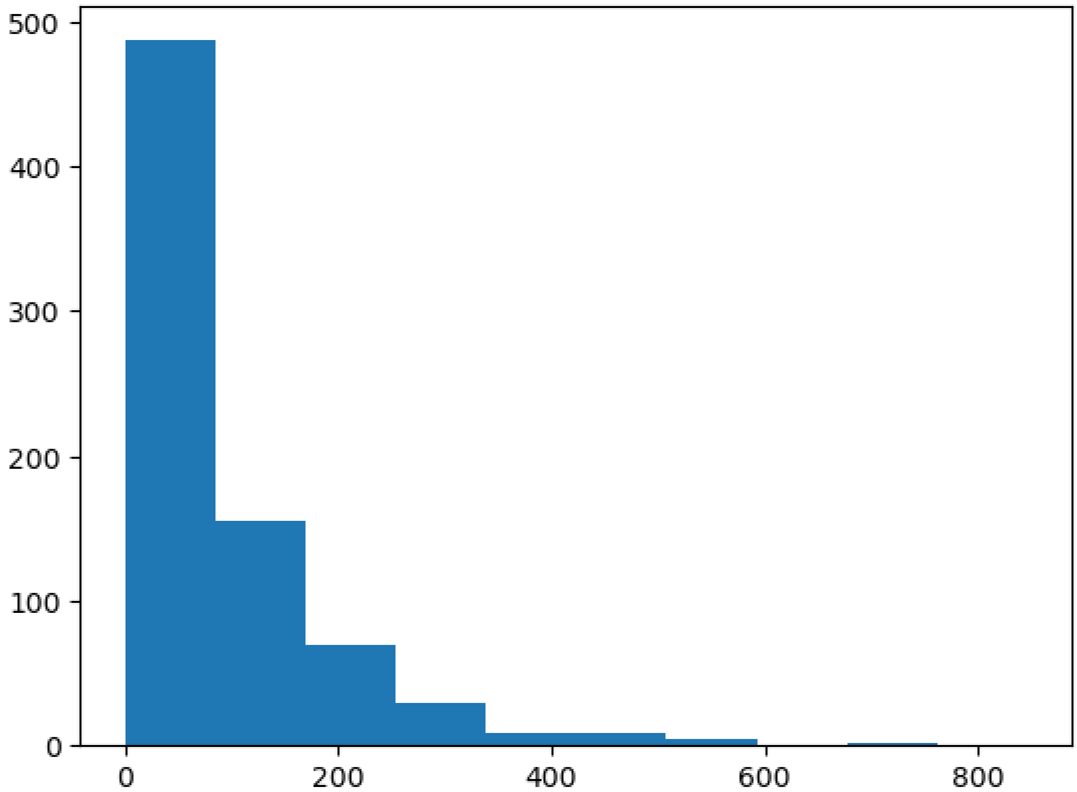
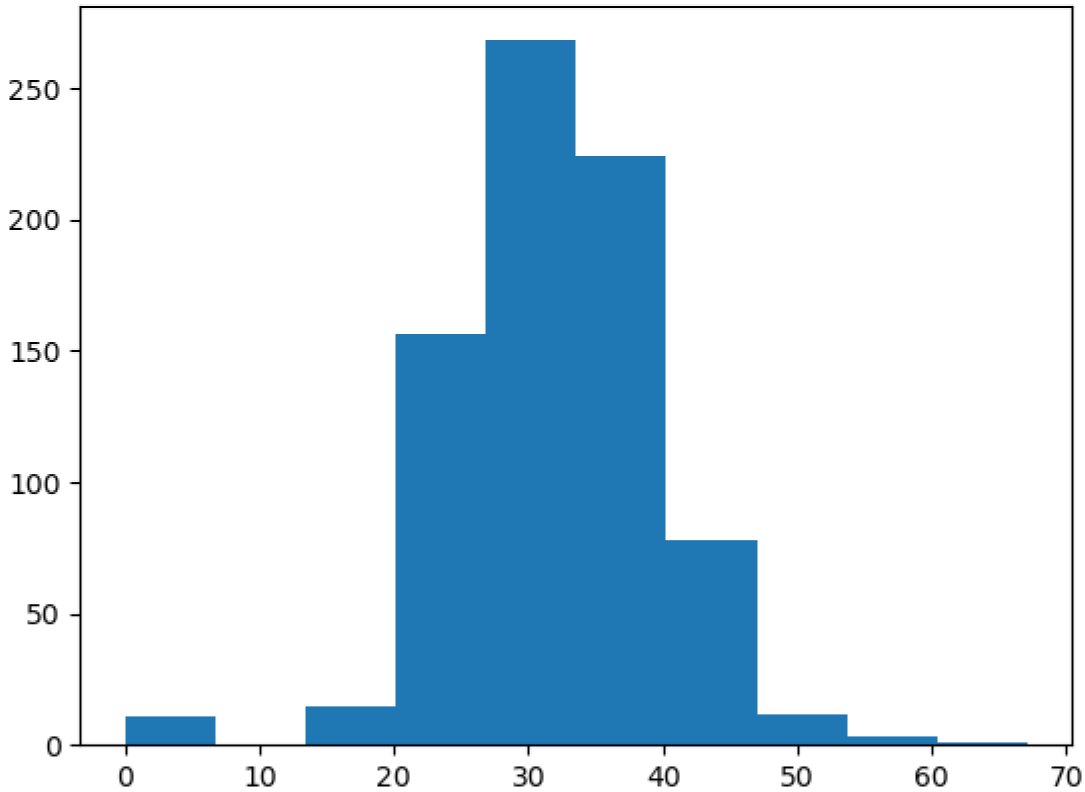


In [20]:
```
data['BMI'].value_counts().head(7)
```

Out[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
```

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

Out[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 ]),
 <BarContainer object of 10 artists>)
```



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

Out[22]:

	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 [ ]:

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

Out[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  ]),
 [<matplotlib.patches.Polygon at 0x15f6b8b19d0>])
```

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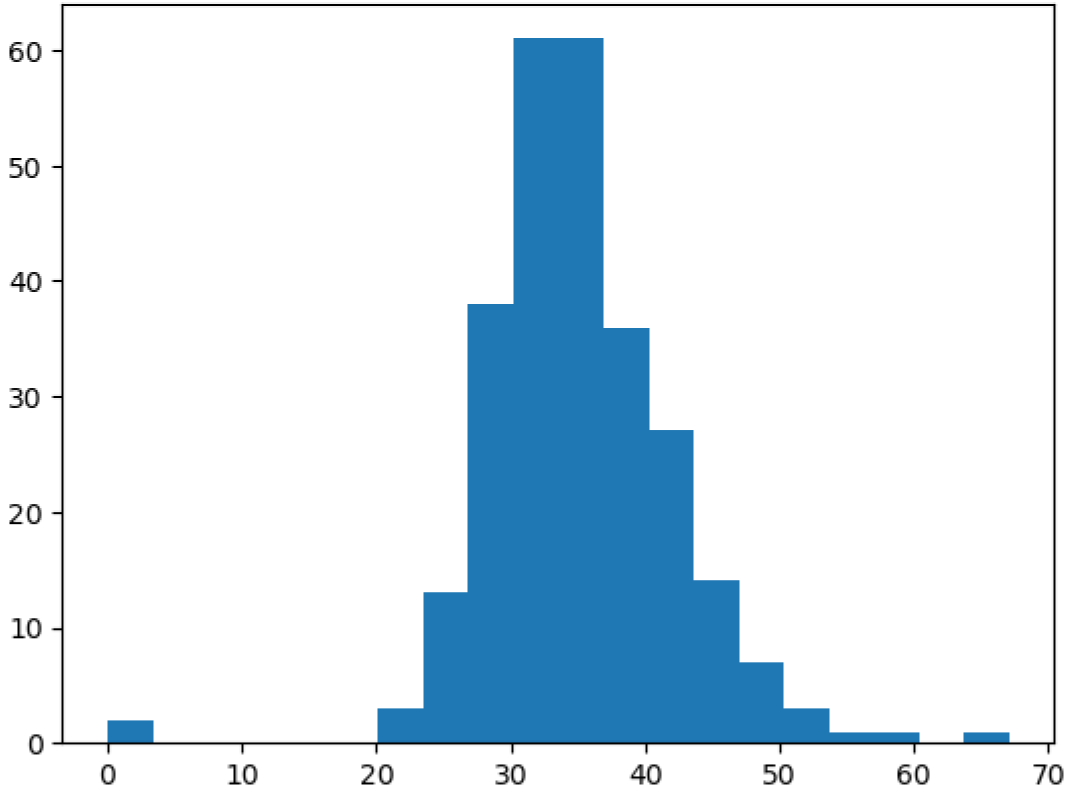
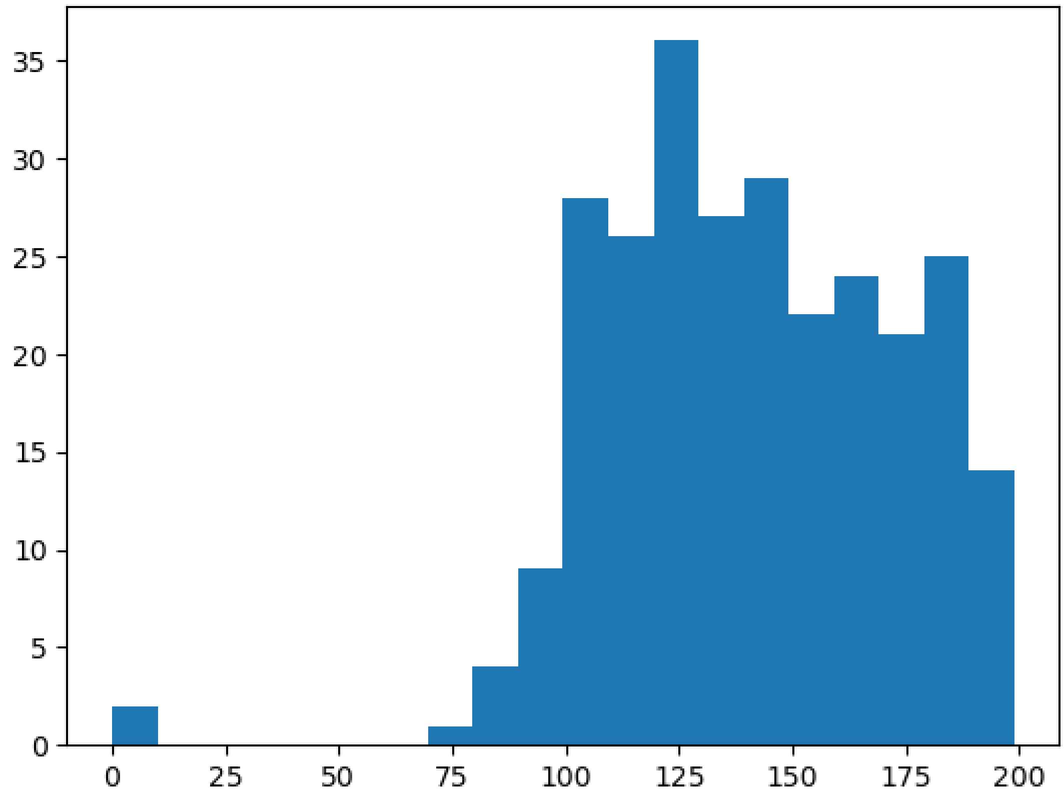


In [24]:
```
Positive['BMI'].value_counts().head(7)
```

Out[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
```

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

Out[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.  ]),
 [<matplotlib.patches.Polygon at 0x15f6b921700>])
```

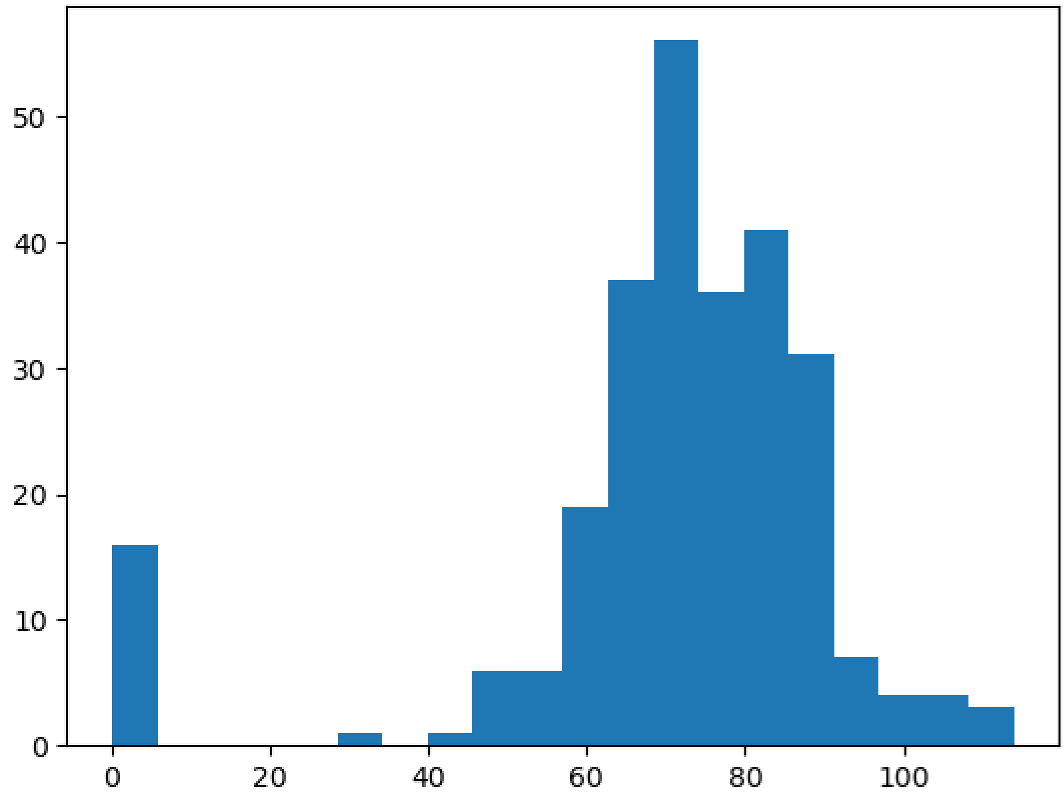


In [26]:
```
Positive['Glucose'].value_counts().head(7)
```

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

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

Out[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. ]),
 [<matplotlib.patches.Polygon at 0x15f6b9d8220>])
```



In [28]:
```
Positive['BloodPressure'].value_counts().head(7)
```
Out[28]:
```
70    23
76    18
78    17
74    17
72    16
0     16
80    13
Name: BloodPressure, dtype: int64
```

In [29]:
```
plt.hist(Positive['SkinThickness'],histtype='stepfilled',bins=20)
```
Out[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.  ]),
 [<matplotlib.patches.Polygon at 0x15f6ba2dee0>])
```

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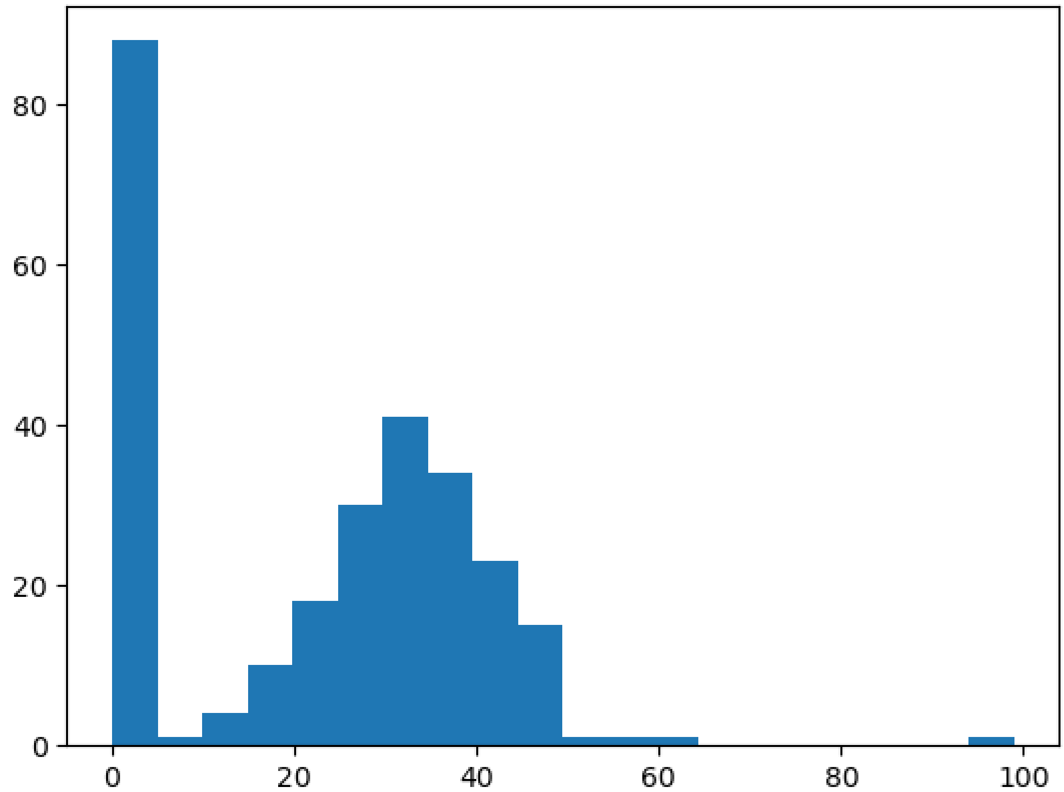

In [30]:
```
Positive['SkinThickness'].value_counts().head(7)
```

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

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

Out[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. ]),
 [<matplotlib.patches.Polygon at 0x15f6ba99370>])
```

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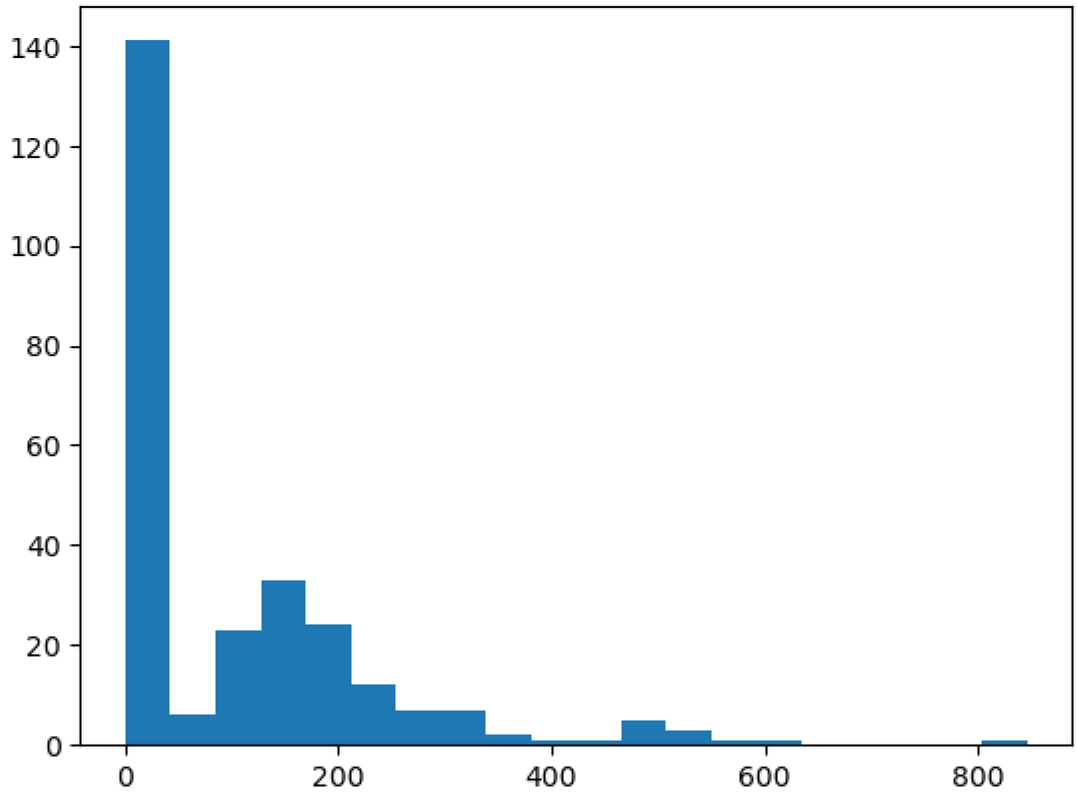
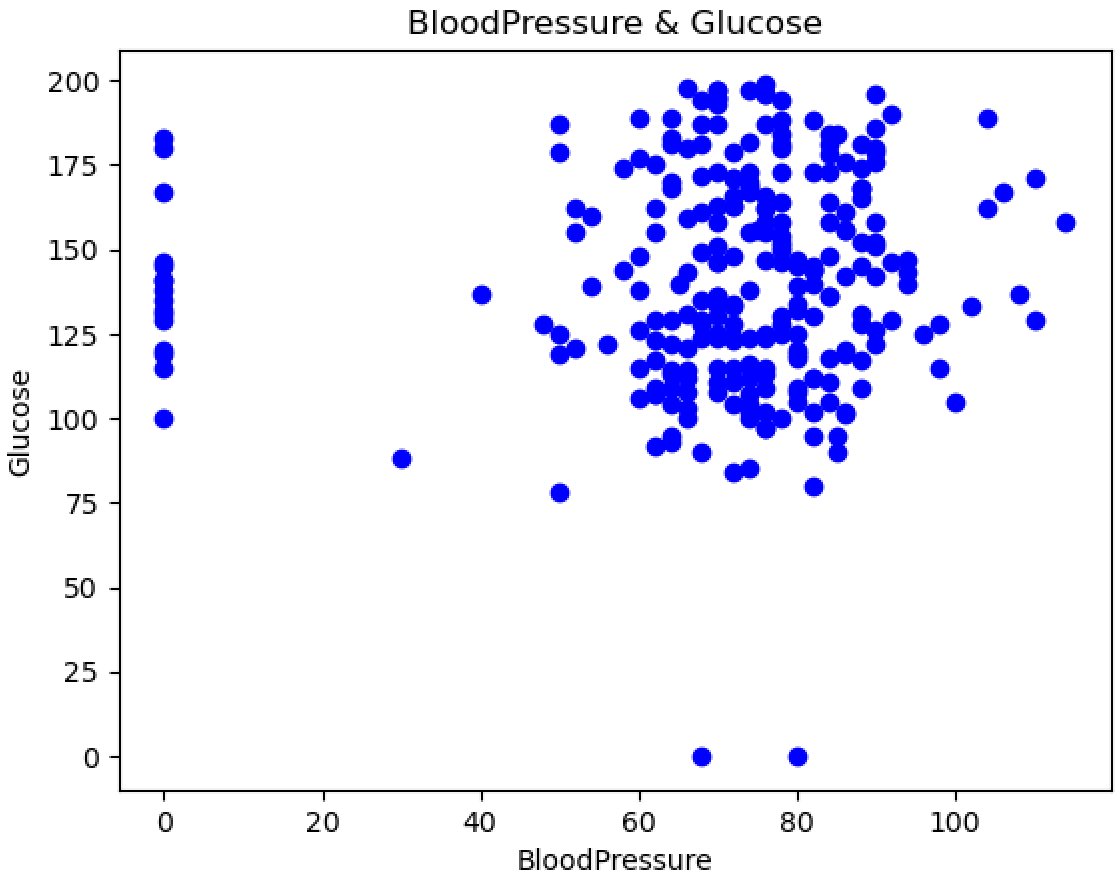


In [32]:
```
Positive['Insulin'].value_counts().head(7)
```

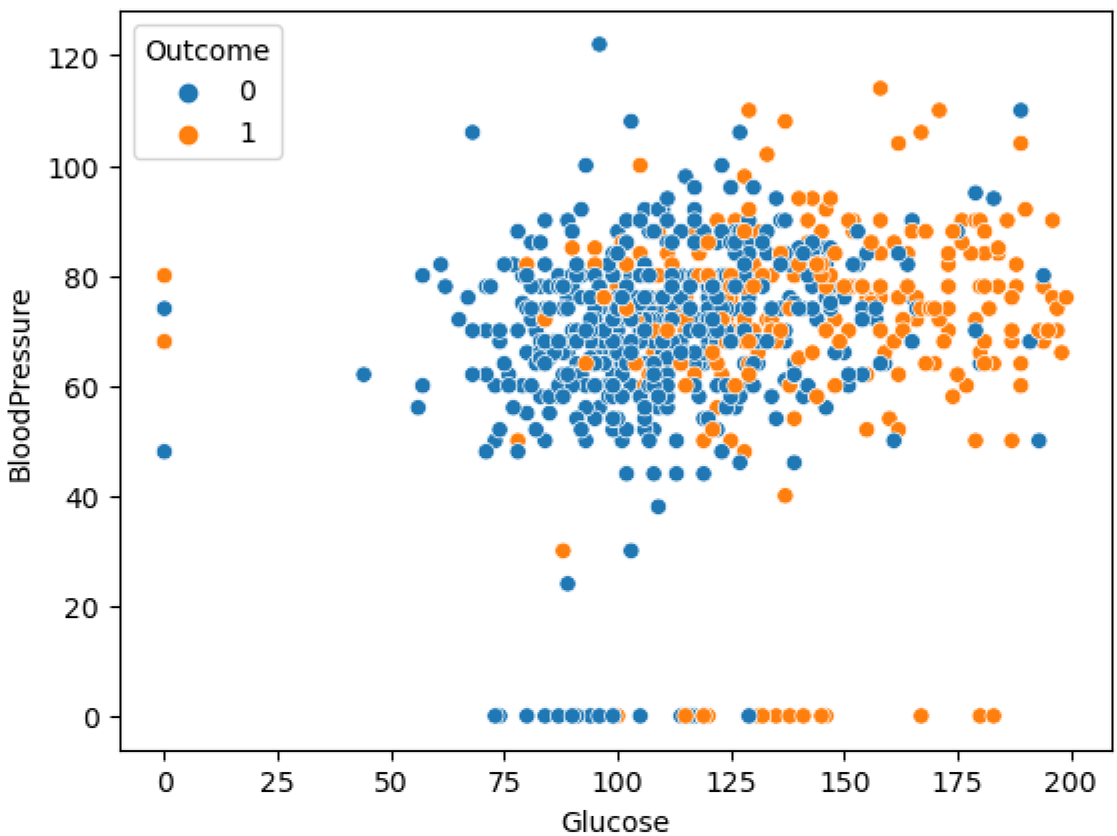
Out[32]:
```
0      138
130      6
180      4
175      3
156      3
185      2
194      2
Name: Insulin, dtype: int64
```

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

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



In [35]:
```
g =sns.scatterplot(x= "Glucose" ,y= "BloodPressure",
                   hue="Outcome",
                   data=data);
```



In [36]:
```
B =sns.scatterplot(x= "BMI" ,y= "Insulin",
                   hue="Outcome",
                   data=data);
```

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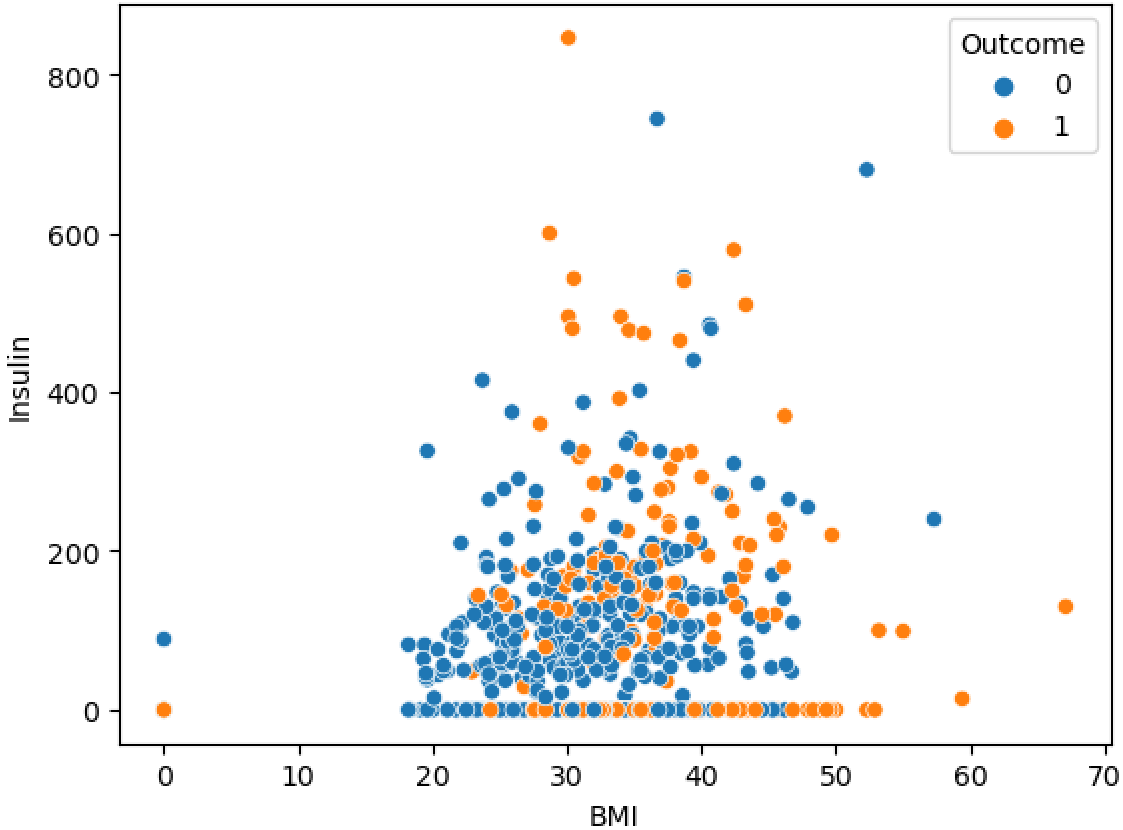
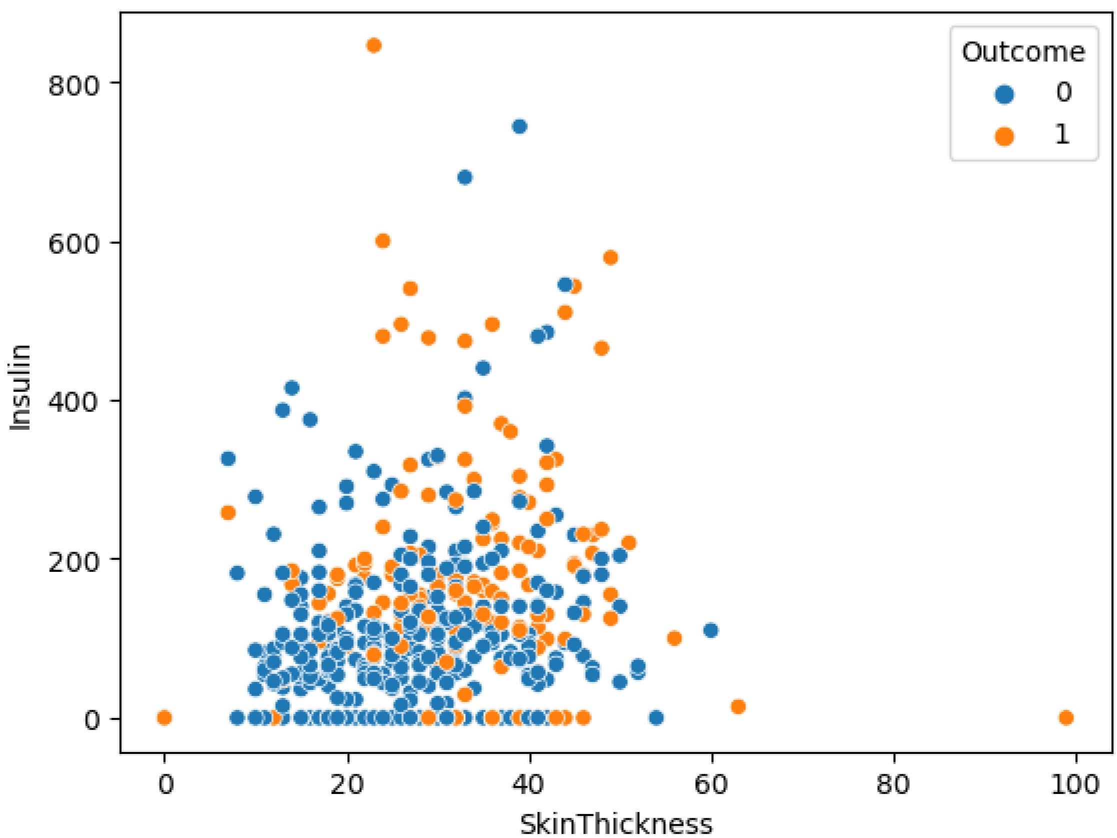


In [37]:
```
S =sns.scatterplot(x= "SkinThickness" ,y= "Insulin",
              hue="Outcome",
              data=data);
```



In [38]:
```
### correlation matrix
data.corr()
```

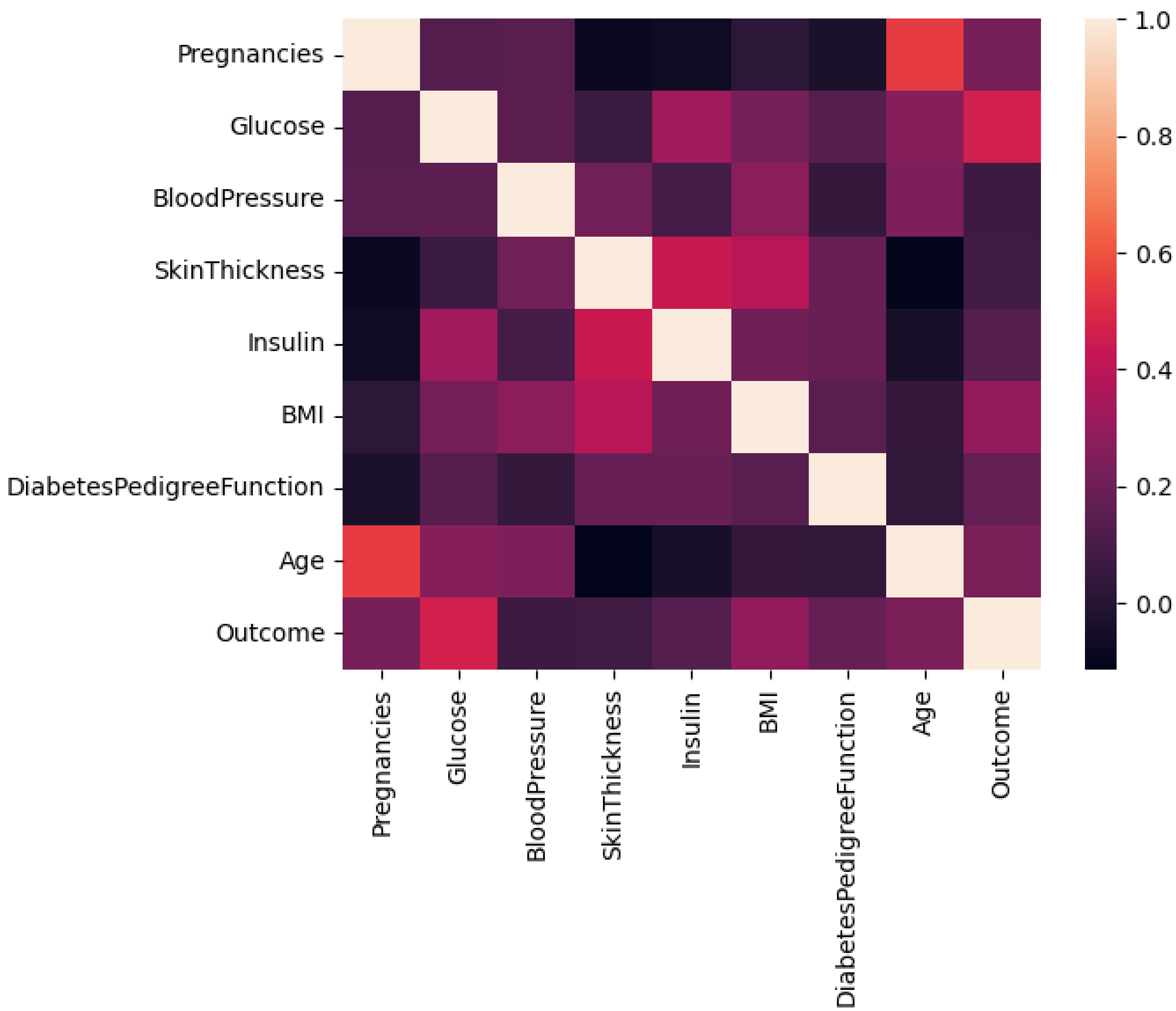
Out[38]:

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

In [39]:

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

Out[39]: <AxesSubplot:>



In [40]:

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

Out[40]: <AxesSubplot:>

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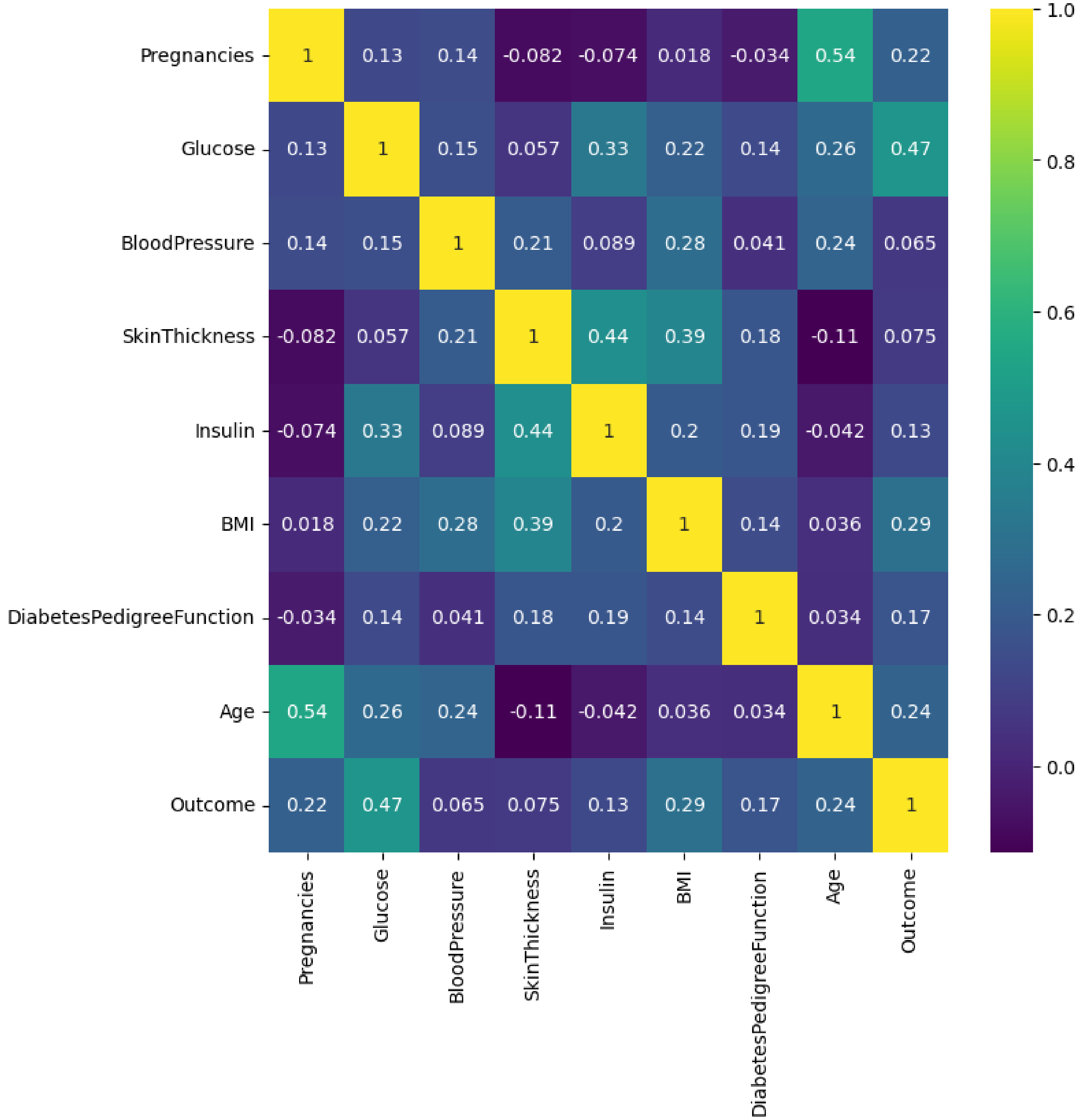
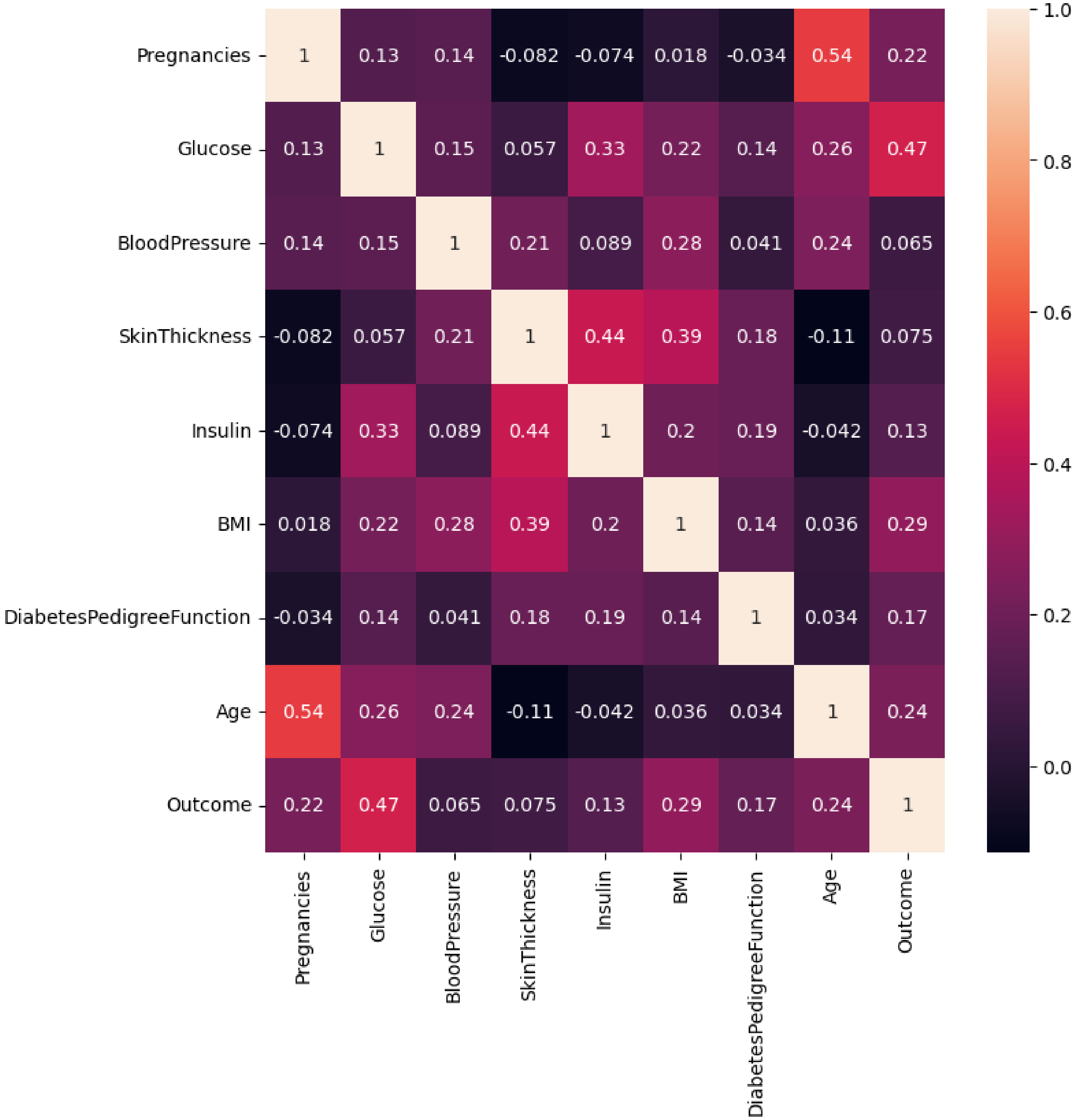


In [41]:
```
plt.subplots(figsize=(8,8))
sns.heatmap(data.corr(),annot=True)   ### gives correlation value
```

Out[41]:
```
<AxesSubplot:>
```



In [42]:
```
data.head(5)
```

Out[42]:

	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 [43]:
```
features = data.iloc[:,[0,1,2,3,4,5,6,7]].values
label = data.iloc[:,8].values
```

In [44]:
```
#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 [45]:
```
#Create model
from sklearn.linear_model import LogisticRegression
model = LogisticRegression()
model.fit(X_train,y_train)
```

Out[45]:
```
LogisticRegression()
```

In [47]:
```
print(model.score(X_train,y_train))
print(model.score(X_test,y_test))
```

```
0.7719869706840391
0.7662337662337663
```

In [48]:
```
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(label,model.predict(features))
cm
```

Out[48]:
```
array([[446,  54],
       [122, 146]], dtype=int64)
```

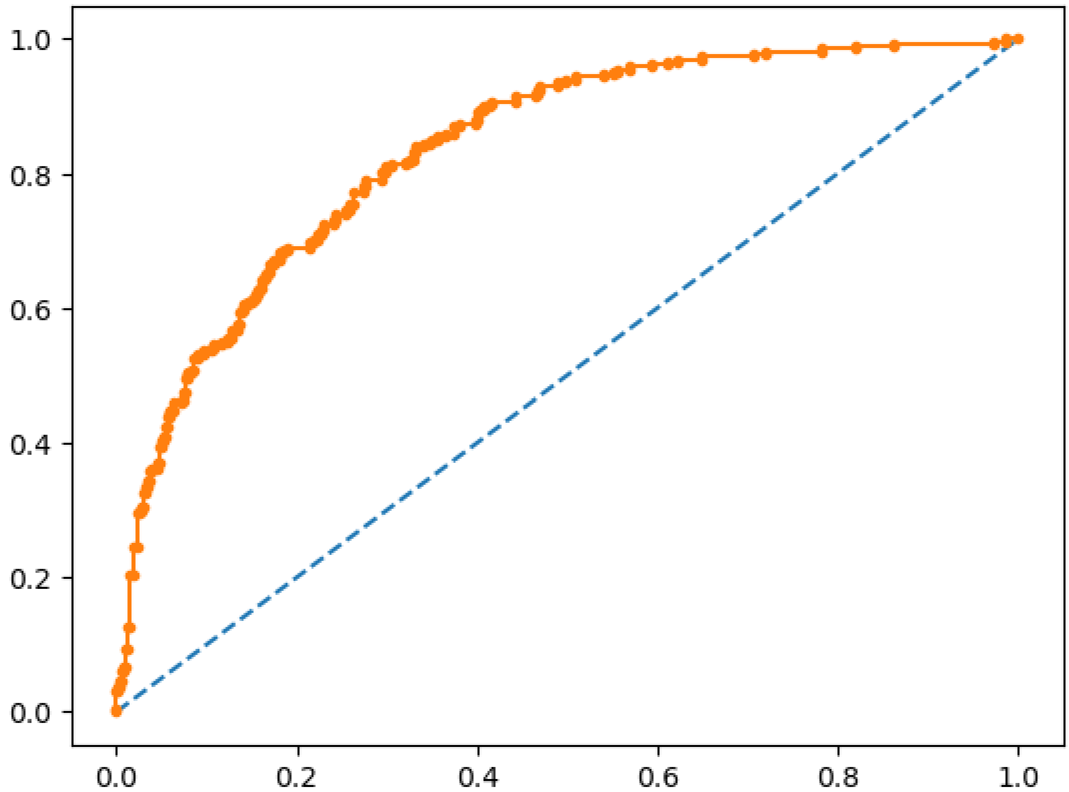
In [49]:
```
from sklearn.metrics import classification_report
print(classification_report(label,model.predict(features)))
```

```
              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 [50]:
```
#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[50]:
```
[<matplotlib.lines.Line2D at 0x15f6e2c1190>]
```



In [51]:
```
#Applying Decission Tree Classifier
from sklearn.tree import DecisionTreeClassifier
model3 = DecisionTreeClassifier(max_depth=5)
model3.fit(X_train,y_train)
```

Out[51]:
```
DecisionTreeClassifier(max_depth=5)
```

In [52]:
```
model3.score(X_train,y_train)
```

Out[52]:
```
0.8289902280130294
```

In [53]:
```
#Applying Random Forest
from sklearn.ensemble import RandomForestClassifier
model4 = RandomForestClassifier(n_estimators=11)
model4.fit(X_train,y_train)
```

Out[53]:
```
RandomForestClassifier(n_estimators=11)
```

In [54]:
```
model4.score(X_train,y_train)
```

Out[54]:
```
0.99185667752443
```

In [55]:
```
model4.score(X_test,y_test)
```

Out[55]:
```
0.7337662337662337
```

In [56]:
```
#Support Vector Classifier

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

Out[56]:
```
SVC(gamma='auto')
```

Loading [MathJax]/extensions/Safe.js

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

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

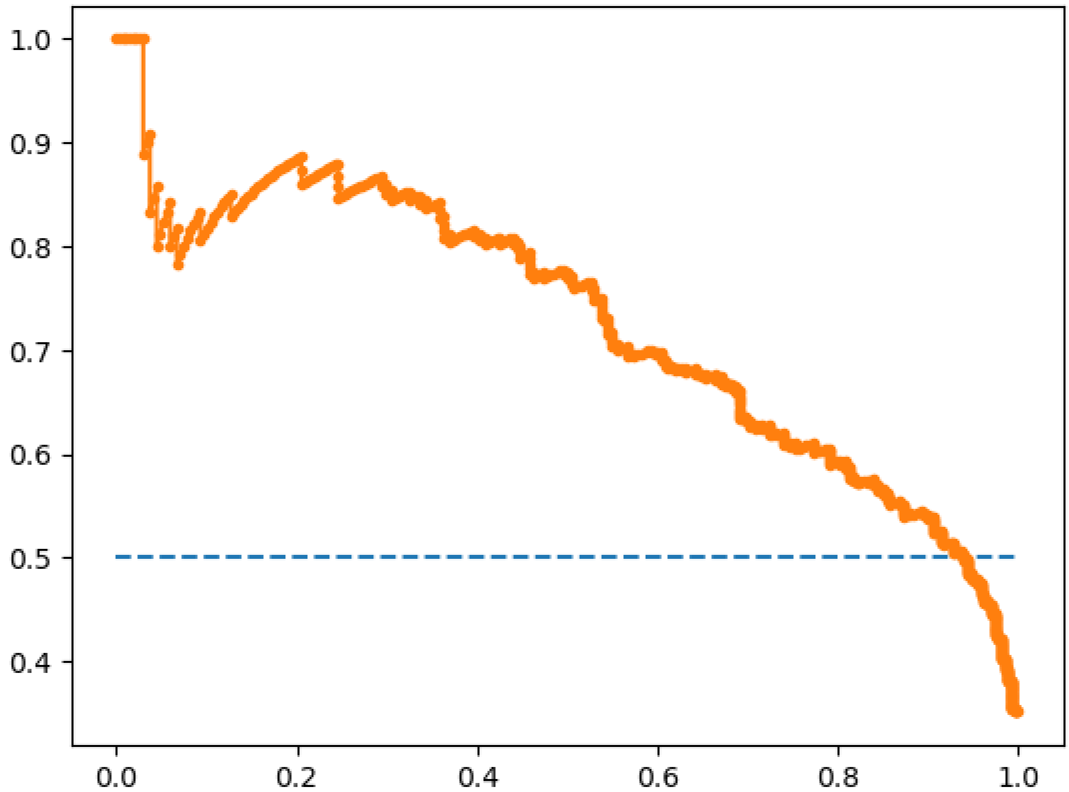
Out[58]:
```
0.6168831168831169
```

In [65]:
```
#Applying K-NN
from sklearn.neighbors import KNeighborsClassifier
model2 = KNeighborsClassifier(n_neighbors=7,
                              metric='minkowski',
                              p = 2)
```

In [68]:
```
#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[68]:
```
[<matplotlib.lines.Line2D at 0x15f6f5f3ee0>]
```



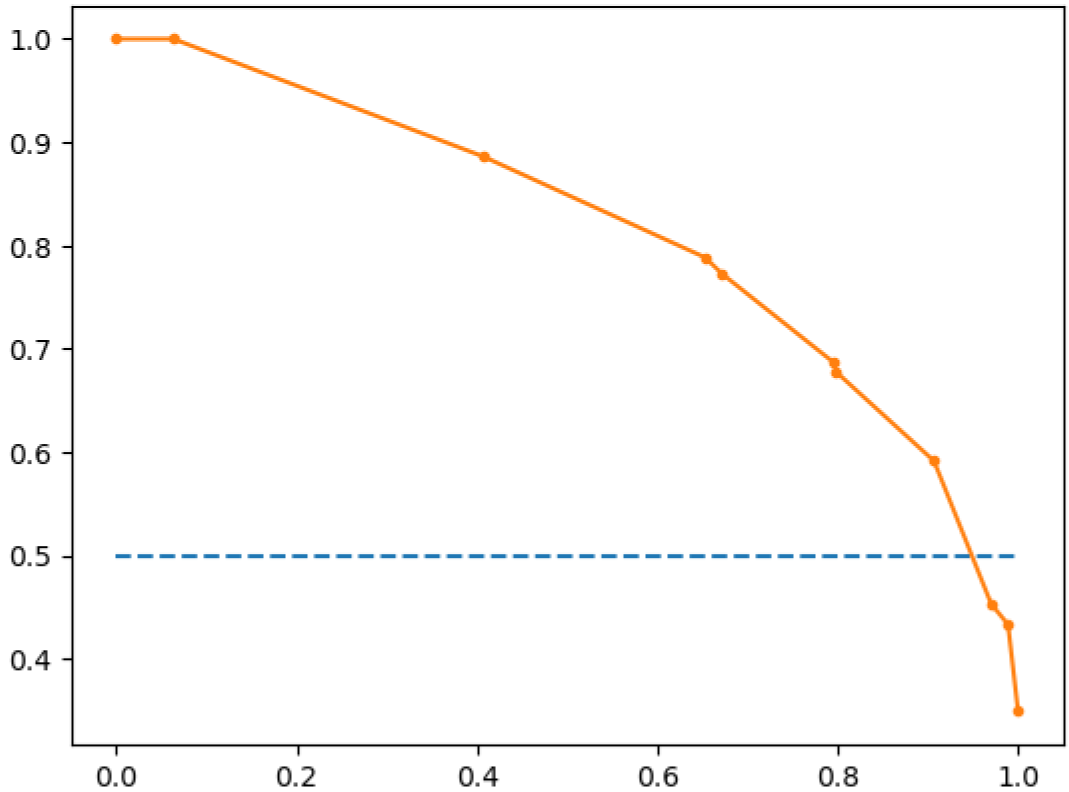
In [72]:

```
#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[72]:

```
[<matplotlib.lines.Line2D at 0x15f6f62b700>]
```



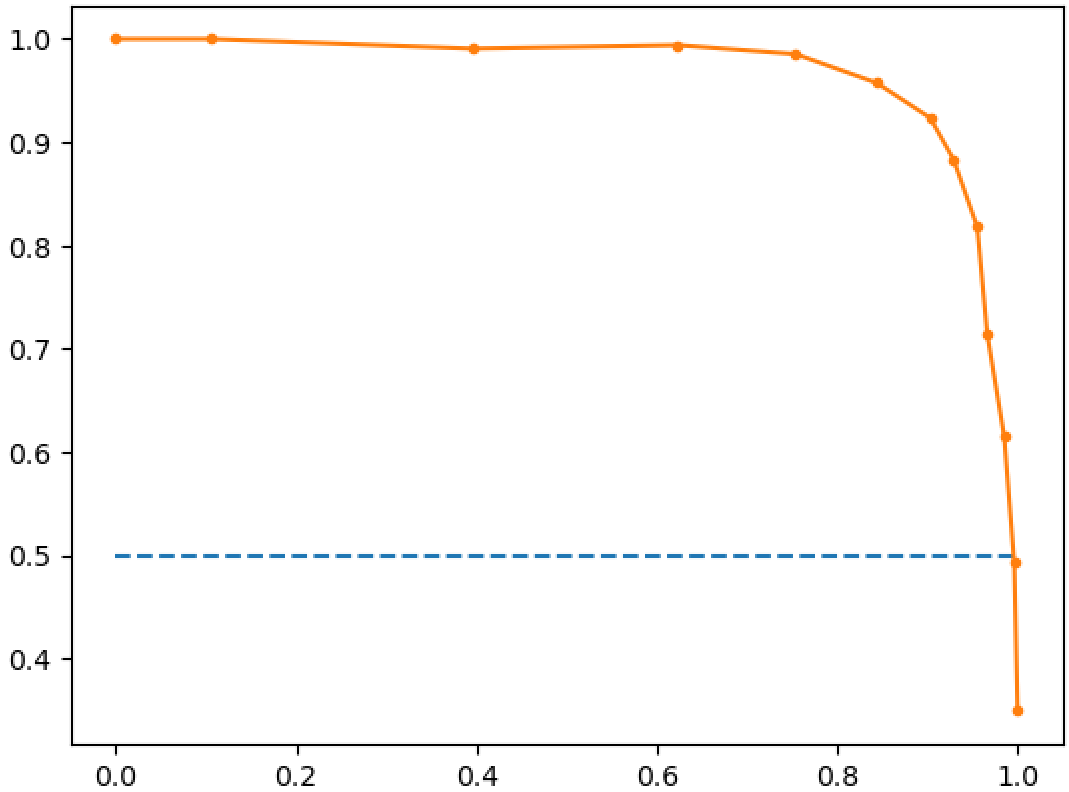
In [73]:

```
#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=0.913 auc=0.967 ap=0.959
```

Out[73]:

```
[<matplotlib.lines.Line2D at 0x15f6f68be80>]
```


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