In [1]:

```
import numpy as np
import pandas as pd


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

%matplotlib inline
```

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]:

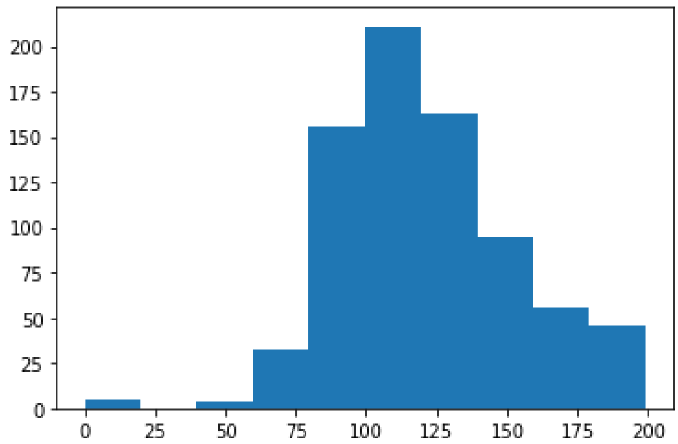
```
99     17
100    17
111    14
129    14
125    14
106    14
112    13
Name: Glucose, dtype: int64
```

In [8]:

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

Out[8]:

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



In [9]:

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

Out[9]:

```
70    57
74    52
78    45
68    45
72    44
64    43
```

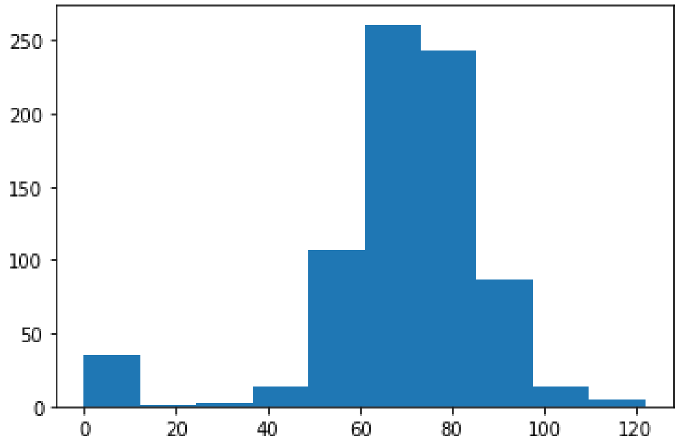
```
80    40
Name: BloodPressure, dtype: int64
```

In [10]:

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

Out[10]:

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



In [11]:

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

Out[11]:

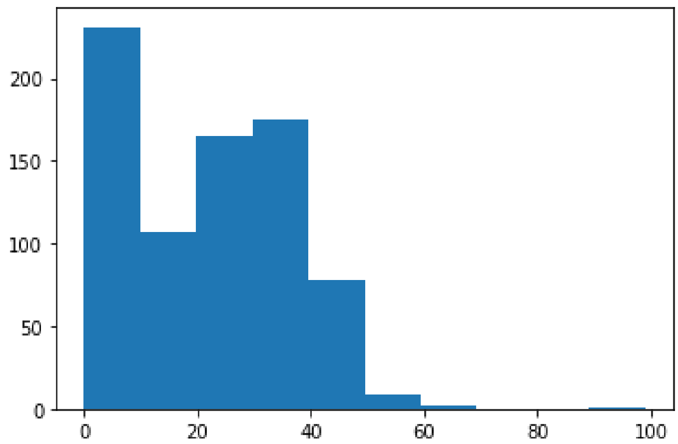
```
0     227
32     31
30     27
27     23
23     22
33     20
28     20
Name: SkinThickness, dtype: int64
```

In [12]:

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

Out[12]:

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



In [13]:

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

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

Out[13]:

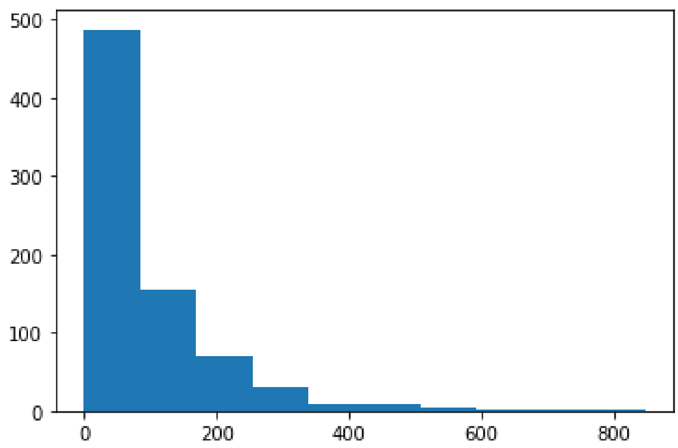
```
0      374
105     11
130      9
140      9
120      8
94       7
180      7
Name: Insulin, dtype: int64
```

In [14]:

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

Out[14]:

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



In [15]:

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

Out[15]:

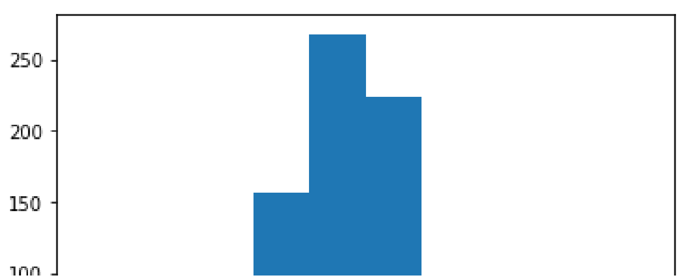
```
32.0    13
31.6    12
31.2    12
0.0     11
32.4    10
33.3    10
30.1     9
Name: BMI, dtype: int64
```

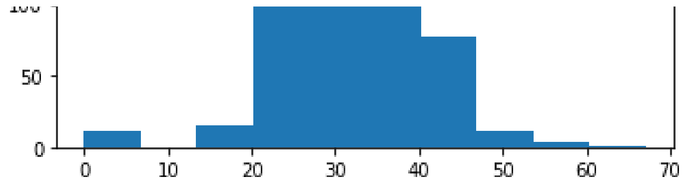
In [16]:

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

Out[16]:

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





In [17]:

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

Out[17]:

	count	mean	std	min	25%	50%	75%	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

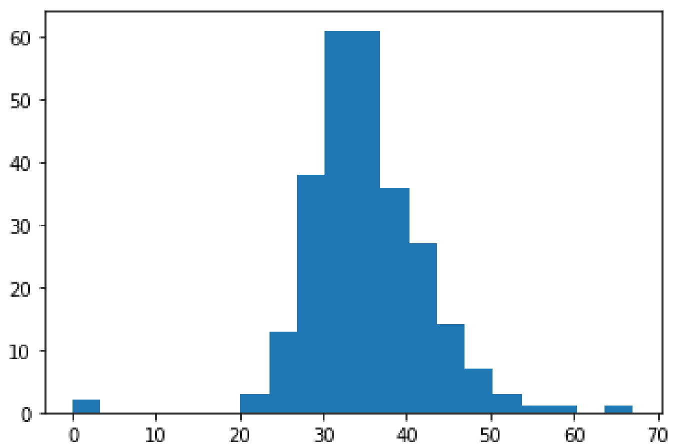
Week 2

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  ]),
 <a list of 1 Patch objects>)
```



In [19]:

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

Out[19]:

```
32.9    8
31.6    7
33.3    6
31.2    5
```

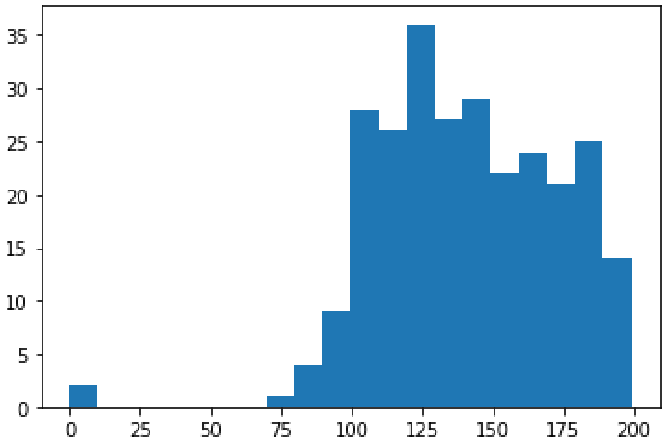
```
30.5    5
32.0    5
34.3    4
Name: BMI, dtype: int64
```

In [20]:

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

Out[20]:

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



In [21]:

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

Out[21]:

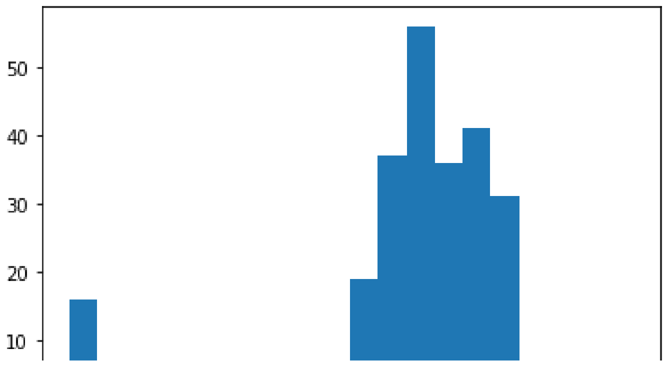
```
125    7
128    6
129    6
115    6
158    6
146    5
124    5
Name: Glucose, dtype: int64
```

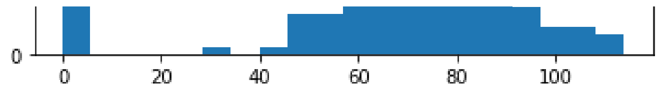
In [22]:

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

Out[22]:

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





In [23]:

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

Out[23]:

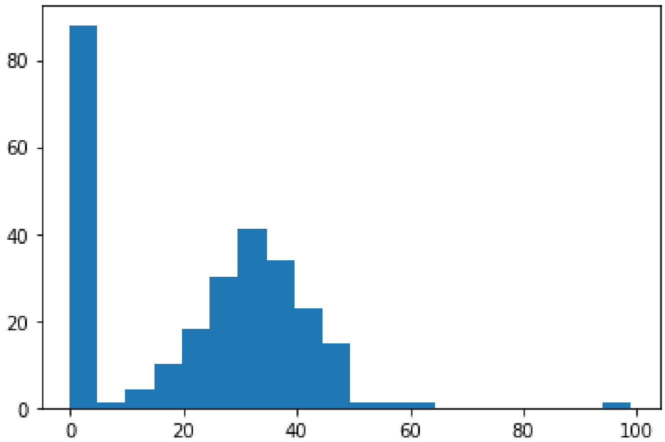
```
70    23
76    18
78    17
74    17
72    16
0     16
80    13
Name: BloodPressure, dtype: int64
```

In [24]:

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

Out[24]:

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



In [25]:

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

Out[25]:

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

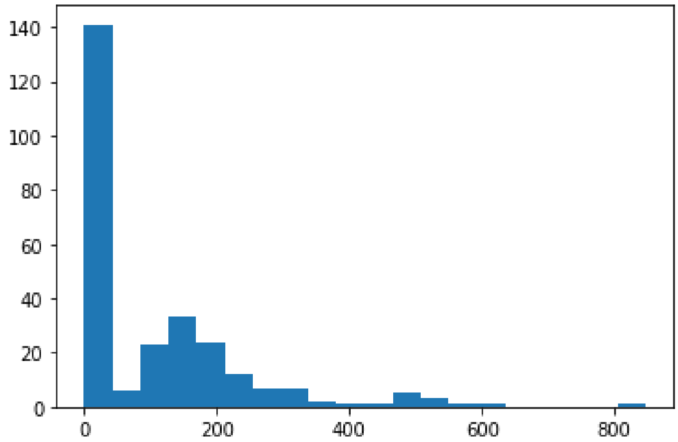
In [26]:

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

Out[26]:

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

```
<a list of 1 Patch objects>)
```



In [27]:

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

Out[27]:

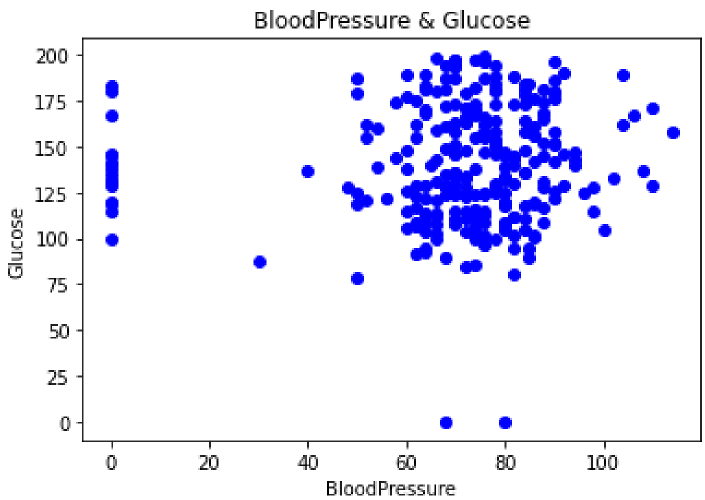
```
0      138
130      6
180      4
175      3
156      3
185      2
194      2
Name: Insulin, dtype: int64
```

In [28]:

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

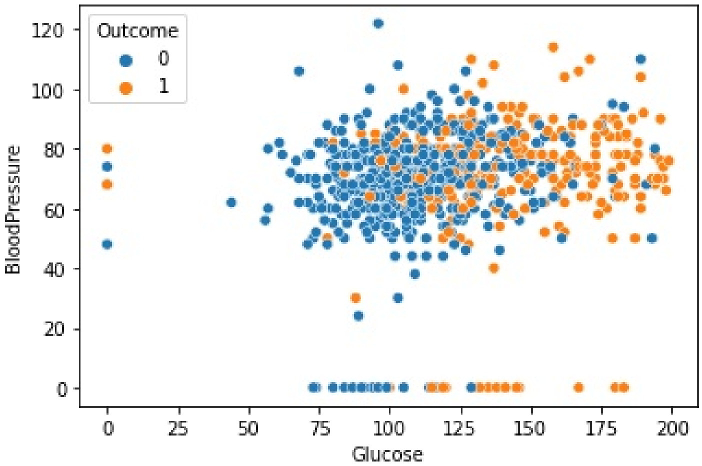
In [29]:

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



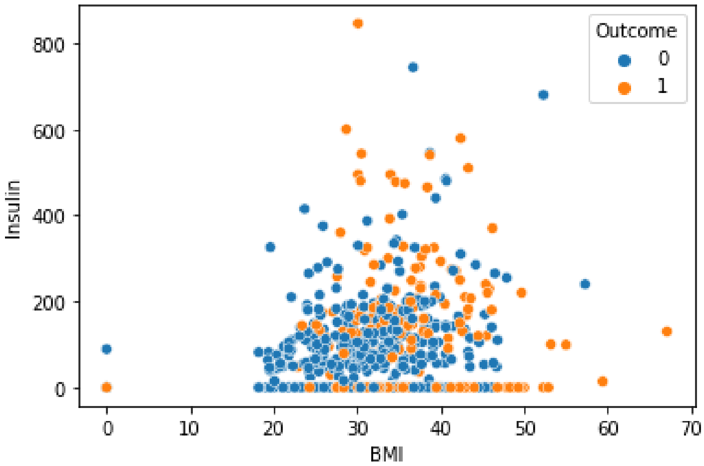
In [30]:

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



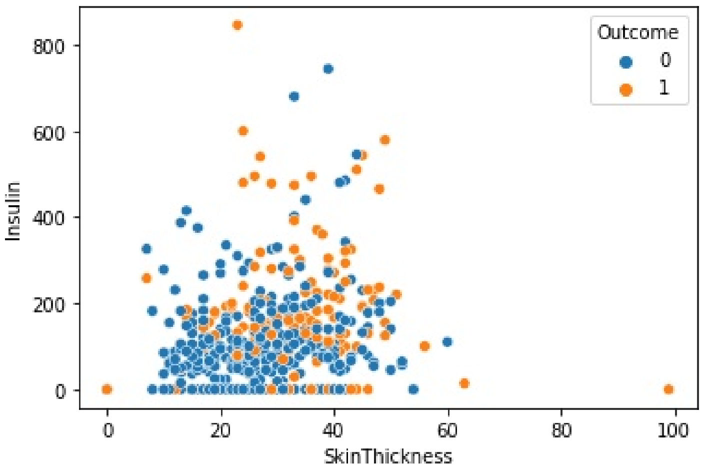
In [31]:

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



In [32]:

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



In [33]:

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

Out[33]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-	0.017683	-0.03352

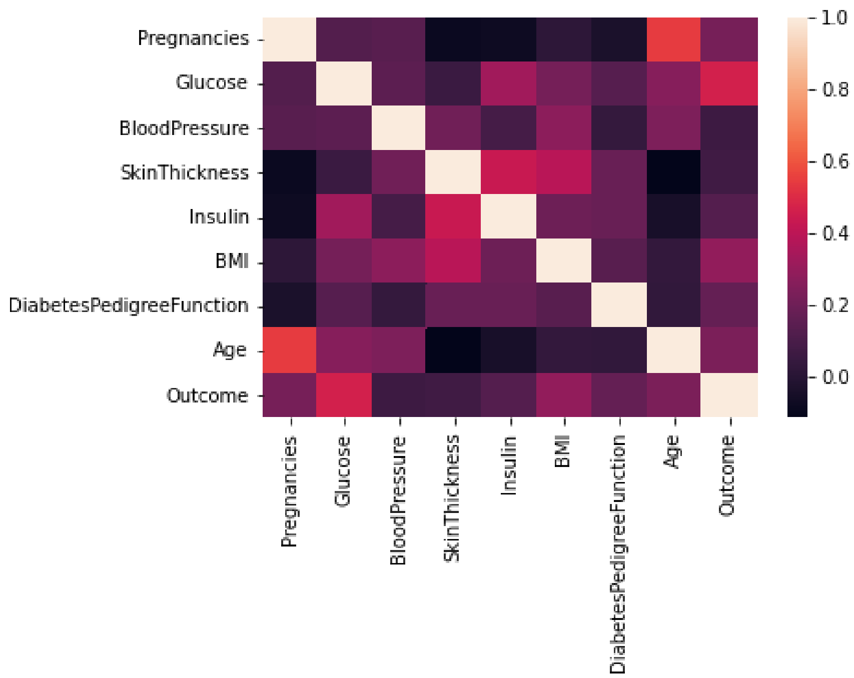
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.221071	0.13733
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.281805	0.04126
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.392573	0.18392
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.197859	0.18507
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.000000	0.14064
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.140647	1.00000
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.036242	0.03356
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.292695	0.17384

In [34]:

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

Out[34]:

<matplotlib.axes._subplots.AxesSubplot at 0x7f4172d4bad0>

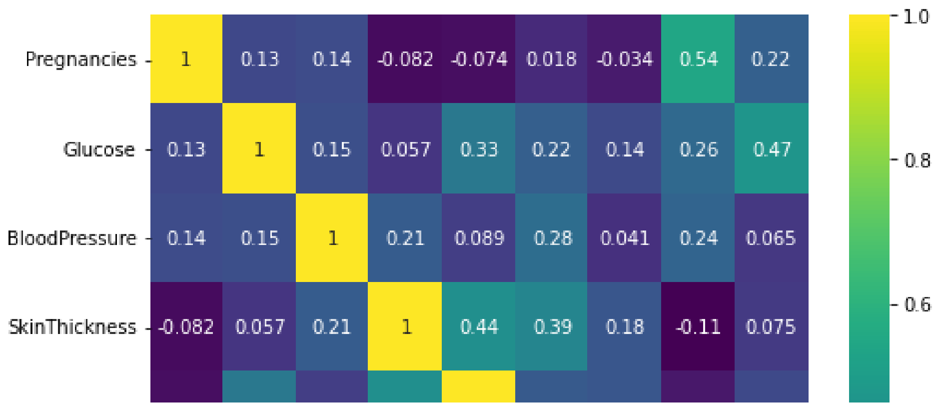


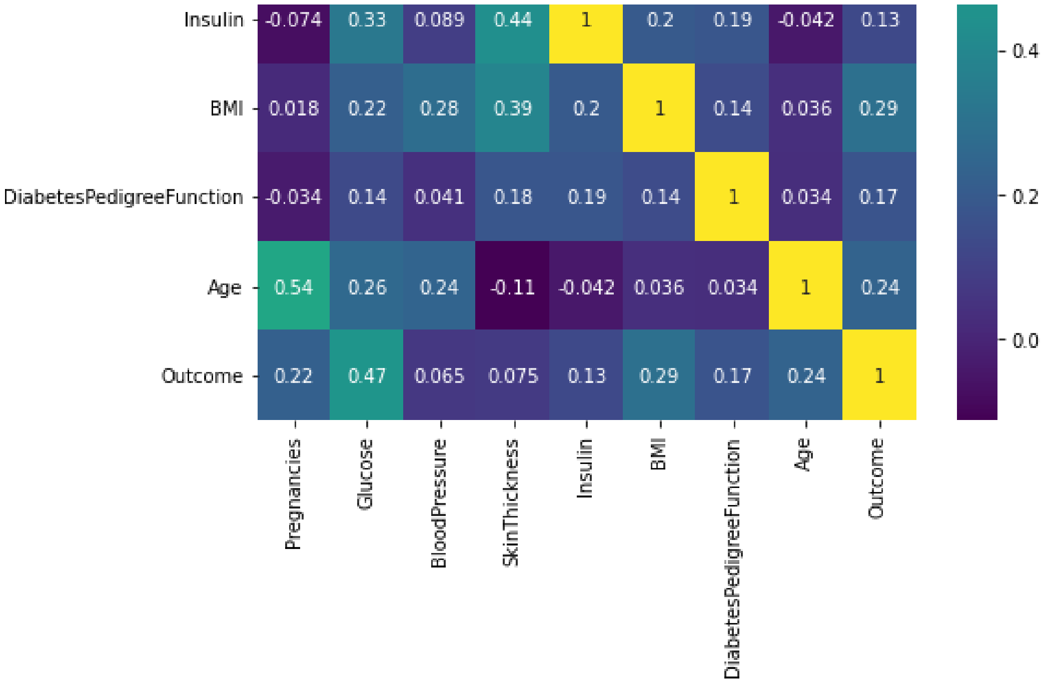
In [35]:

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

Out[35]:

<matplotlib.axes._subplots.AxesSubplot at 0x7f4172fef610>



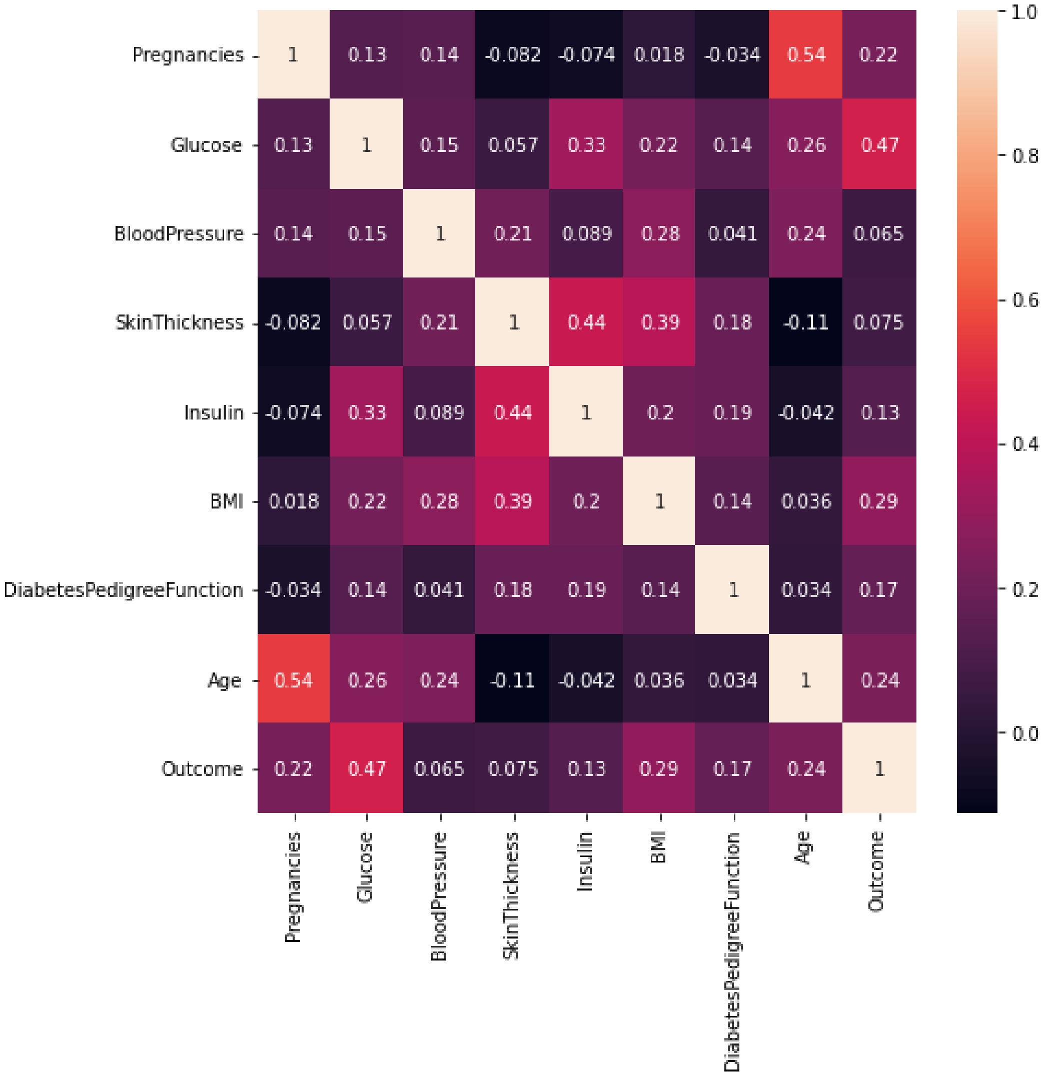


In [36]:

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

Out[36]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f4170398390>
```



In [37]:

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

Out[37]:

	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 [38]:

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

In [39]:

```
#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 [40]:

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

Out[40]:

```
LogisticRegression()
```

In [41]:

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

```
0.7719869706840391
0.7662337662337663
```

In [42]:

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

Out[42]:

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

In [43]:

```
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
```

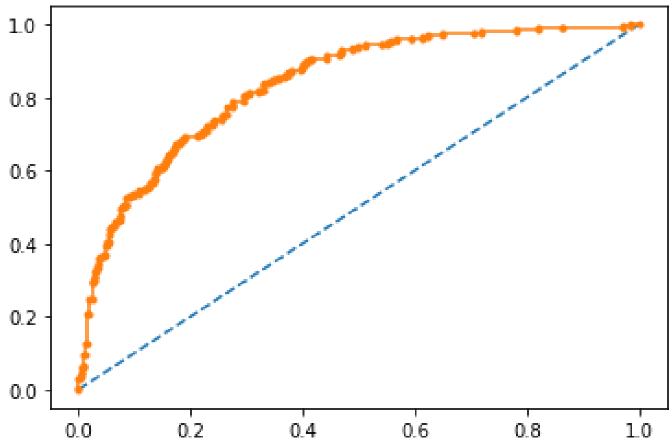
In [44]:

```
#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[44]:

[<matplotlib.lines.Line2D at 0x7f416dc92850>]



In [45]:

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

Out[45]:

DecisionTreeClassifier(max_depth=5)

In [46]:

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

Out[46]:

0.8289902280130294

In [47]:

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

Out[47]:

0.7597402597402597

In [48]:

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

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

Out[48]:

```
RandomForestClassifier(n_estimators=11)
```

In [49]:

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

Out[49]:

```
0.99185667752443
```

In [50]:

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

Out[50]:

```
0.7857142857142857
```

In [51]:

```
#Support Vector Classifier

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

Out[51]:

```
SVC(gamma='auto')
```

In [52]:

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

Out[52]:

```
0.6168831168831169
```

In [54]:

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

Out[54]:

```
KNeighborsClassifier(n_neighbors=7)
```

In [55]:

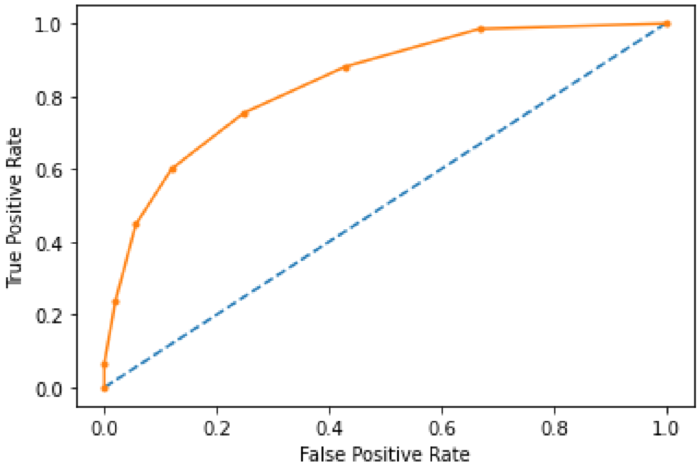
```
#Preparing ROC Curve (Receiver Operating Characteristics Curve)
from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score

# 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 0.571
42857 0.42857143
 0.28571429 0.14285714 0.        ]
```

Out[55]:

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



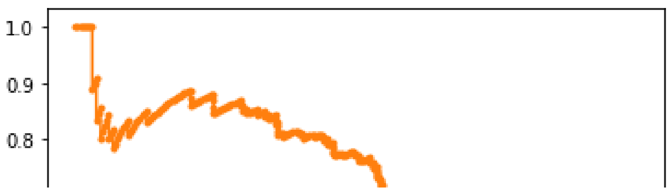
In [56]:

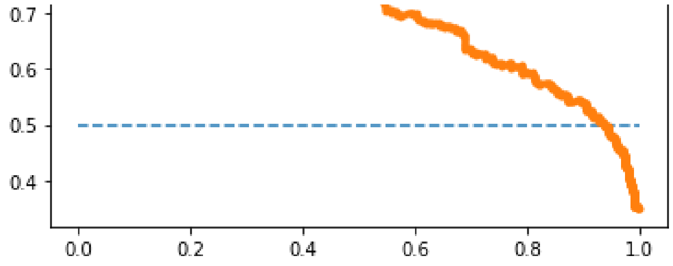
```
#Precision Recall Curve for Logistic Regression

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[56]:

```
[<matplotlib.lines.Line2D at 0x7f416d521510>]
```





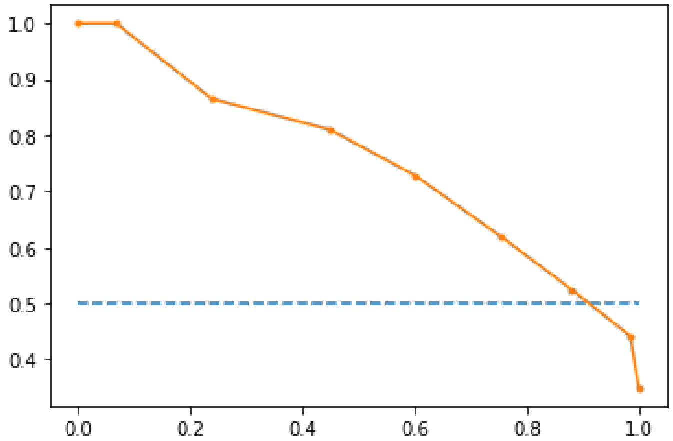
In [57]:

```
#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[57]:

```
[<matplotlib.lines.Line2D at 0x7f416d48dc50>]
```



In [58]:

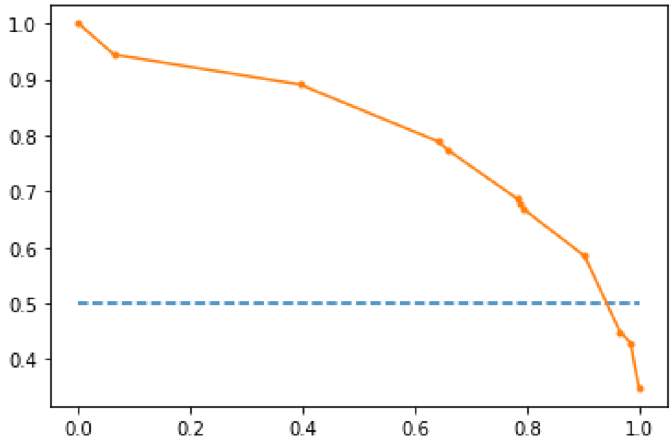
```
#Precision Recall Curve for Decission Tree Classifier

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=0.708 auc=0.800 ap=0.761
```

Out[58]:

```
[<matplotlib.lines.Line2D at 0x7f416d558a90>]
```



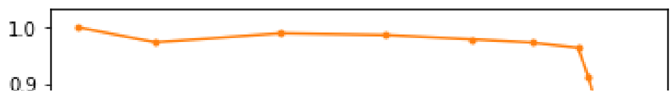
In [59]:

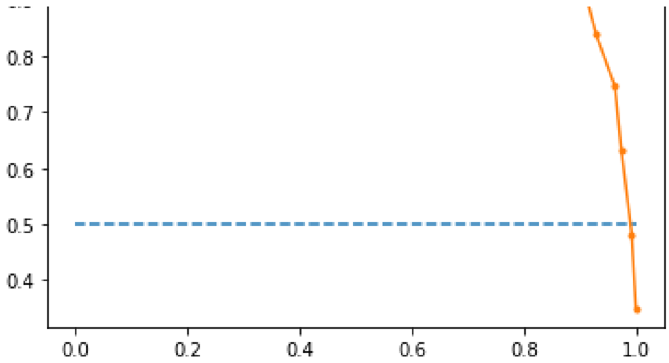
```
#Precision Recall Curve for Random Forest

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=0.926 auc=0.958 ap=0.951
```

Out[59]:

```
[<matplotlib.lines.Line2D at 0x7f416d3d4510>]
```





In [ ]: