In [64]:
```
import pandas as pd

import numpy as np

import matplotlib.pyplot as plt
%matplotlib inline

import warnings
warnings.filterwarnings("ignore")

import seaborn as sns
```

In [65]:
```
data = pd.read_csv('Health Care Diabetes.csv')
```

In [66]:
```
data.head()
```

Out[66]:

	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 [67]:
```
data.isnull().sum()
```

Out[67]:
```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

In [68]:
```
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 [69]:
```
Positive = data[data['Outcome']==1]
Positive.head(5)
```

Out[69]:

	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

Week 1

Data Exploration:

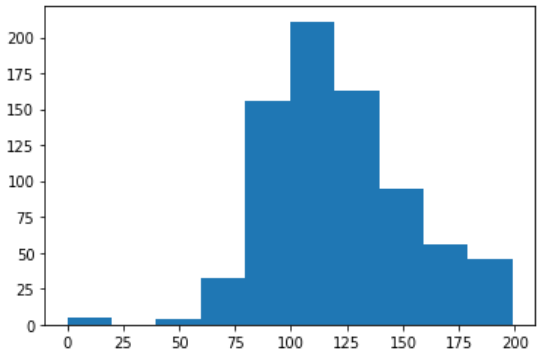
Glucose Descriptive Analysis

In [70]:
```
data['Glucose'].value_counts().head(7)
```

Out[70]:
```
100    17
99     17
129    14
125    14
111    14
106    14
95     13
Name: Glucose, dtype: int64
```

In [71]:
```
plt.hist(data['Glucose'])
```

Out[71]:
```
(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>)
```



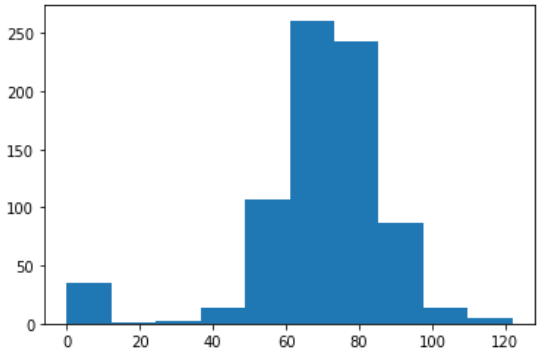
Blood Pressure Descriptive Analysis

In [72]:
```
data['BloodPressure'].value_counts().head(7)
```

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

In [73]:
```
plt.hist(data['BloodPressure'])
```

Out[73]:
```
(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>)
```



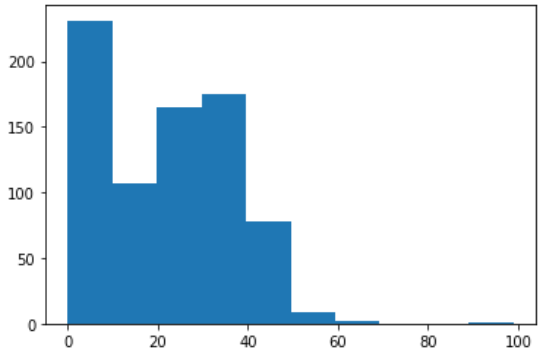
Skin Thickness Descriptive Analysis

In [74]:
```
data['SkinThickness'].value_counts().head(7)
```

Out[74]:
```
0     227
32     31
30     27
27     23
23     22
33     20
18     20
Name: SkinThickness, dtype: int64
```

In [75]:
```
plt.hist(data['SkinThickness'])
```

Out[75]:
```
(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>)
```



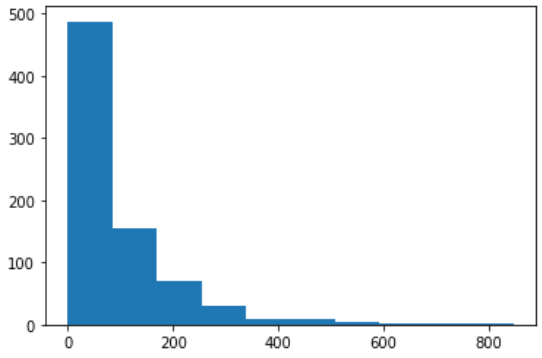
Insulin Descriptive Analysis

In [76]:
```
data['Insulin'].value_counts().head(7)
```

Out[76]:
```
0      374
105     11
140      9
130      9
120      8
100      7
94       7
Name: Insulin, dtype: int64
```

In [77]:
```
plt.hist(data['Insulin'])
```

Out[77]:
```
(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>)
```



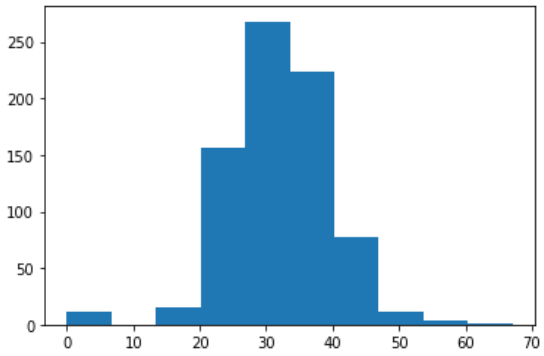
BMI Descriptive Analysis

In [78]:
```
data['BMI'].value_counts().head(7)
```

Out[78]:
```
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 [79]:
```
plt.hist(data['BMI'])
```

Out[79]:
```
(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>)
```



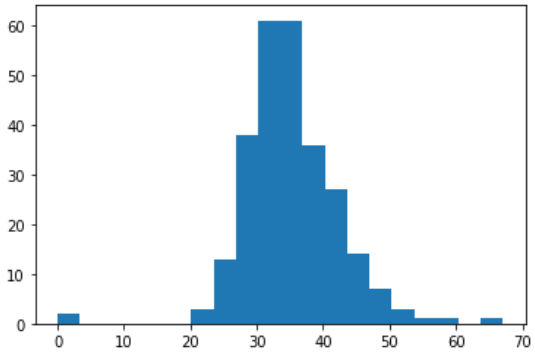
In [80]:
```
data.describe().transpose()
```

Out[80]:

	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 [81]:
```
plt.hist(Positive['BMI'],histtype='stepfilled',bins=20)
```

Out[81]:
```
(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>)
```

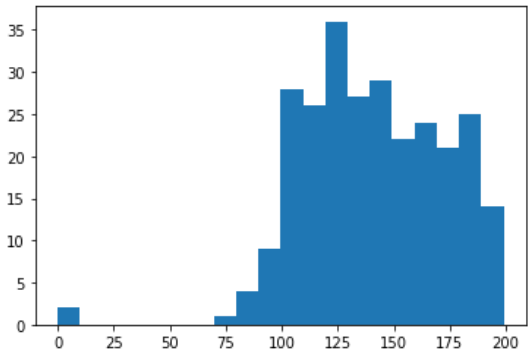


In [82]:
```
Positive['BMI'].value_counts().head(7)
```

Out[82]:
```
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 [83]:
```
plt.hist(Positive['Glucose'],histtype='stepfilled',bins=20)
```

Out[83]:
```
(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>)
```

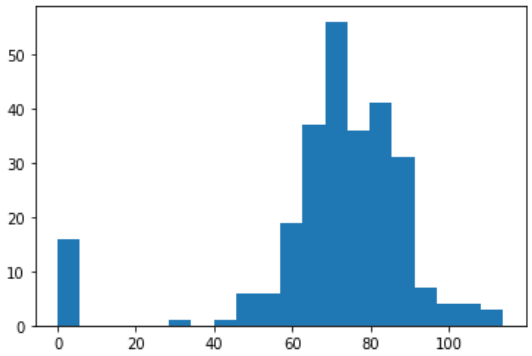


In [84]:
```
Positive['Glucose'].value_counts().head(7)
```

Out[84]:
```
125    7
158    6
128    6
115    6
129    6
146    5
162    5
Name: Glucose, dtype: int64
```

In [85]:
```
plt.hist(Positive['BloodPressure'],histtype='stepfilled',bins=20)
```

Out[85]:
```
(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>)
```

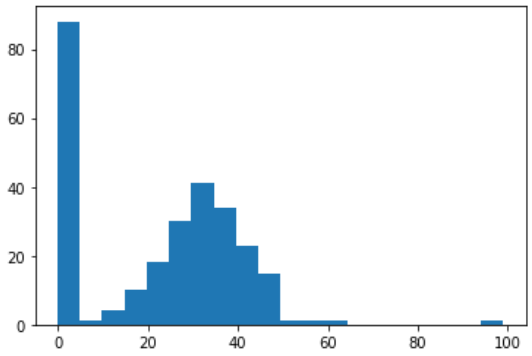


In [86]:
```
Positive['BloodPressure'].value_counts().head(7)
```

Out[86]:
```
70    23
76    18
78    17
74    17
72    16
0     16
82    13
Name: BloodPressure, dtype: int64
```

In [87]:
```
plt.hist(Positive['SkinThickness'],histtype='stepfilled',bins=20)
```

Out[87]:
```
(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>)
```

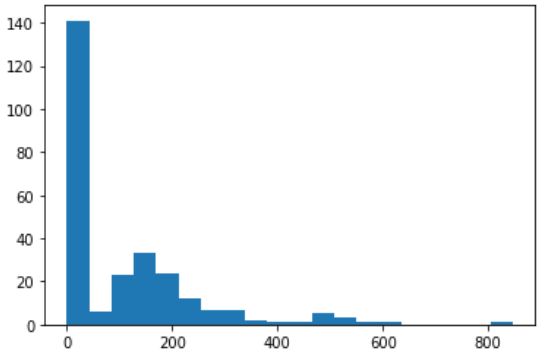


In [88]:
```
Positive['SkinThickness'].value_counts().head(7)
```

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

In [89]:
```
plt.hist(Positive['Insulin'],histtype='stepfilled',bins=20)
```

Out[89]:
```
(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 [90]:
```
Positive['Insulin'].value_counts().head(7)
```

Out[90]:
```
0      138
130      6
180      4
156      3
175      3
194      2
125      2
Name: Insulin, dtype: int64
```

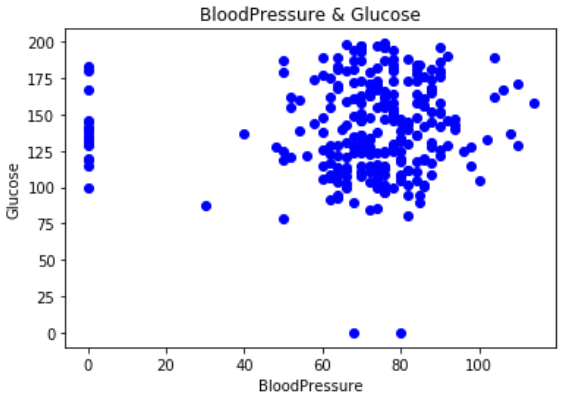
Week 2

Data Exploration:

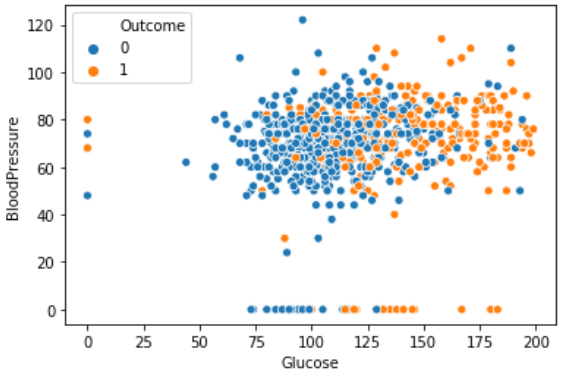
In [91]:
```
BloodPressure = Positive['BloodPressure']
Glucose = Positive['Glucose']
SkinThickness = Positive['SkinThickness']
Insulin = Positive['Insulin']
BMI = Positive['BMI']
```

Scatter Plot

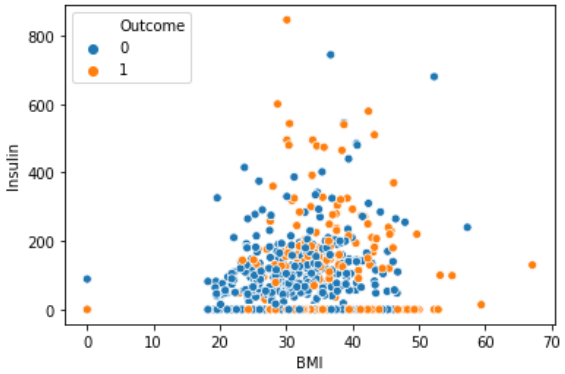
In [92]:
```
plt.scatter(BloodPressure, Glucose, color=['b'])
plt.xlabel('BloodPressure')
plt.ylabel('Glucose')
plt.title('BloodPressure & Glucose')
plt.show()
```



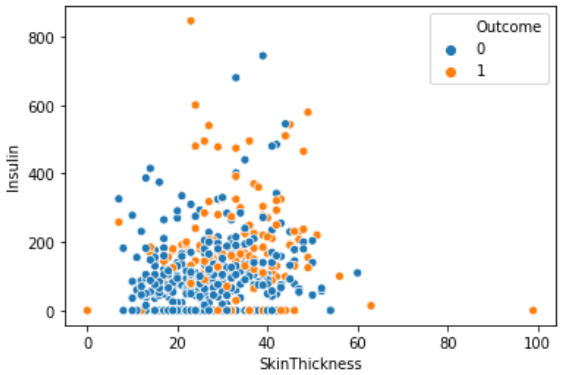
In [93]:
```
g =sns.scatterplot(x= "Glucose" ,y= "BloodPressure",
                   hue="Outcome",
                   data=data);
```



In [94]:
```
B =sns.scatterplot(x= "BMI" ,y= "Insulin",
                   hue="Outcome",
                   data=data);
```



In [95]:
```
S =sns.scatterplot(x= "SkinThickness" ,y= "Insulin",
                   hue="Outcome",
                   data=data);
```



Correlation Matrix

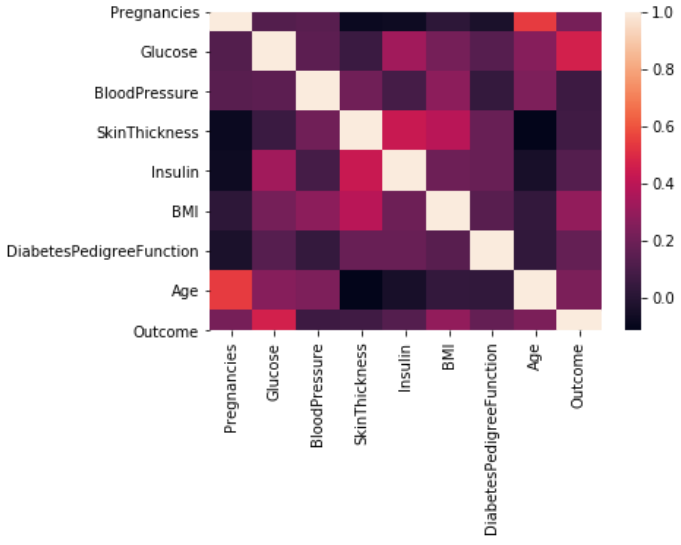
In [96]:
```
data.corr()
```

Out[96]:

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
Pregnancies	1.000000	0.129459	0.141282	-0.081672	-0.073535	0.017683	-0.033523	0.544341
Glucose	0.129459	1.000000	0.152590	0.057328	0.331357	0.221071	0.137337	0.263514
BloodPressure	0.141282	0.152590	1.000000	0.207371	0.088933	0.281805	0.041265	0.239528
SkinThickness	-0.081672	0.057328	0.207371	1.000000	0.436783	0.392573	0.183928	-0.113970
Insulin	-0.073535	0.331357	0.088933	0.436783	1.000000	0.197859	0.185071	-0.042163
BMI	0.017683	0.221071	0.281805	0.392573	0.197859	1.000000	0.140647	0.036242
DiabetesPedigreeFunction	-0.033523	0.137337	0.041265	0.183928	0.185071	0.140647	1.000000	0.033561
Age	0.544341	0.263514	0.239528	-0.113970	-0.042163	0.036242	0.033561	1.000000
Outcome	0.221898	0.466581	0.065068	0.074752	0.130548	0.292695	0.173844	0.238356

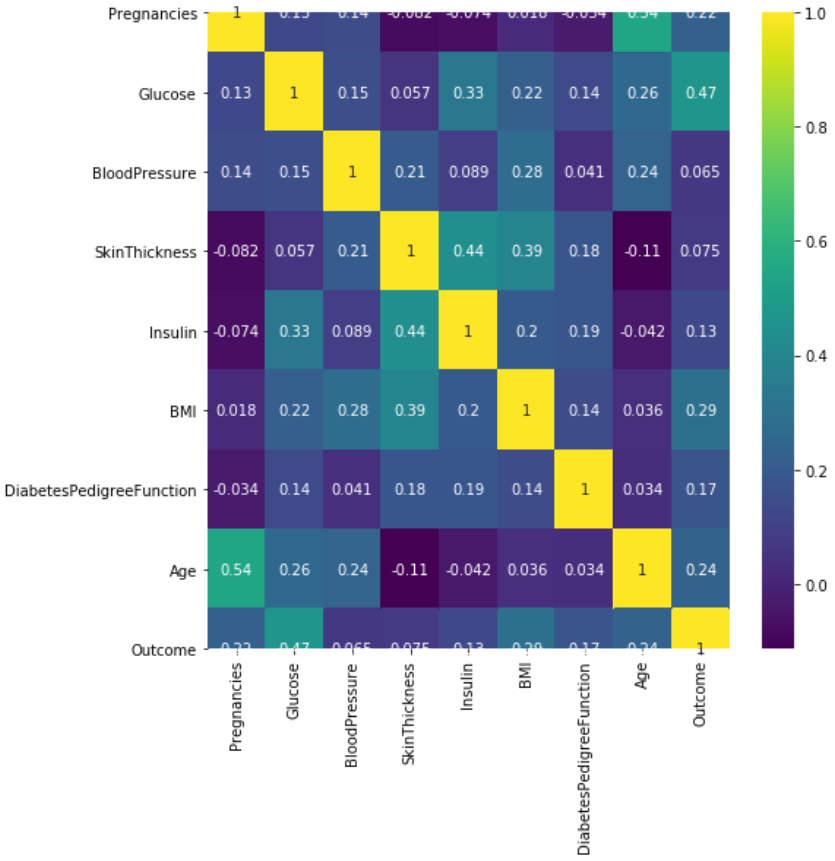
In [97]:
```
sns.heatmap(data.corr())
```

Out[97]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x13b945d5f28>
```



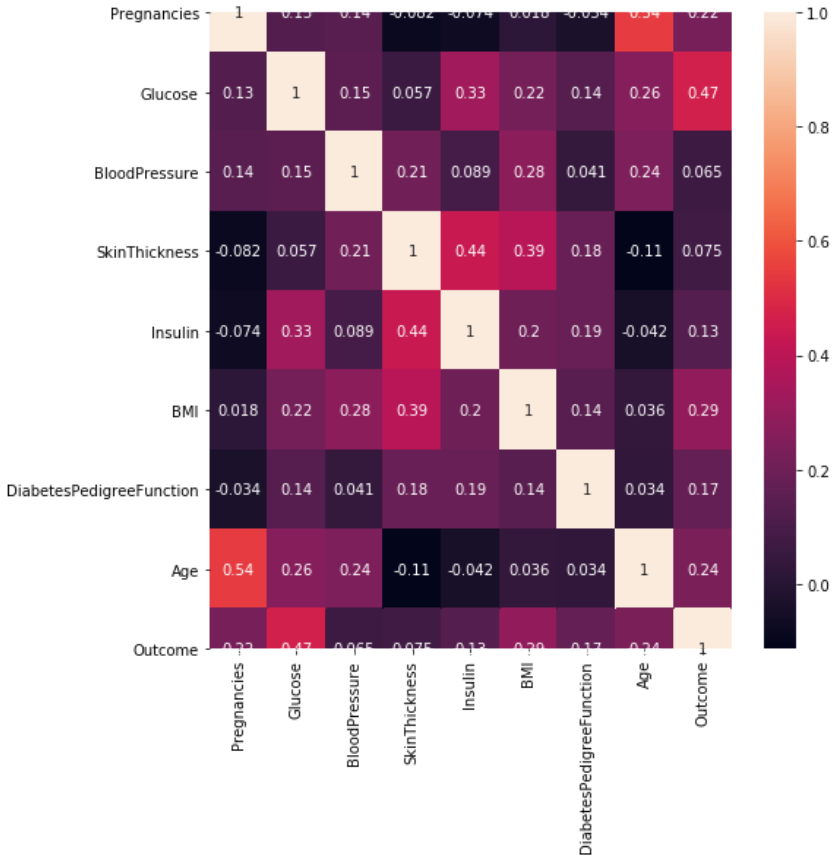
In [98]:
```
plt.subplots(figsize=(8,8))
sns.heatmap(data.corr(),annot=True,cmap='viridis')
```

Out[98]: <matplotlib.axes._subplots.AxesSubplot at 0x13b9467fc50>



In [99]:
```
plt.subplots(figsize=(8,8))
sns.heatmap(data.corr(),annot=True)
```

Out[99]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x13b9492ea58>
```



In [100]:
```
data.head(5)
```

Out[100]:

	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

Week 3

Data Modelling

Logistic Regreation and Model Building

In [101]:
```
features = data.iloc[:,[0,1,2,3,4,5,6,7]].values
label = data.iloc[:,8].values
```

Train Test Split

In [102]:
```
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)
```

Creating Model

In [103]:
```
from sklearn.linear_model import LogisticRegression
model = LogisticRegression()
model.fit(X_train,y_train)
```

Out[103]:
```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, l1_ratio=None, max_iter=100,
                   multi_class='auto', n_jobs=None, penalty='l2',
                   random_state=None, solver='lbfgs', tol=0.0001, verbose=0,
                   warm_start=False)
```

In [104]:
```
print(model.score(X_train,y_train))
print(model.score(X_test,y_test))
```

```
0.7719869706840391
0.7662337662337663
```

In [105]:
```
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(label,model.predict(features))
cm
```

Out[105]:
```
array([[446,  54],
       [122, 146]], dtype=int64)
```

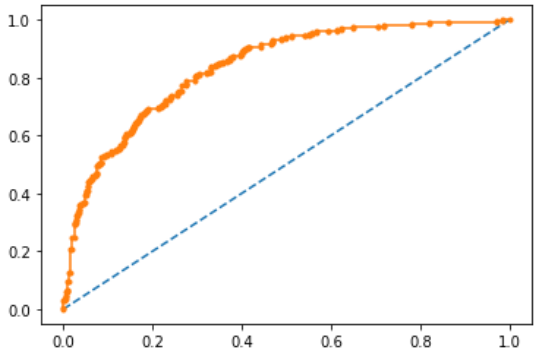
In [106]:
```
from sklearn.metrics import classification_report
print(classification_report(label,model.predict(features)))
```

```
              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 [107]:
```
#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]
# Calculating AUC
auc = roc_auc_score(label, probs)
print('AUC: %.3f' % auc)
# Calculating 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[107]:
```
[<matplotlib.lines.Line2D at 0x13b94855a58>]
```



Applying Decission Tree Classifier

In [108]:
```
from sklearn.tree import DecisionTreeClassifier
model3 = DecisionTreeClassifier(max_depth=5)
model3.fit(X_train,y_train)
```

Out[108]:
```
DecisionTreeClassifier(ccp_alpha=0.0, 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='deprecated',
                       random_state=None, splitter='best')
```

In [109]:
```
model3.score(X_train,y_train)
```

Out[109]:
```
0.8289902280130294
```

In [110]:
```
model3.score(X_test,y_test)
```

Out[110]:
```
0.7727272727272727
```

Applying Random Forest

In [111]:
```
from sklearn.ensemble import RandomForestClassifier
model4 = RandomForestClassifier(n_estimators=11)
model4.fit(X_train,y_train)
```

Out[111]:
```
RandomForestClassifier(bootstrap=True, ccp_alpha=0.0, class_weight=None,
                       criterion='gini', max_depth=None, max_features='auto',
                       max_leaf_nodes=None, max_samples=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 [112]:
```
model4.score(X_train,y_train)
```

Out[112]:
```
0.988599348534202
```

In [113]:
```
model4.score(X_test,y_test)
```

Out[113]:
```
0.7272727272727273
```

Support Vector Classifier

In [114]:
```
from sklearn.svm import SVC
model5 = SVC(kernel='rbf', gamma='auto')
model5.fit(X_train,y_train)
```

Out[114]:
```
SVC(C=1.0, break_ties=False, 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 [115]:
```
model5.score(X_train,y_train)
```

Out[115]:
```
1.0
```

In [116]:
```
model5.score(X_test,y_test)
```

Out[116]:
```
0.6168831168831169
```

Applying K-NN

In [117]:
```
from sklearn.neighbors import KNeighborsClassifier
model2 = KNeighborsClassifier(n_neighbors=7,
                              metric='minkowski',
                              p = 2)
model2.fit(X_train,y_train)
```

Out[117]:
```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=7, p=2,
                     weights='uniform')
```

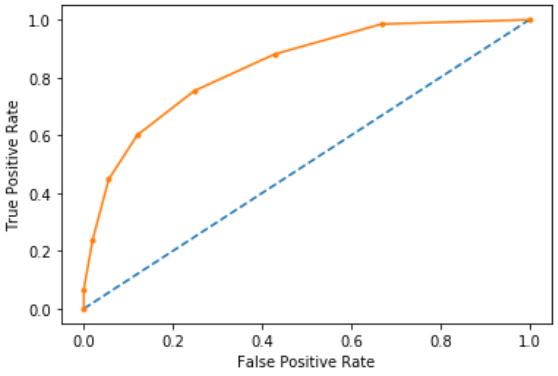
Week 4

Data Modelling:

In [118]:
```
#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]
# Calculating AUC
auc = roc_auc_score(label, probs)
print('AUC: %.3f' % auc)
# Calculating 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.        ]
```

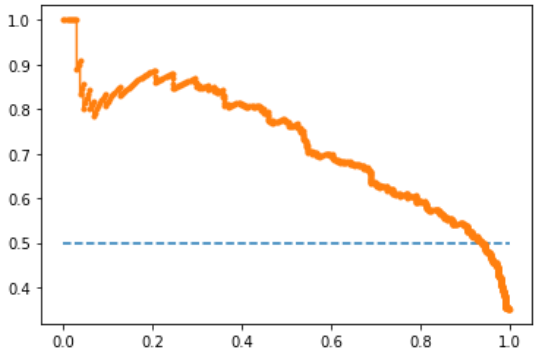
Out[118]: Text(0, 0.5, 'True Positive Rate')



In [119]:
```
#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)
# Calculating precision-recall curve
precision, recall, thresholds = precision_recall_curve(label, probs)
# Calculating F1 score
f1 = f1_score(label, yhat)
# Calculating precision-recall AUC
auc = auc(recall, precision)
# Calculating 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
```

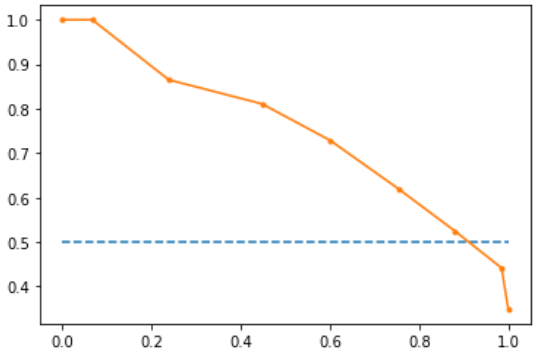
Out[119]:
```
[<matplotlib.lines.Line2D at 0x13b94b575f8>]
```



In [120]:
```
#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)
# Calculating precision-recall curve
precision, recall, thresholds = precision_recall_curve(label, probs)
# Calculating F1 score
f1 = f1_score(label, yhat)
# Calculating precision-recall AUC
auc = auc(recall, precision)
# Calculating 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
```

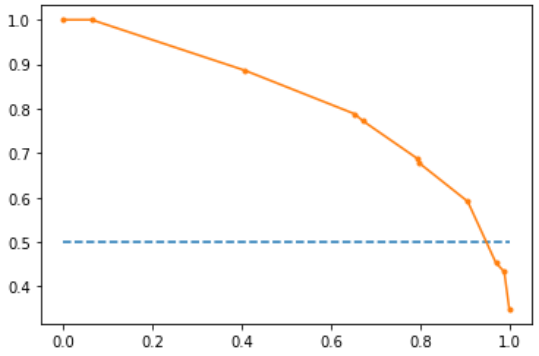
Out[120]:
```
[<matplotlib.lines.Line2D at 0x13b94bb73c8>]
```



In [121]:
```
#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)
# Calculating precision-recall curve
precision, recall, thresholds = precision_recall_curve(label, probs)
# Calculating F1 score
f1 = f1_score(label, yhat)
# Calculating precision-recall AUC
auc = auc(recall, precision)
# Calculating 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[121]:
```
[<matplotlib.lines.Line2D at 0x13b94be8dd8>]
```



In [122]:
```
#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)
# Calculating precision-recall curve
precision, recall, thresholds = precision_recall_curve(label, probs)
# Calculating F1 score
f1 = f1_score(label, yhat)
# Calculating precision-recall AUC
auc = auc(recall, precision)
# Calculating 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=0.906 auc=0.959 ap=0.950
```

Out[122]:
```
[<matplotlib.lines.Line2D at 0x13b95dc18d0>]
```