%matplotlib inline ### import libraries import numpy as np import pandas as pd import matplotlib.pyplot as plt from matplotlib import style import seaborn as sns

In [2]:

```
data = pd.read_csv('health care diabetes.csv')
```

In [3]:

```
data.head()
```

Out[3]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

In [4]:

```
data.isnull().any()
```

Out[4]:

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

In [5]:

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
Pregnancies                 768 non-null int64
Glucose                     768 non-null int64
BloodPressure               768 non-null int64
SkinThickness               768 non-null int64
Insulin                     768 non-null int64
BMI                         768 non-null float64
DiabetesPedigreeFunction    768 non-null float64
Age                         768 non-null int64
Outcome                     768 non-null int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

In [41]:

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

Out[41]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
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 [43]:

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

Out[43]:

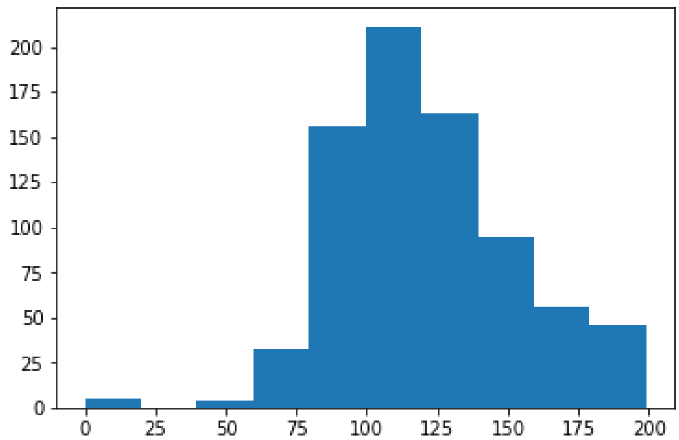
```
100    17
99     17
129    14
125    14
111    14
106    14
95     13
Name: Glucose, dtype: int64
```

In [35]:

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

Out[35]:

```
(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 [33]:

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

Out[33]:

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

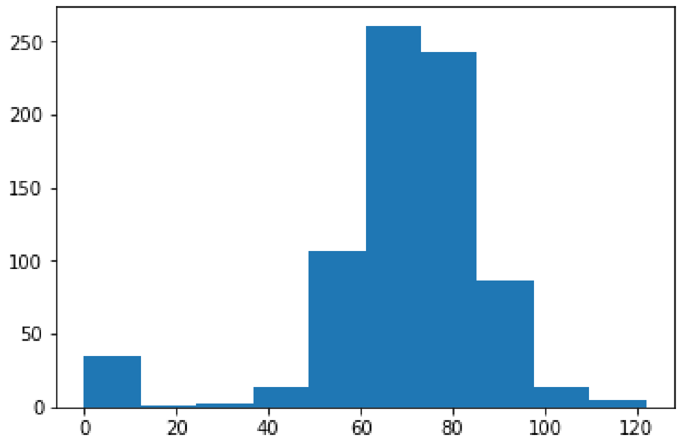
In [36]:

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

Out[36]:

```
(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. ]),
```

```
 &lt;a list of 10 Patch objects&gt;)
```



In [32]:

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

Out[32]:

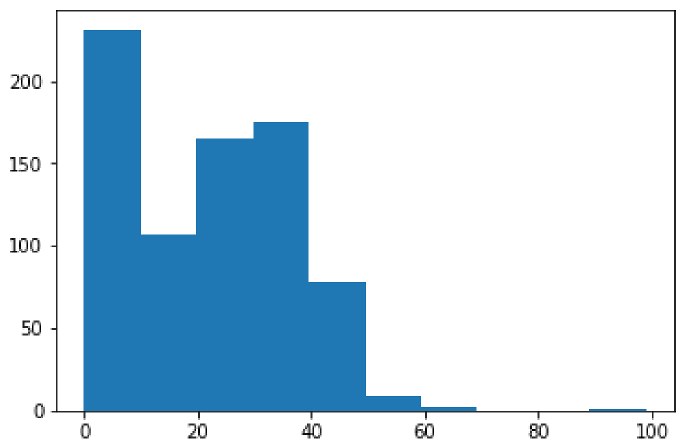
```
0      227
32      31
30      27
27      23
23      22
33      20
18      20
Name: SkinThickness, dtype: int64
```

In [37]:

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

Out[37]:

```
(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 [30]:

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

Out[30]:

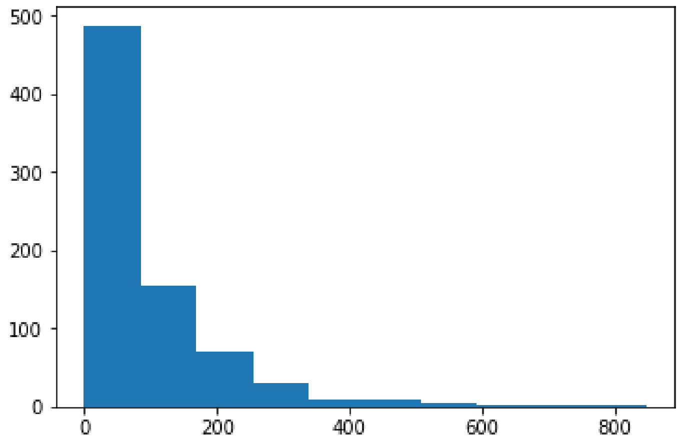
```
0      374
105     11
140      9
130      9
120      8
100      7
94       7
Name: Insulin, dtype: int64
```

In [38]:

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

Out[38]:

```
(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 [29]:

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

Out[29]:

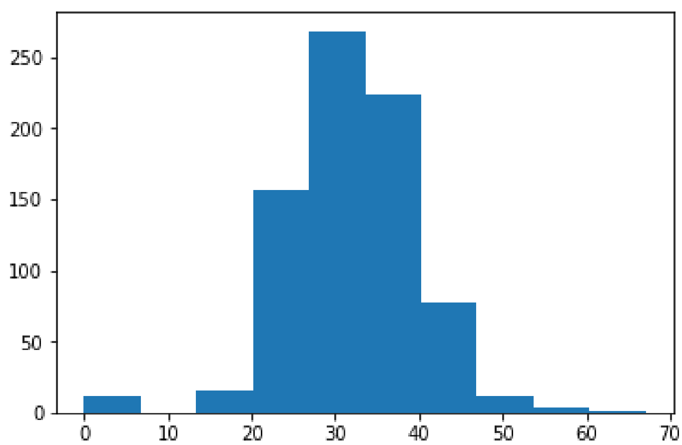
```
32.0    13
31.6    12
31.2    12
0.0     11
33.3    10
32.4    10
32.8     9
Name: BMI, dtype: int64
```

In [39]:

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

Out[39]:

```
(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 [9]:

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

Out[9]:

	count	mean	std	min	25%	50%	75%	max
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	99.00
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	846.00
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	67.10
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

In [ ]:

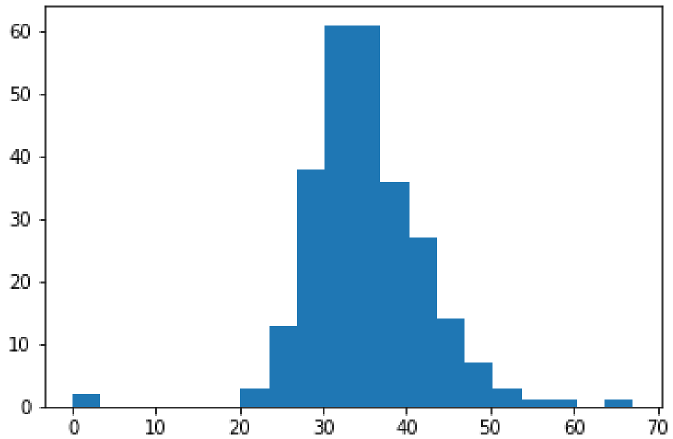
Week 2

In [49]:

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

Out[49]:

```
(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 [55]:

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

Out[55]:

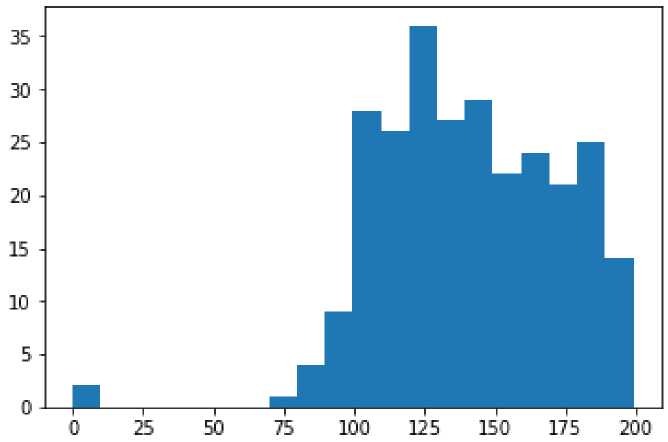
```
32.9    8
31.6    7
33.3    6
30.5    5
32.0    5
31.2    5
32.4    4
Name: BMI, dtype: int64
```

In [61]:

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

Out[61]:

```
(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 [56]:

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

Out[56]:

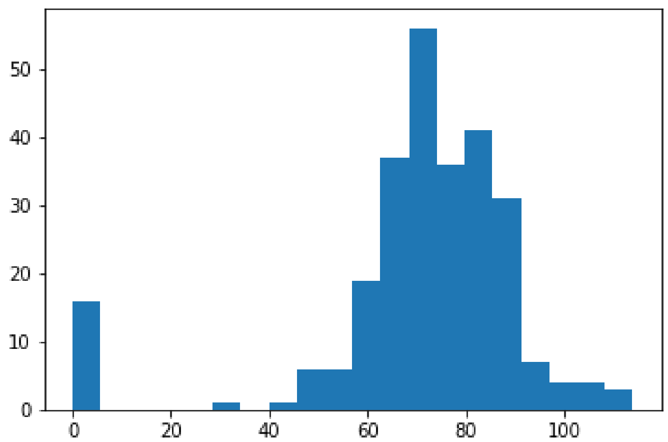
```
125    7
158    6
128    6
115    6
129    6
146    5
162    5
Name: Glucose, dtype: int64
```

In [62]:

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

Out[62]:

```
(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 [57]:

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

Out[57]:

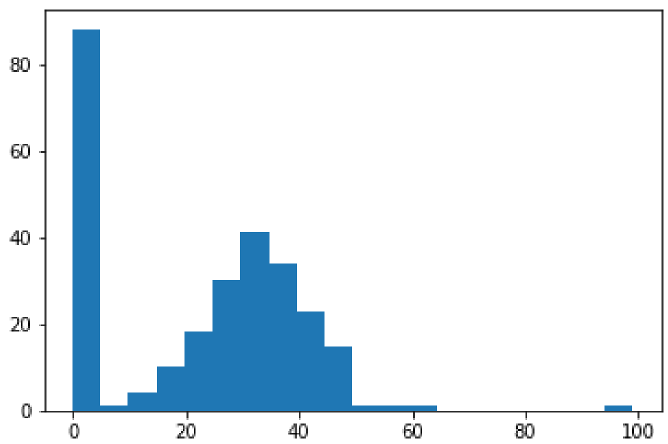
```
70    23
76    18
78    17
74    17
72    16
0     16
82    13
Name: BloodPressure, dtype: int64
```

In [63]:

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

Out[63]:

```
(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 [60]:

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

Out[60]:

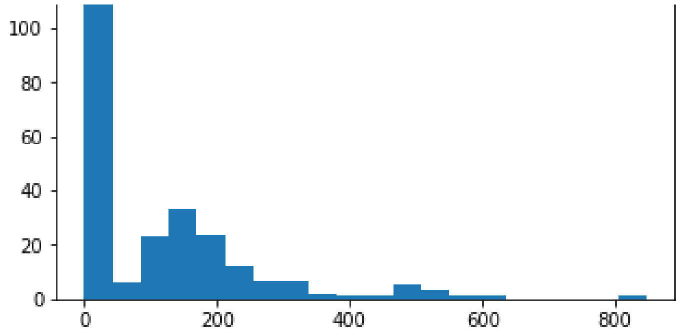
```
0     88
32    14
33     9
30     9
39     8
35     8
36     8
Name: SkinThickness, dtype: int64
```

In [64]:

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

Out[64]:

```
(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 [59]:

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

Out[59]:

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

In [65]:

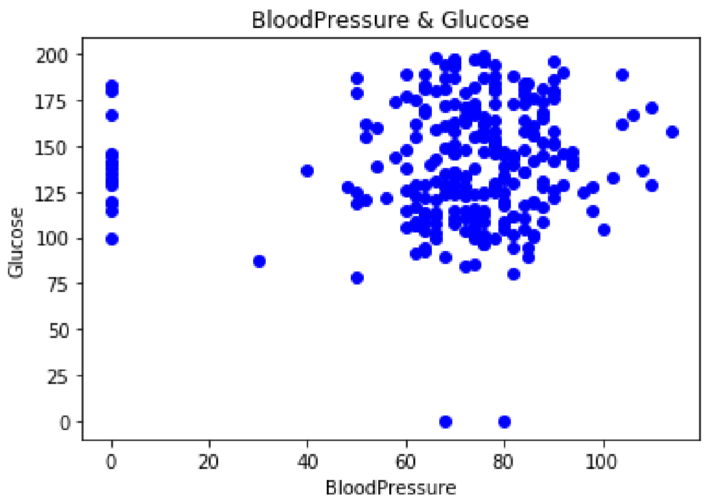
```
#Scatter plot
```

In [68]:

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

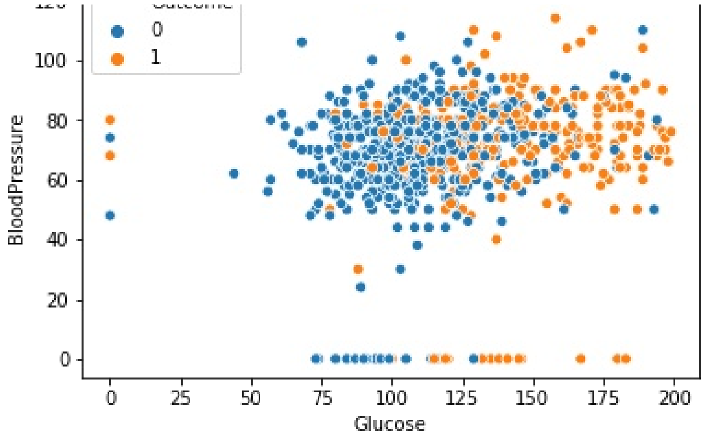
In [85]:

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



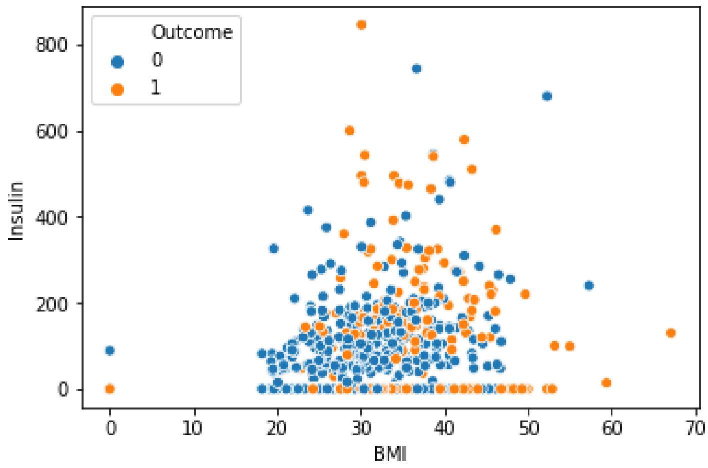
In [101]:

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



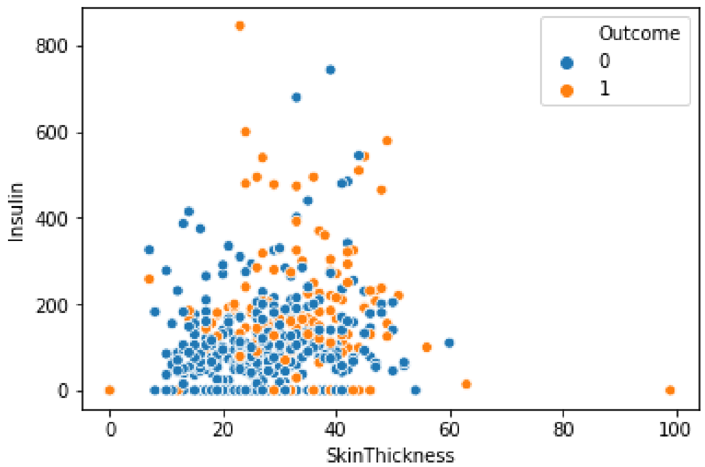
In [100]:

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



In [107]:

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



In [104]:

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

Out[104]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.017683	-0.03352

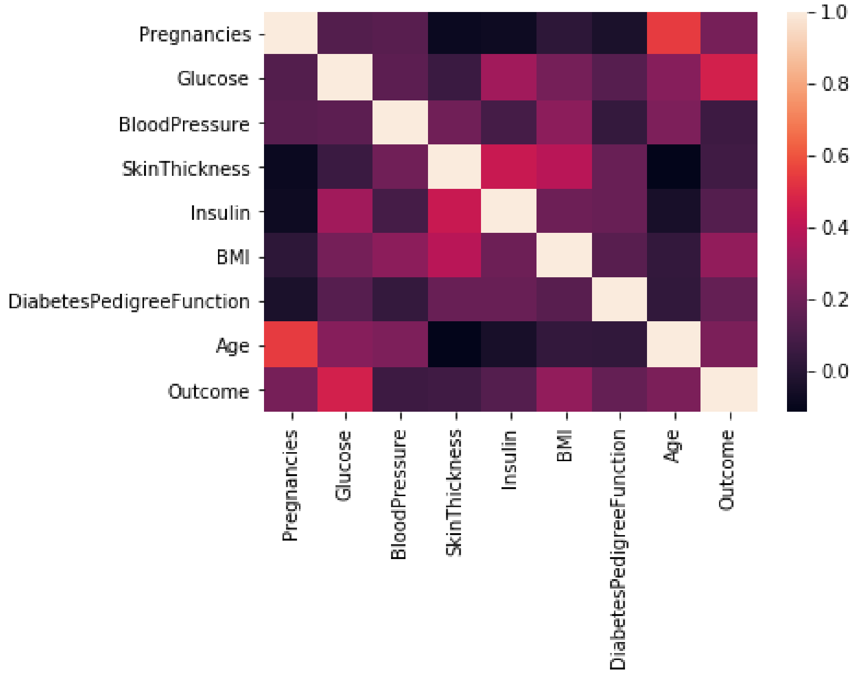
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunctio
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.221071	0.13733
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.281805	0.04126
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.392573	0.18392
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 [105]:

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

Out[105]:

<matplotlib.axes._subplots.AxesSubplot at 0x2278a586278>

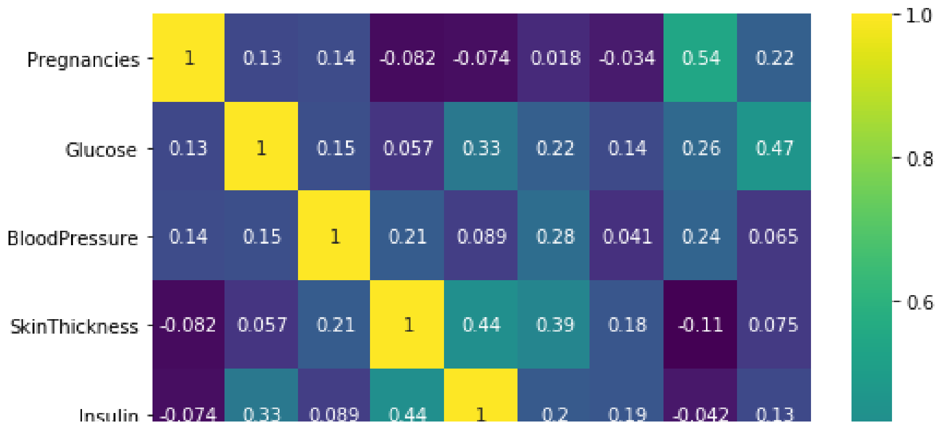


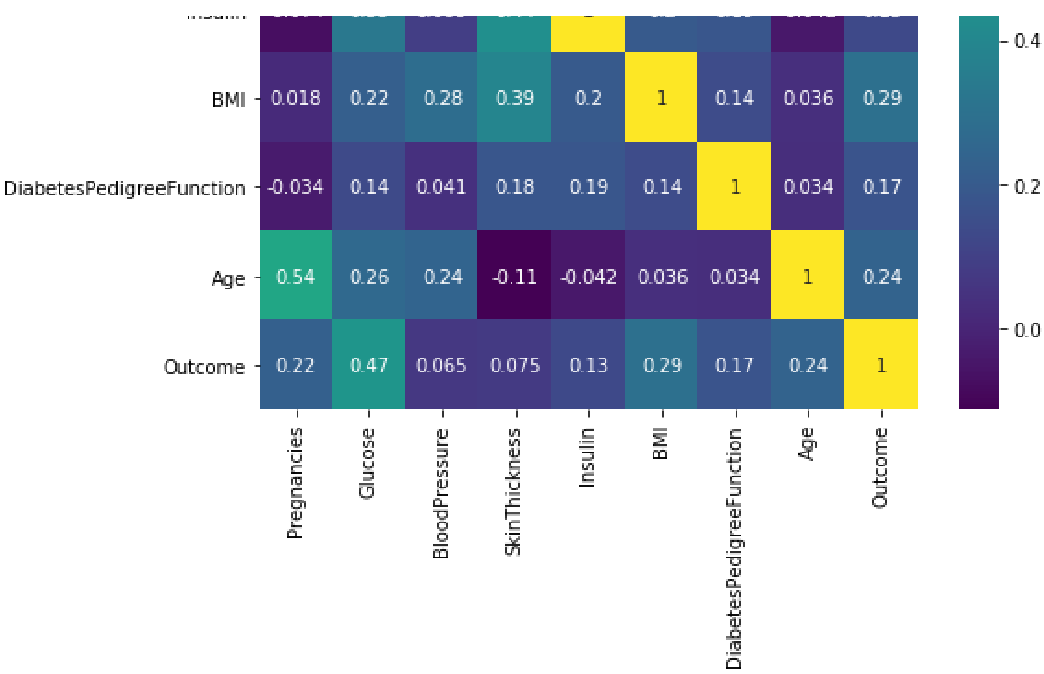
In [106]:

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

Out[106]:

<matplotlib.axes._subplots.AxesSubplot at 0x2278a71d710>



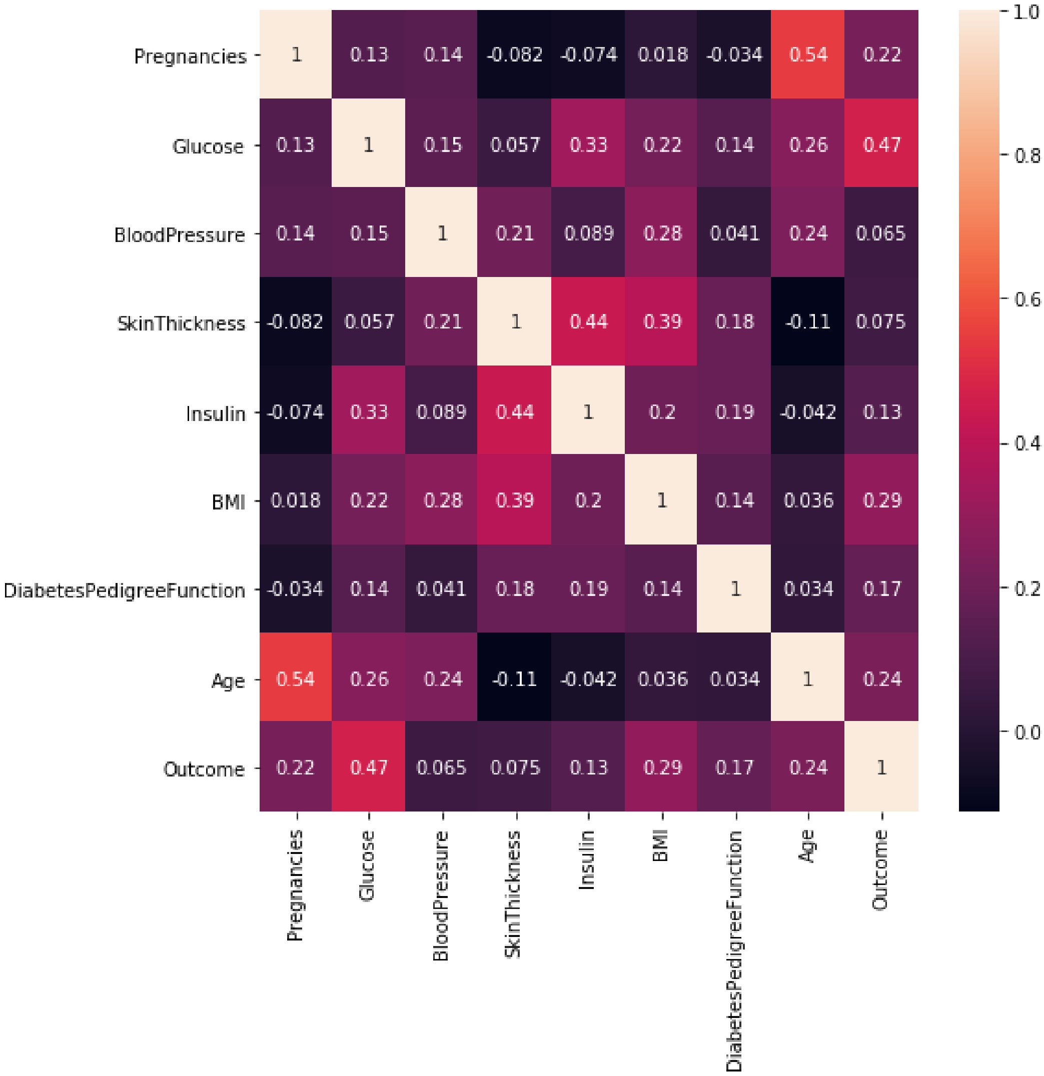


In [116]:

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

Out[116]:

<matplotlib.axes._subplots.AxesSubplot at 0x2278bde9f28>



In [113]:

```
# Logistic Regreation and model building
```

In [117]:

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

Out[117]:

	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 [130]:

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

In [136]:

```
#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 [137]:

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

```
C:\ProgramData\Anaconda3\lib\site-packages\sklearn\linear_model\logistic.py:433: FutureWa
rning: Default solver will be changed to 'lbfgs' in 0.22. Specify a solver to silence thi
s warning.
  FutureWarning)
```

Out[137]:

```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
          intercept_scaling=1, max_iter=100, multi_class='warn',
          n_jobs=None, penalty='l2', random_state=None, solver='warn',
          tol=0.0001, verbose=0, warm_start=False)
```

In [138]:

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

```
0.7833876221498371
0.7337662337662337
```

In [139]:

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

Out[139]:

```
array([[452,  48],
       [126, 142]], dtype=int64)
```

In [140]:

```
from sklearn.metrics import classification_report
print(classification_report(label,model.predict(features)))
```

```
              precision    recall  f1-score   support

           0       0.78      0.90      0.84       500
           1       0.75      0.53      0.62       268

   micro avg       0.77      0.77      0.77       768
   macro avg       0.76      0.72      0.73       768
weighted avg       0.77      0.77      0.76       768
```

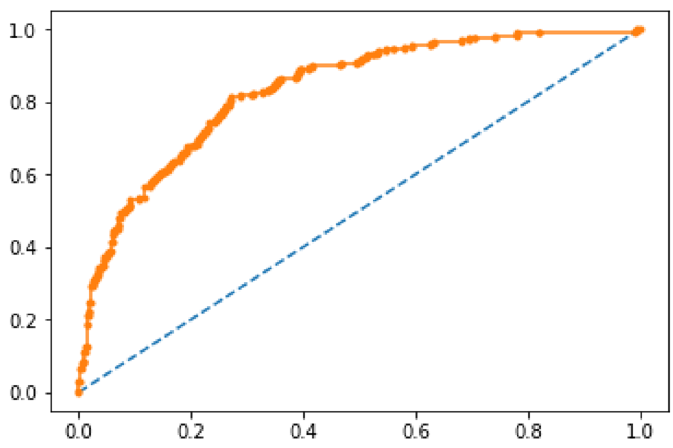
In [141]:

```
#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: 0.834

Out[141]:

[<matplotlib.lines.Line2D at 0x2278c4fba90>]



In [152]:

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

Out[152]:

```
DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=5,
            max_features=None, max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, presort=False, random_state=None,
            splitter='best')
```

In [163]:

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

Out[163]:

```
0.990228013029316
```

In [164]:

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

Out[164]:

```
0.7532467532467533
```

In [162]:

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

Out[162]:

```
RandomForestClassifier(bootstrap=True, class_weight=None, criterion='gini',
            max_depth=None, max_features='auto', max_leaf_nodes=None,
            min_impurity_decrease=0.0, min_impurity_split=None,
            min_samples_leaf=1, min_samples_split=2,
            min_weight_fraction_leaf=0.0, n_estimators=11, n_jobs=None,
            oob_score=False, random_state=None, verbose=0,
            warm_start=False)
```

In [165]:

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

Out[165]:

```
0.990228013029316
```

In [166]:

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

Out[166]:

```
0.7532467532467533
```

In [169]:

```
#Support Vector Classifier

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

Out[169]:

```
SVC(C=1.0, cache_size=200, class_weight=None, coef0=0.0,
  decision_function_shape='ovr', degree=3, gamma='auto', kernel='rbf',
  max_iter=-1, probability=False, random_state=None, shrinking=True,
  tol=0.001, verbose=False)
```

In [170]:

```
model5model.score(X_test,y_test).score(X_train,y_train)
```

Out[170]:

```
1.0
```

In [171]:

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

Out[171]:

```
0.6168831168831169
```

In [142]:

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

Out[142]:

```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
           metric_params=None, n_jobs=None, n_neighbors=7, p=2,
           weights='uniform')
```

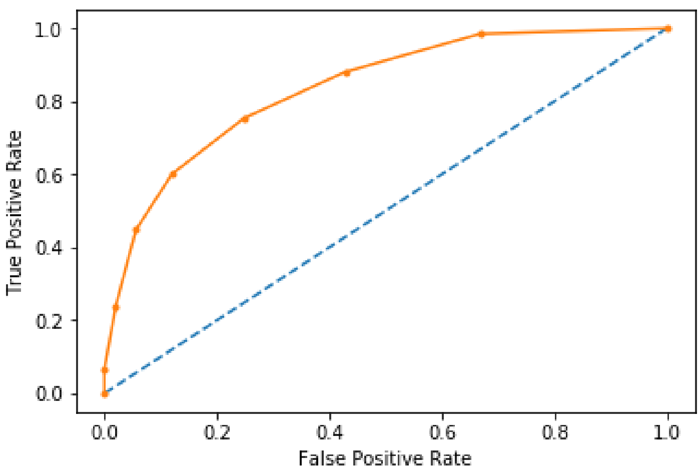
In [143]:

```
#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[143]:

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



In [144]:

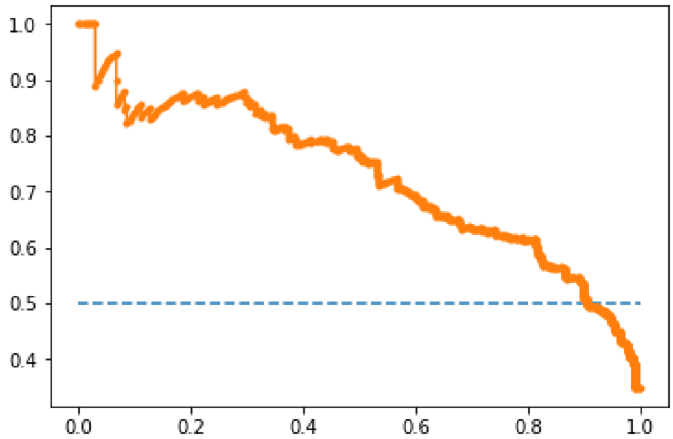
```
#Precision Recall Curve for Logistic Regression
```

```python
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=0.620 auc=0.728 ap=0.728
```

Out[144]:

```
[<matplotlib.lines.Line2D at 0x2278d0052e8>]
```



In [145]:

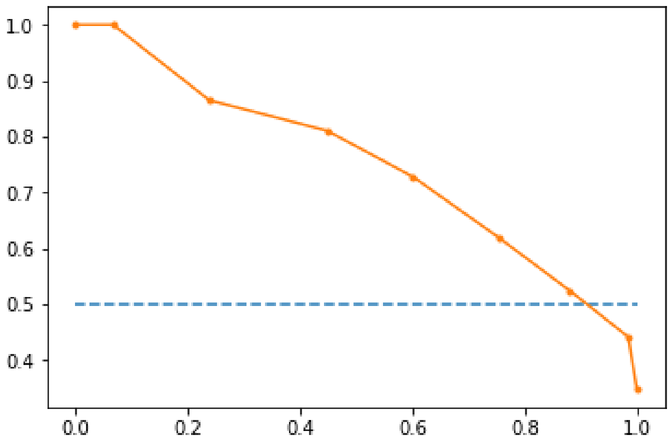
```python
#Precision Recall Curve for KNN

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[145]:

```
[<matplotlib.lines.Line2D at 0x2278d025908>]
```



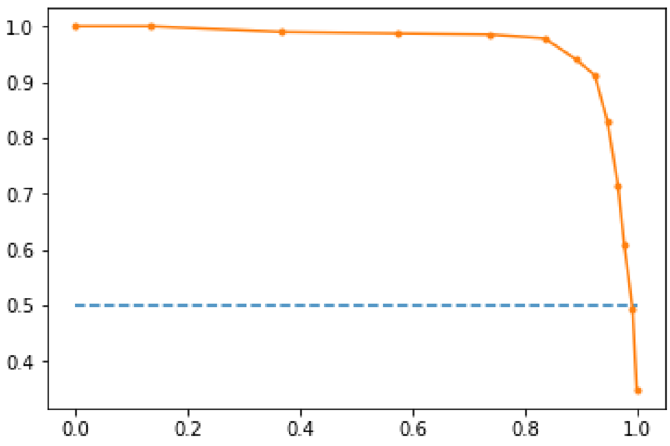
In [167]:

```
#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=0.916 auc=0.966 ap=0.958
```

Out[167]:

```
[<matplotlib.lines.Line2D at 0x2278bde2a20>]
```



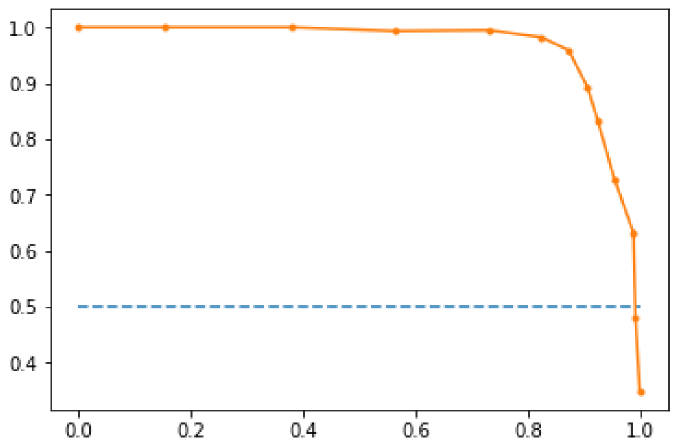
In [168]:

```
#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=0.914 auc=0.968 ap=0.960
```

Out[168]:

```
[<matplotlib.lines.Line2D at 0x2278a747cf8>]
```



In [ ]: