Healthcare Analysis Project

December 20, 2021

Healthcare Project 2

DESCRIPTION

Problem Statement NIDDK (National Institute of Diabetes and Digestive and Kidney Diseases) research creates knowledge about and treatments for the most chronic, costly, and consequential diseases. The dataset used in this project is originally from NIDDK. The objective is to predict whether or not a patient has diabetes, based on certain diagnostic measurements included in the dataset. Build a model to accurately predict whether the patients in the dataset have diabetes or not.

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


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

%matplotlib inline
```

[2]:
```
data = pd.read_csv('health care diabetes.csv')
```

[3]:
```
data.head()
```

[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

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

[4]:

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

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

[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
```

[6]:
```
data.describe()
```

[6]:

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

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

[7]:
```
data.isnull().any()
```

[7]:
```
Pregnancies                 False
Glucose                     False
BloodPressure               False
SkinThickness               False
Insulin                     False
BMI                         False
DiabetesPedigreeFunction    False
Age                         False
Outcome                     False
dtype: bool
```

[8]:
```
Positive = data[data['Outcome']==1]
Positive.head(5)
```

[8]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35        0  33.6
2            8      183             64              0        0  23.3
4            0      137             40             35      168  43.1
6            3       78             50             32       88  31.0
8            2      197             70             45      543  30.5

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

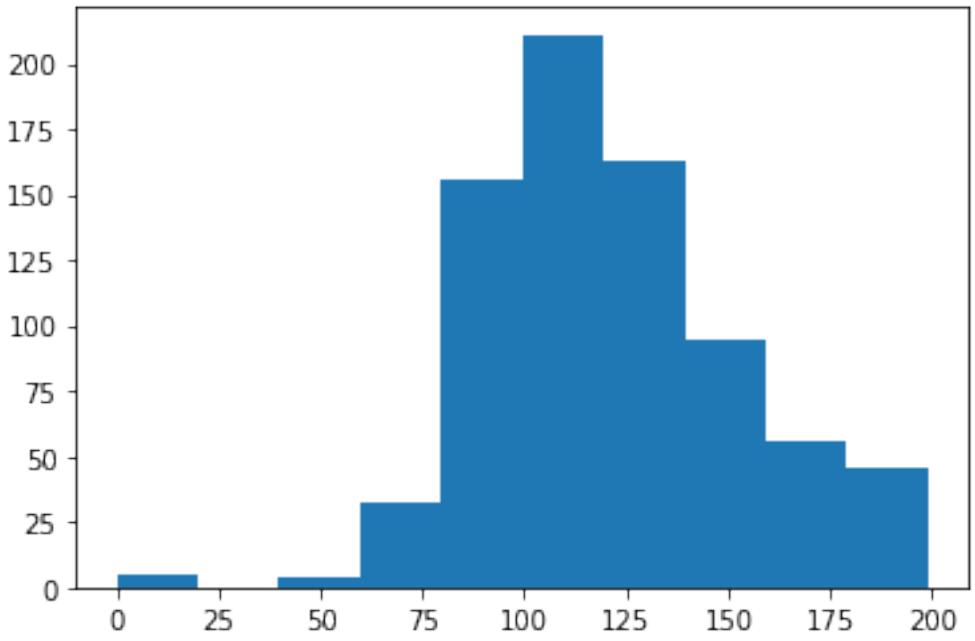
[9]:
```
data['Glucose'].value_counts().head(7)
```

[9]:
```
100    17
99     17
129    14
125    14
111    14
```

```
106    14
95     13
Name: Glucose, dtype: int64
```

[10]:
```
plt.hist(data['Glucose'])
```

[10]:
```
(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>)
```

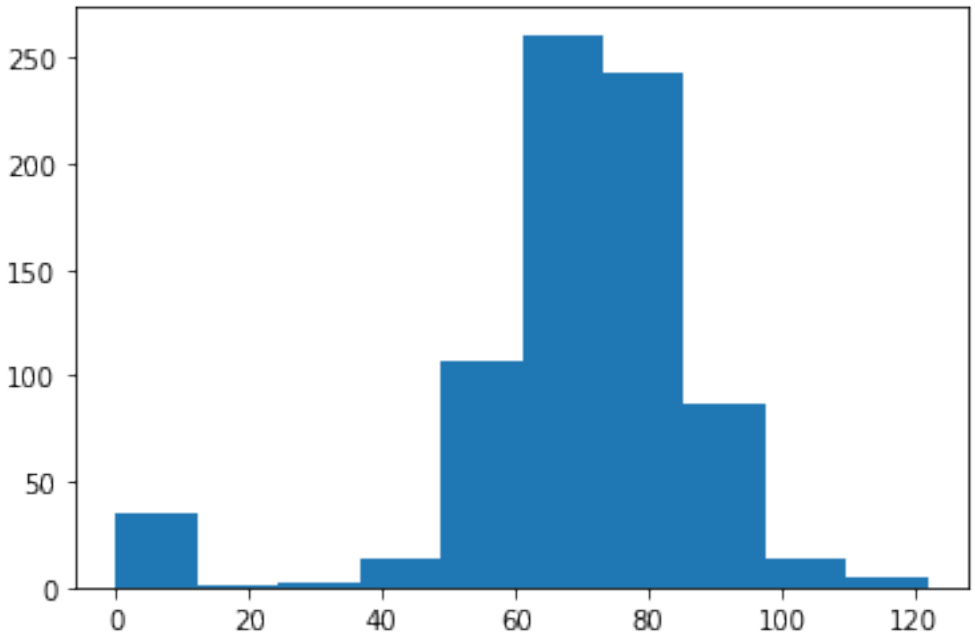


[11]:
```
data['BloodPressure'].value_counts().head(7)
```

[11]:
```
70    57
74    52
68    45
78    45
72    44
64    43
80    40
Name: BloodPressure, dtype: int64
```

[12]:
```
plt.hist(data['BloodPressure'])
```

[12]:
```
(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>)
```

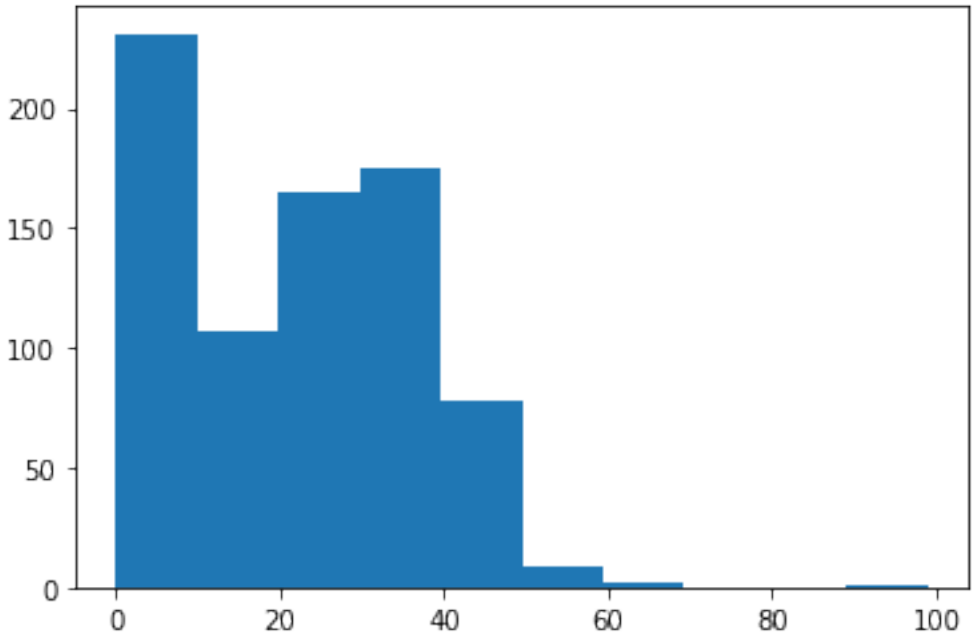


[13]:
```
data['SkinThickness'].value_counts().head(7)
```

[13]:
```
0     227
32     31
30     27
27     23
23     22
33     20
18     20
Name: SkinThickness, dtype: int64
```

[14]:
```
plt.hist(data['SkinThickness'])
```

[14]:
```
(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>)
```

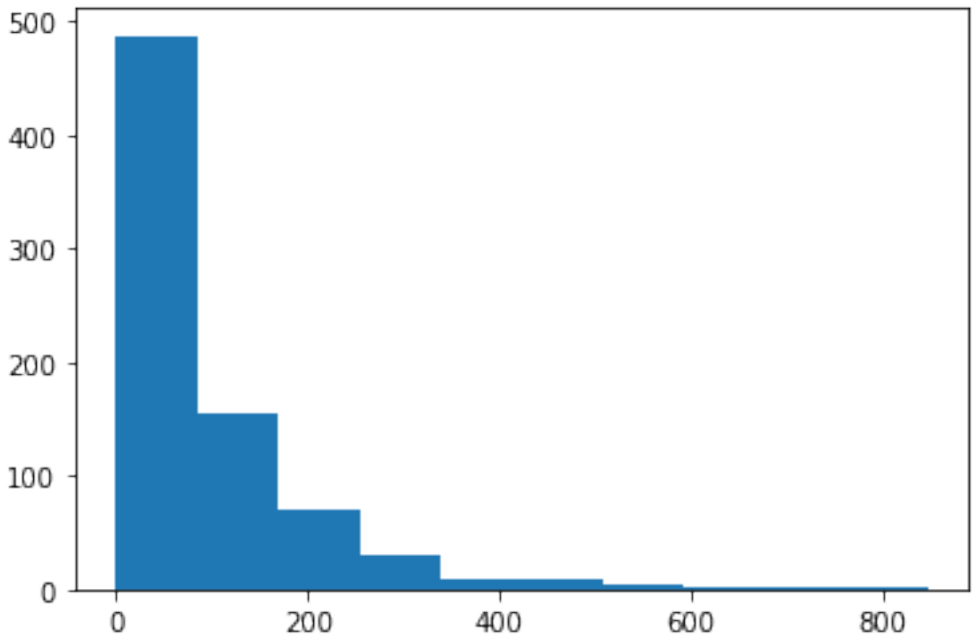


[15]:
```
data['Insulin'].value_counts().head(7)
```

[15]:
```
0      374
105     11
140      9
130      9
120      8
100      7
94       7
Name: Insulin, dtype: int64
```

[16]:
```
plt.hist(data['Insulin'])
```

[16]:
```
(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>)
```

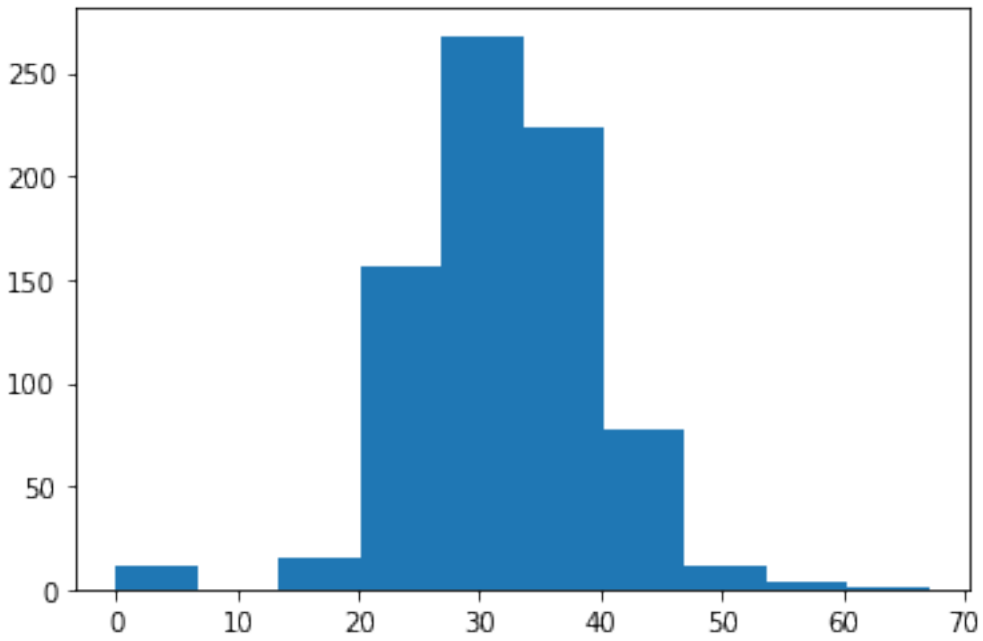


[17]:
```
data['BMI'].value_counts().head(7)
```

[17]:
```
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
```

[18]:
```
plt.hist(data['BMI'])
```

[18]:
```
(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>)
```



[19]:
```
data.describe().transpose()
```

[19]:

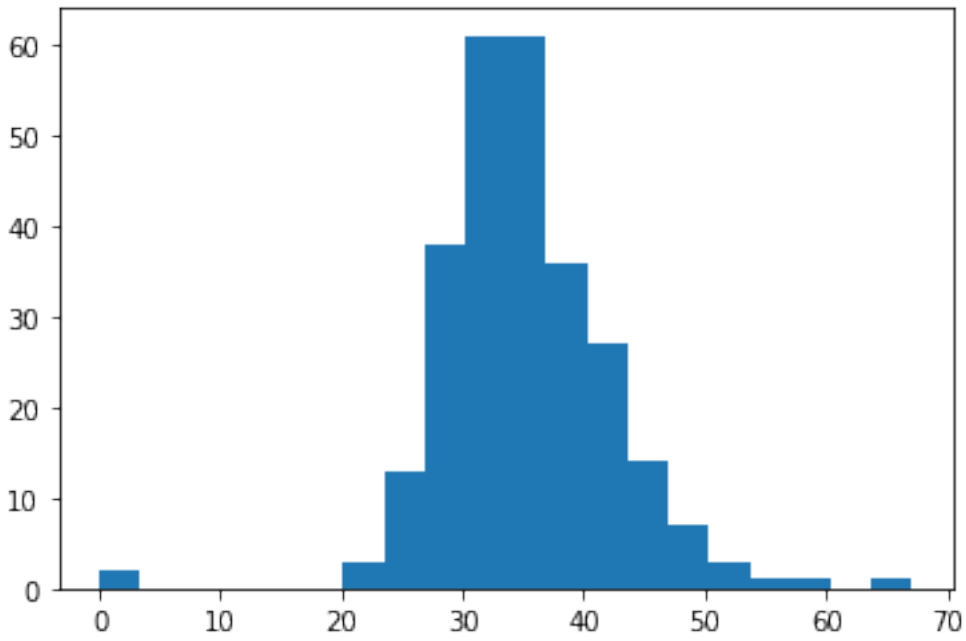
	count	mean	std	min	25%	\
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	
Glucose	768.0	120.894531	31.972618	0.000	99.00000	
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	
Insulin	768.0	79.799479	115.244002	0.000	0.00000	
BMI	768.0	31.992578	7.884160	0.000	27.30000	
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	
Age	768.0	33.240885	11.760232	21.000	24.00000	
Outcome	768.0	0.348958	0.476951	0.000	0.00000	

	50%	75%	max
Pregnancies	3.0000	6.00000	17.00
Glucose	117.0000	140.25000	199.00
BloodPressure	72.0000	80.00000	122.00
SkinThickness	23.0000	32.00000	99.00
Insulin	30.5000	127.25000	846.00
BMI	32.0000	36.60000	67.10
DiabetesPedigreeFunction	0.3725	0.62625	2.42
Age	29.0000	41.00000	81.00
Outcome	0.0000	1.00000	1.00

Project Task Week 2

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

[20]:
```
(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 0x7f4810352a50>])
```



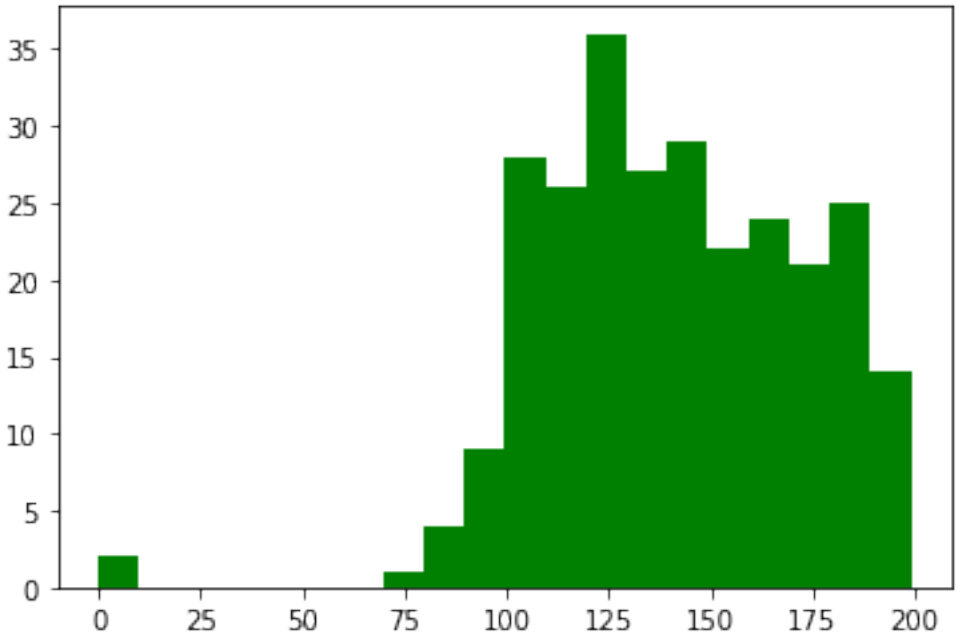
[21]:
```
Positive['BMI'].value_counts().head(7)
```

[21]:
```
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
```

[22]:
```
plt.hist(Positive['Glucose'],histtype='stepfilled',bins=20,color='g')
```

[22]:
```
(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 0x7f48105eaf50>])
```

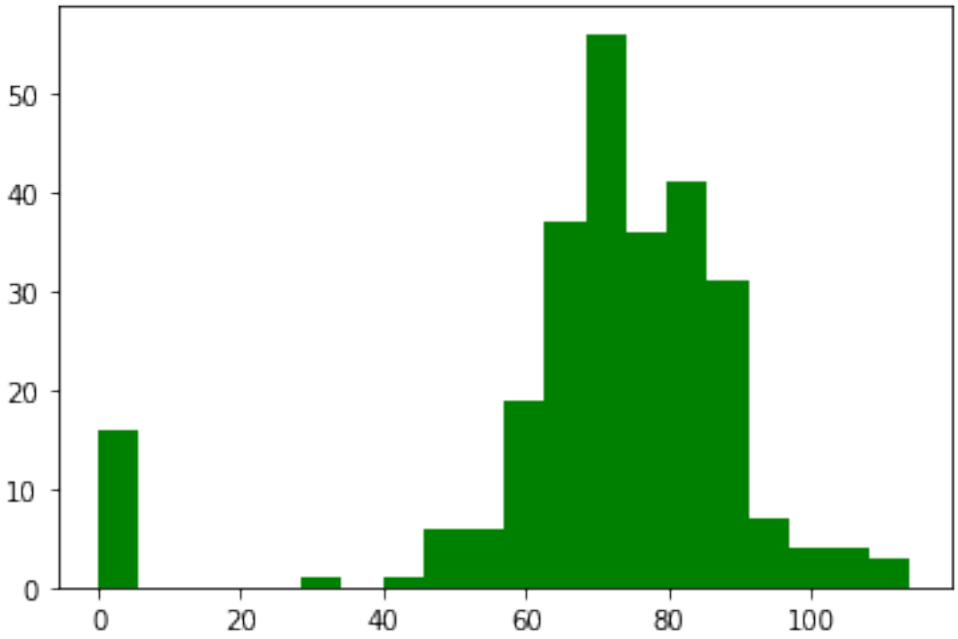


[23]:
```
Positive['Glucose'].value_counts().head(7)
```

[23]:
```
125    7
158    6
128    6
115    6
129    6
146    5
162    5
Name: Glucose, dtype: int64
```

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

[25]:
```
(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 0x7f4810076090>])
```

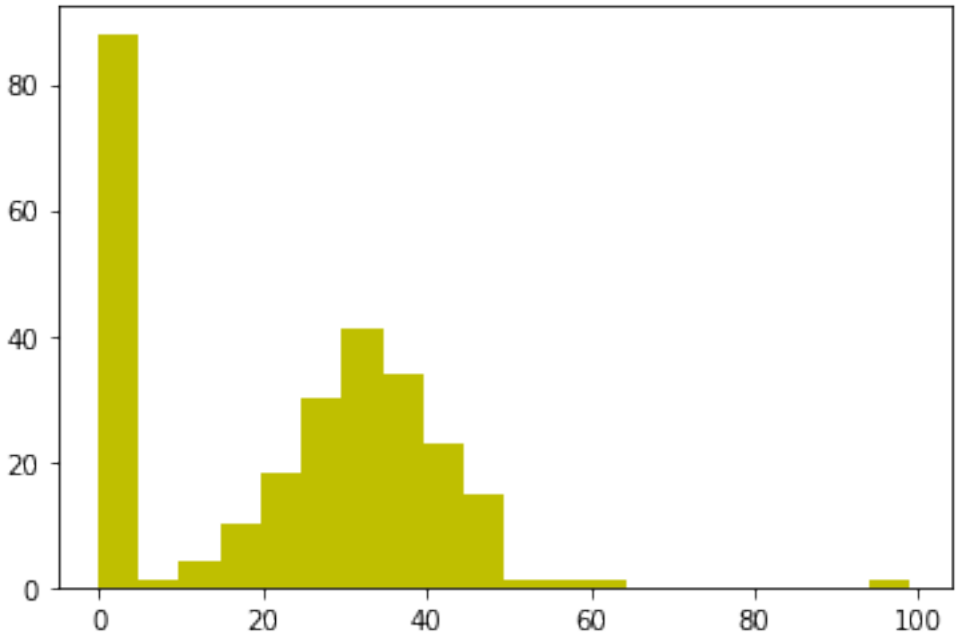


[26]:
```
Positive['BloodPressure'].value_counts().head(7)
```

[26]:
```
70    23
76    18
78    17
74    17
72    16
0     16
82    13
Name: BloodPressure, dtype: int64
```

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

[27]:
```
(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 0x7f480ffcf410>])
```

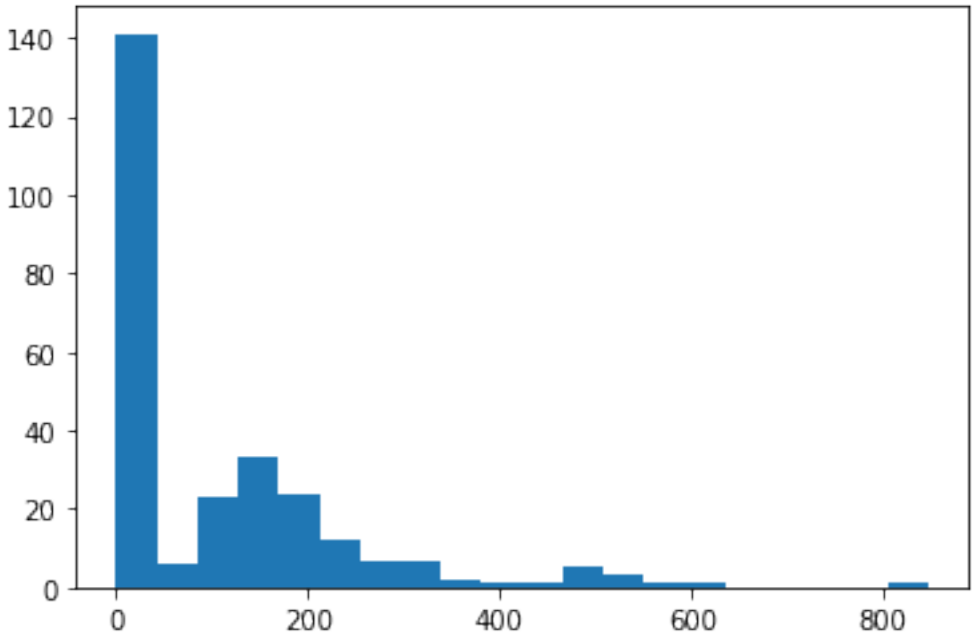


[28]:
```
Positive['SkinThickness'].value_counts().head(7)
```

[28]:
```
0     88
32    14
33     9
30     9
39     8
35     8
36     8
Name: SkinThickness, dtype: int64
```

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

[29]:
```
(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 0x7f480ffa7f90>])
```

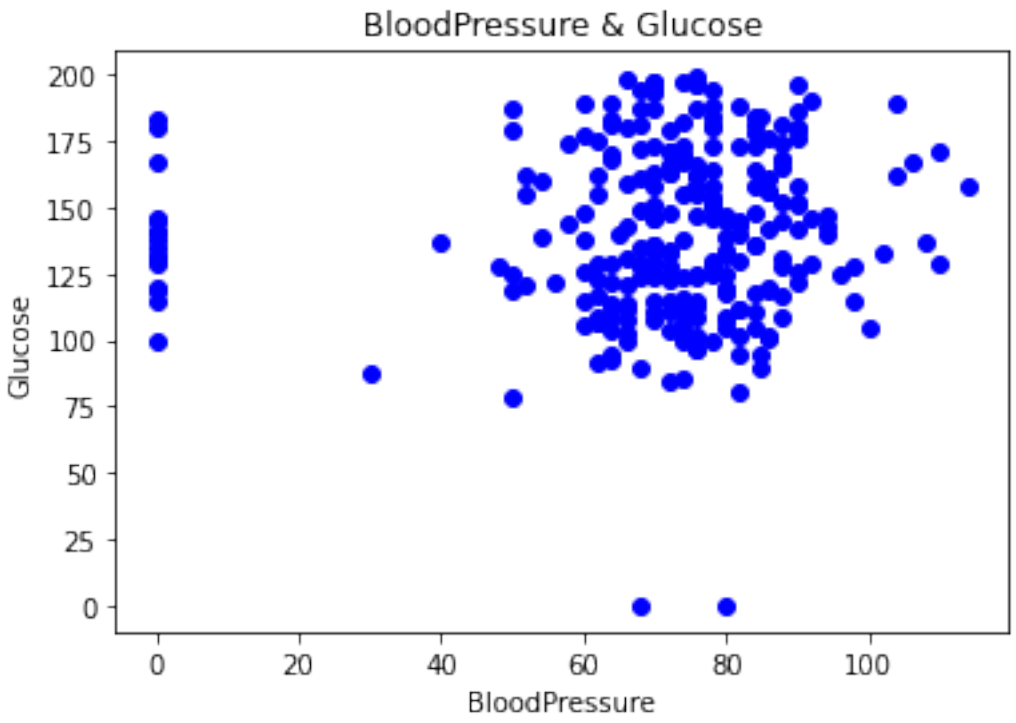


[30]:
```
Positive['Insulin'].value_counts().head(7)
```

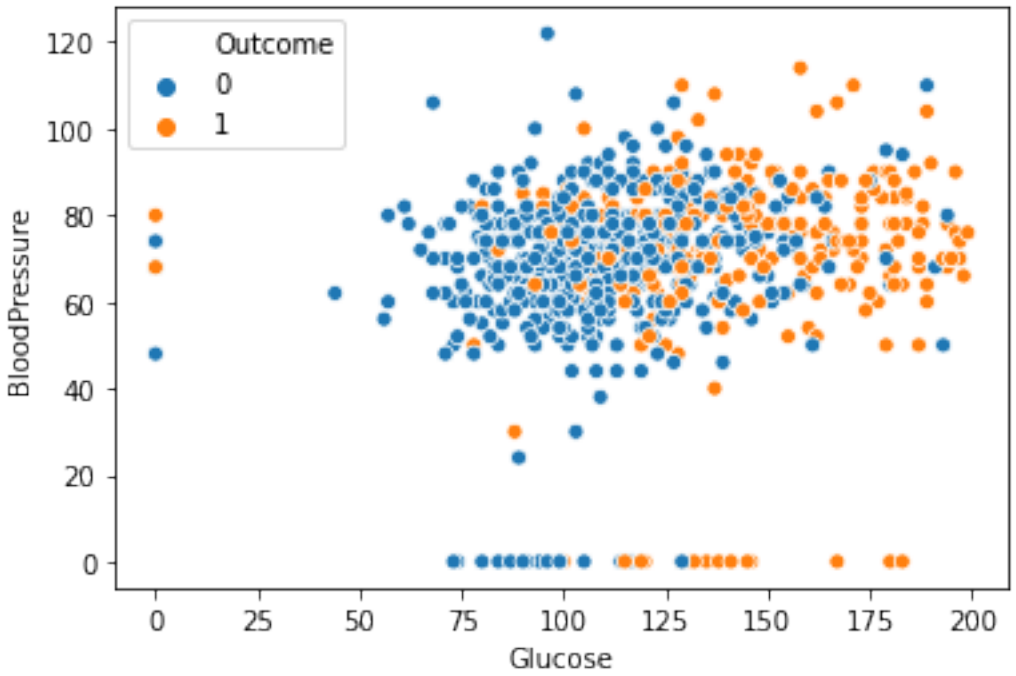
[30]:
```
0      138
130      6
180      4
156      3
175      3
194      2
125      2
Name: Insulin, dtype: int64
```

[32]:
```
BloodPressure = Positive['BloodPressure']
Glucose = Positive['Glucose']
SkinThickness = Positive['SkinThickness']
Insulin = Positive['Insulin']
BMI = Positive['BMI']
```

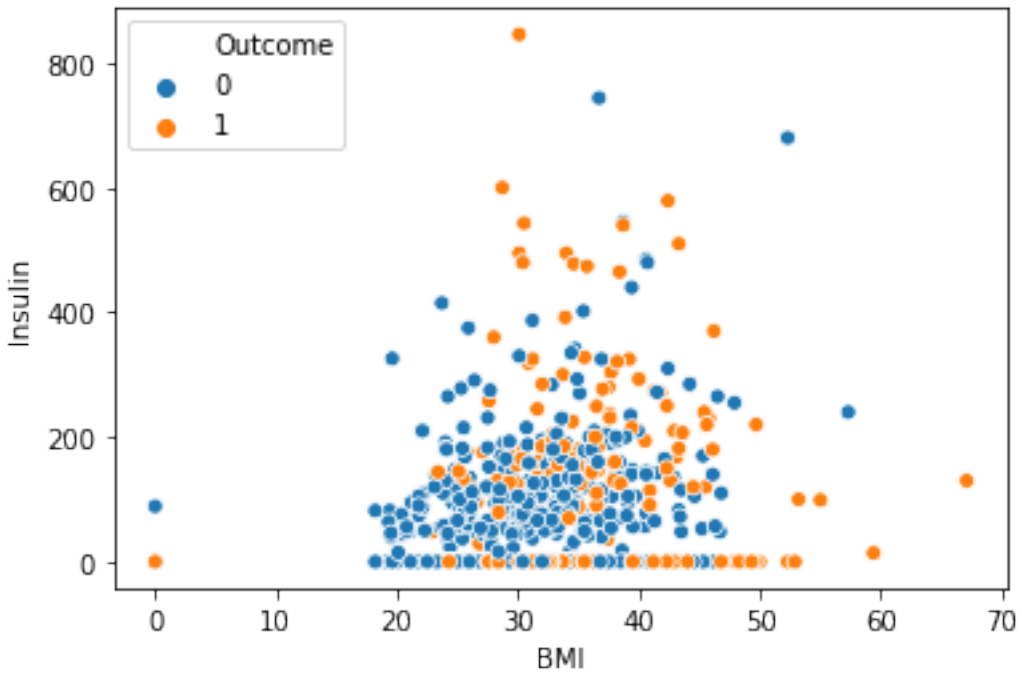
[33]:
```
plt.scatter(BloodPressure, Glucose, color=['b'])
plt.xlabel('BloodPressure')
plt.ylabel('Glucose')
plt.title('BloodPressure & Glucose')
plt.show()
```



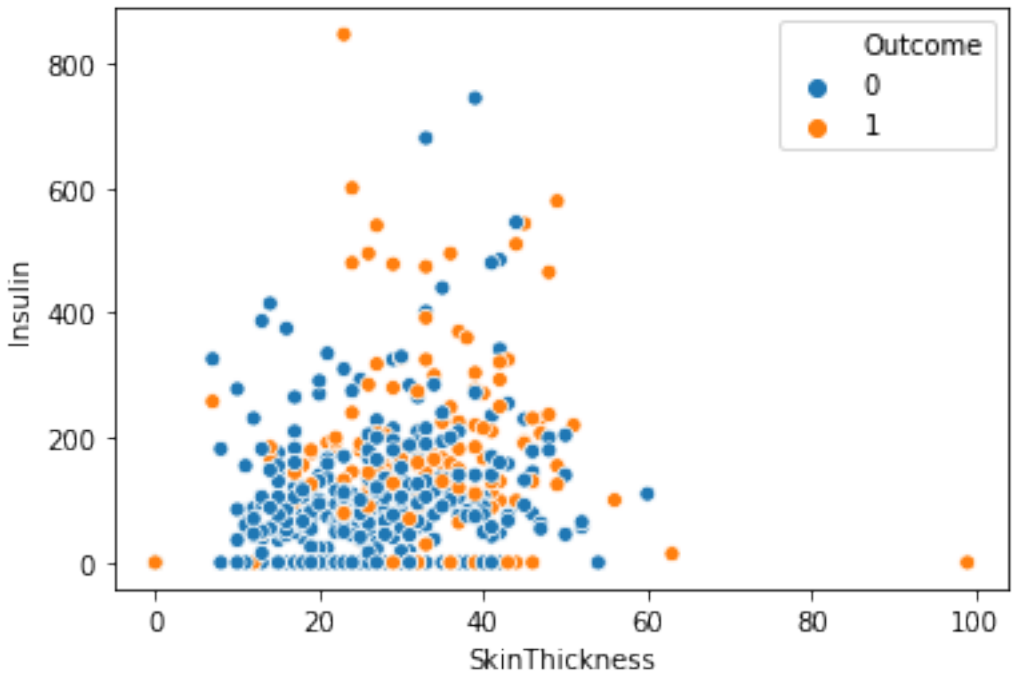
[34]:
```
g =sns.scatterplot(x= "Glucose" ,y= "BloodPressure",
                   hue="Outcome",
                   data=data);
```



[35]:
```
B =sns.scatterplot(x= "BMI" ,y= "Insulin",
                   hue="Outcome",
                   data=data);
```



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



[37]:
```
### correlation matrix
data.corr()
```

[37]:

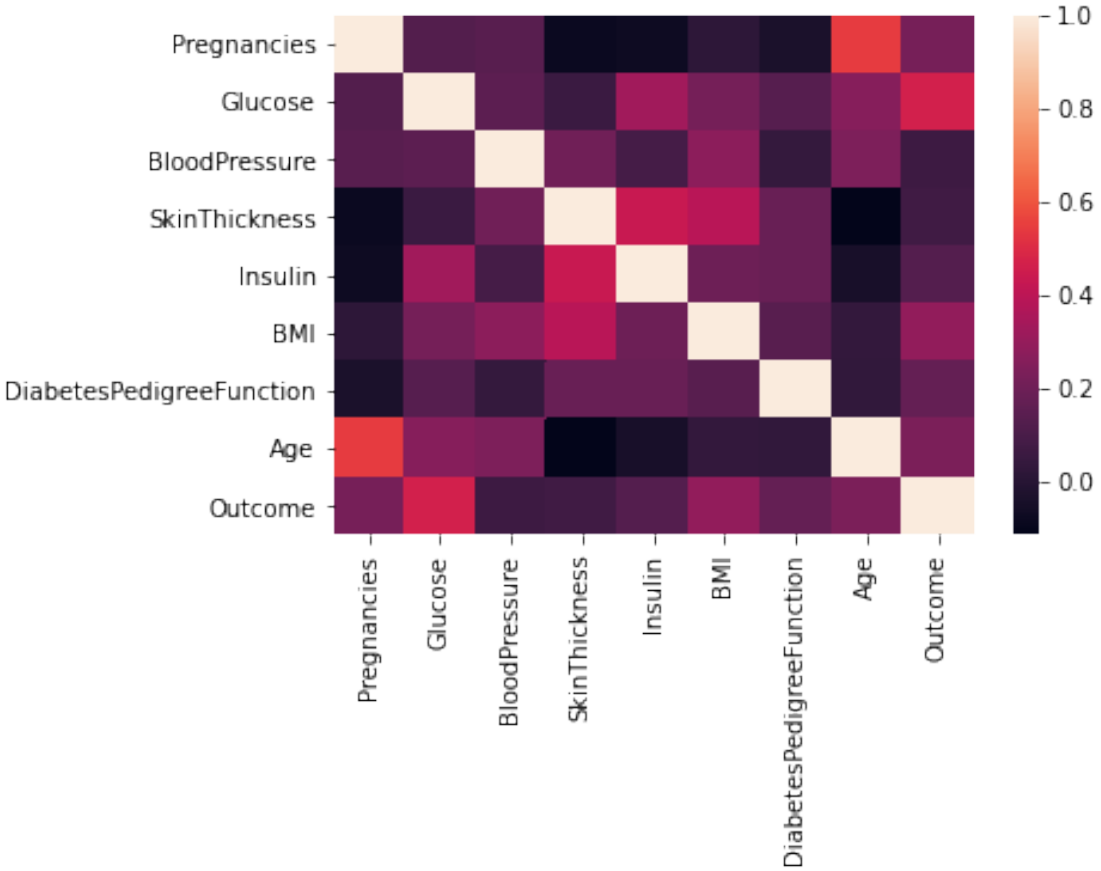
	Pregnancies	Glucose	BloodPressure	SkinThickness	\
Pregnancies	1.000000	0.129459	0.141282	-0.081672	
Glucose	0.129459	1.000000	0.152590	0.057328	
BloodPressure	0.141282	0.152590	1.000000	0.207371	
SkinThickness	-0.081672	0.057328	0.207371	1.000000	
Insulin	-0.073535	0.331357	0.088933	0.436783	
BMI	0.017683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

	Insulin	BMI	DiabetesPedigreeFunction	\
Pregnancies	-0.073535	0.017683	-0.033523	
Glucose	0.331357	0.221071	0.137337	
BloodPressure	0.088933	0.281805	0.041265	
SkinThickness	0.436783	0.392573	0.183928	
Insulin	1.000000	0.197859	0.185071	
BMI	0.197859	1.000000	0.140647	
DiabetesPedigreeFunction	0.185071	0.140647	1.000000	
Age	-0.042163	0.036242	0.033561	
Outcome	0.130548	0.292695	0.173844	

	Age	Outcome
Pregnancies	0.544341	0.221898
Glucose	0.263514	0.466581
BloodPressure	0.239528	0.065068
SkinThickness	-0.113970	0.074752
Insulin	-0.042163	0.130548
BMI	0.036242	0.292695
DiabetesPedigreeFunction	0.033561	0.173844
Age	1.000000	0.238356
Outcome	0.238356	1.000000

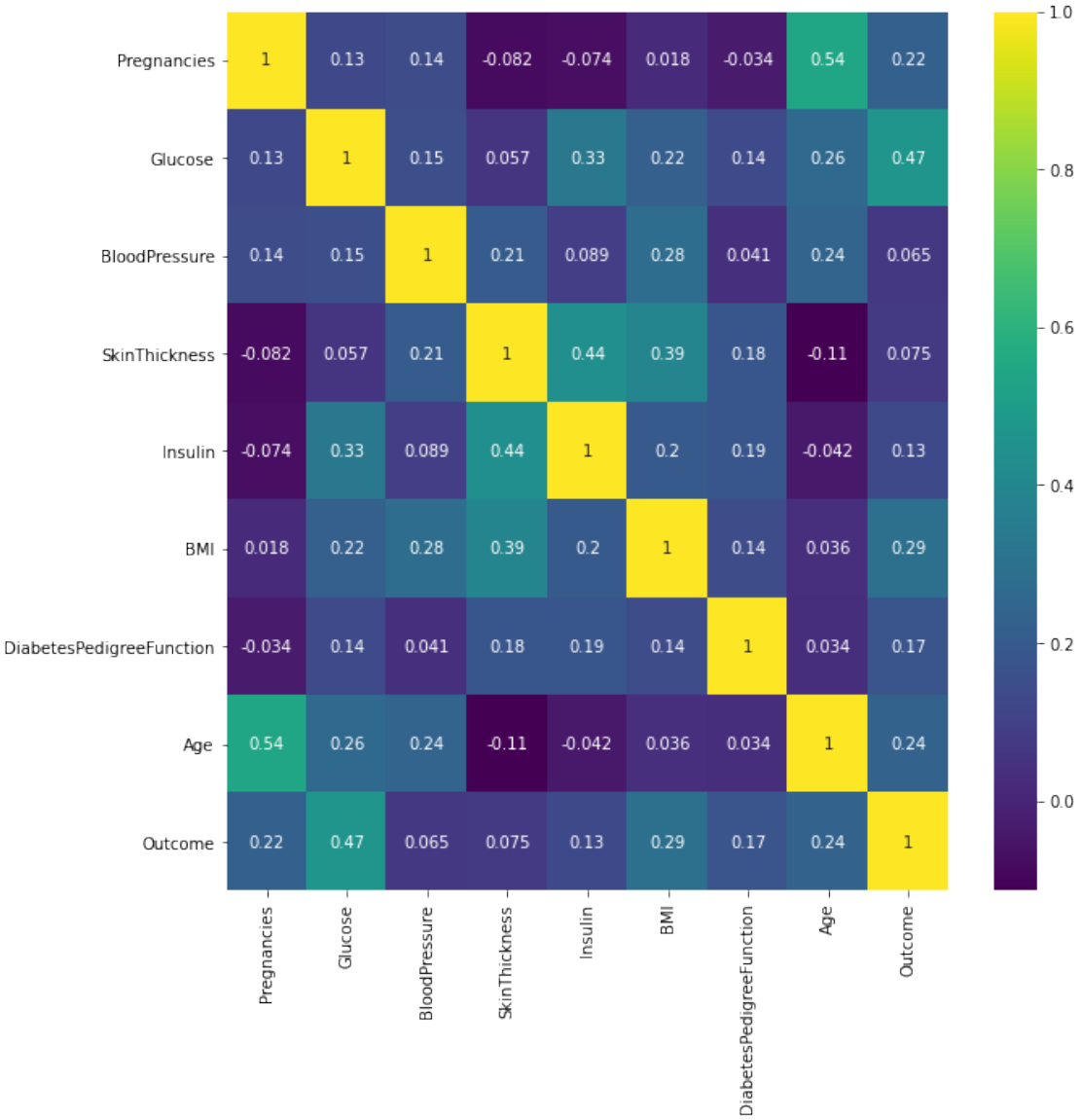
[38]:
```
### create correlation heat map
sns.heatmap(data.corr())
```

[38]: <AxesSubplot:>



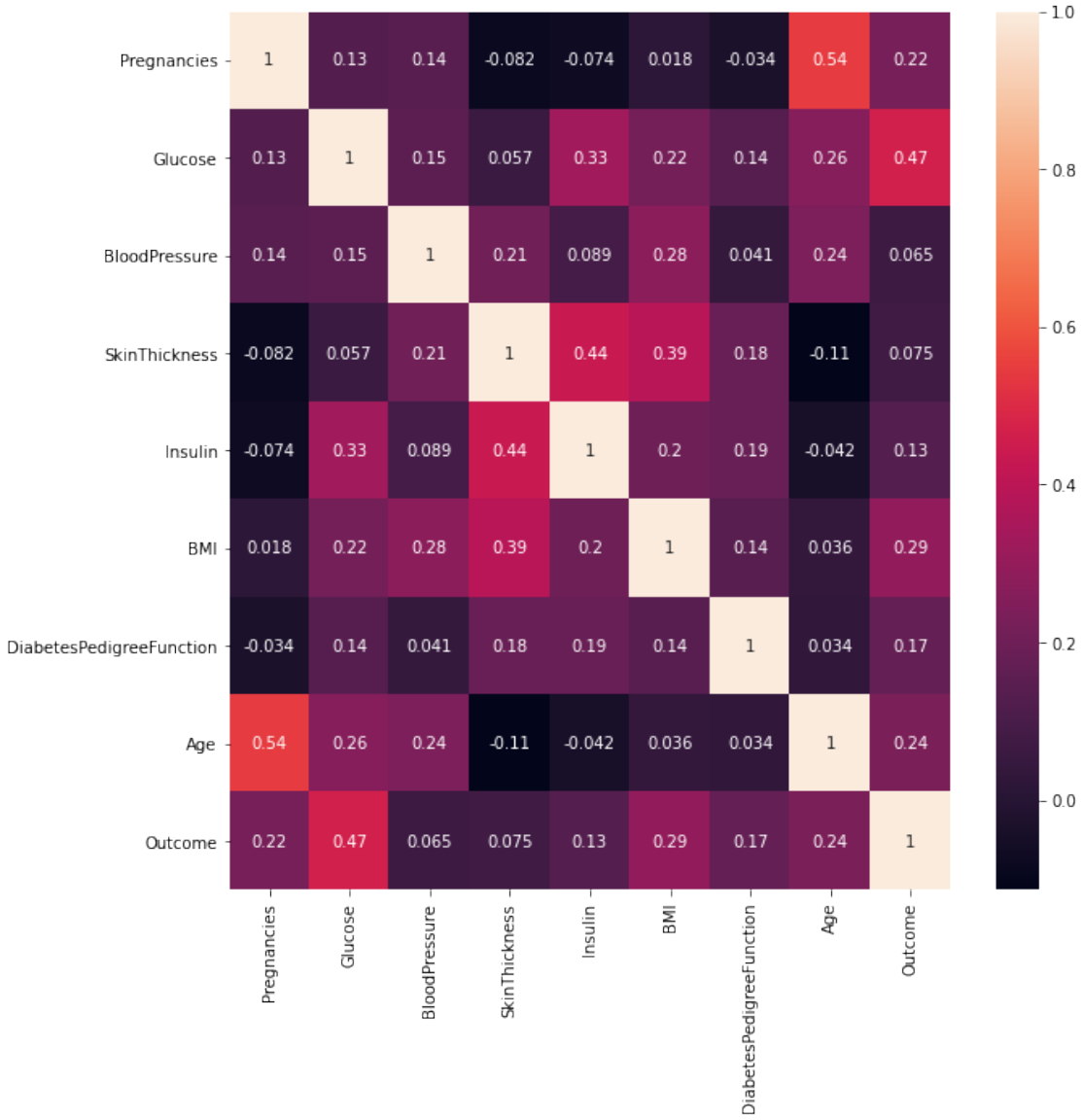
[39]:
```
plt.subplots(figsize=(10,10))
sns.heatmap(data.corr(),annot=True,cmap='viridis')  ### gives correlation value
```

[39]: <AxesSubplot:>



[40]:
```
plt.subplots(figsize=(10,10))
sns.heatmap(data.corr(),annot=True)  ### gives correlation value
```

[40]: <AxesSubplot:>



Project Task Week 3

[41]:
```
data.head(5)
```

[41]:
```
   Pregnancies  Glucose  BloodPressure  SkinThickness  Insulin   BMI  \
0            6      148             72             35        0  33.6
1            1       85             66             29        0  26.6
2            8      183             64              0        0  23.3
3            1       89             66             23       94  28.1
4            0      137             40             35      168  43.1

   DiabetesPedigreeFunction  Age  Outcome
```

```
0                       0.627   50          1
1                       0.351   31          0
2                       0.672   32          1
3                       0.167   21          0
4                       2.288   33          1
```

[42]:
```
features = data.iloc[:,[0,1,2,3,4,5,6,7]].values
label = data.iloc[:,8].values
```

[43]:
```
#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)
```

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

[44]:
```
LogisticRegression()
```

[45]:
```
print(model.score(X_train,y_train))
print(model.score(X_test,y_test))
```

```
0.7719869706840391
0.7662337662337663
```

[46]:
```
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(label,model.predict(features))
cm
```

[46]:
```
array([[446,  54],
       [122, 146]])
```

[47]:
```
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
```

[48]:
```
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
```

[52]:
```
#Applying Random Forest
from sklearn.ensemble import RandomForestClassifier
model4 = RandomForestClassifier(n_estimators=11)
model4.fit(X_train,y_train)
```

[52]:
```
RandomForestClassifier(n_estimators=11)
```

[53]:
```
model4.score(X_train,y_train)
```

[53]:
```
0.9837133550488599
```

[54]:
```
model4.score(X_test,y_test)
```

[54]:
```
0.7467532467532467
```

[57]:
```
#Applying K-NN
from sklearn.neighbors import KNeighborsClassifier
model2 = KNeighborsClassifier(n_neighbors=7,
                              metric='minkowski',
                              p = 2)
```

[58]:
```
#Applying K-NN
from sklearn.neighbors import KNeighborsClassifier
model2 = KNeighborsClassifier(n_neighbors=7,
                              metric='minkowski',
                              p = 2)
```

[59]:
```
#Applying K-NN
from sklearn.neighbors import KNeighborsClassifier
model2 = KNeighborsClassifier(n_neighbors=7,
                              metric='minkowski',
                              p = 2)
```

[60]:
```
#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")
```

```
      ␣
↪---------------------------------------------------------------------------

       NotFittedError                                Traceback (most recent call␣
↪last)

       <ipython-input-60-0cbf62257b3a> in <module>
         3 from sklearn.metrics import roc_auc_score
         4 # predict probabilities
   ----> 5 probs = model2.predict_proba(features)
         6 # keep probabilities for the positive outcome only
         7 probs = probs[:, 1]


       /usr/local/lib/python3.7/site-packages/sklearn/neighbors/_classification.
↪py in predict_proba(self, X)
       239         X = check_array(X, accept_sparse='csr')
       240
   --> 241         neigh_dist, neigh_ind = self.kneighbors(X)
       242
       243         classes_ = self.classes_


       /usr/local/lib/python3.7/site-packages/sklearn/neighbors/_base.py in␣
↪kneighbors(self, X, n_neighbors, return_distance)
```

```
      647                 [2]]…)
      648         """
--> 649         check_is_fitted(self)
      650
      651         if n_neighbors is None:


      /usr/local/lib/python3.7/site-packages/sklearn/utils/validation.py in
↪inner_f(*args, **kwargs)
       61             extra_args = len(args) - len(all_args)
       62             if extra_args <= 0:
---> 63                 return f(*args, **kwargs)
       64
       65             # extra_args > 0


      /usr/local/lib/python3.7/site-packages/sklearn/utils/validation.py in
↪check_is_fitted(estimator, attributes, msg, all_or_any)
     1096
     1097     if not attrs:
-> 1098         raise NotFittedError(msg % {'name': type(estimator).
↪__name__})
     1099
     1100


      NotFittedError: This KNeighborsClassifier instance is not fitted yet.
↪Call 'fit' with appropriate arguments before using this estimator.
```

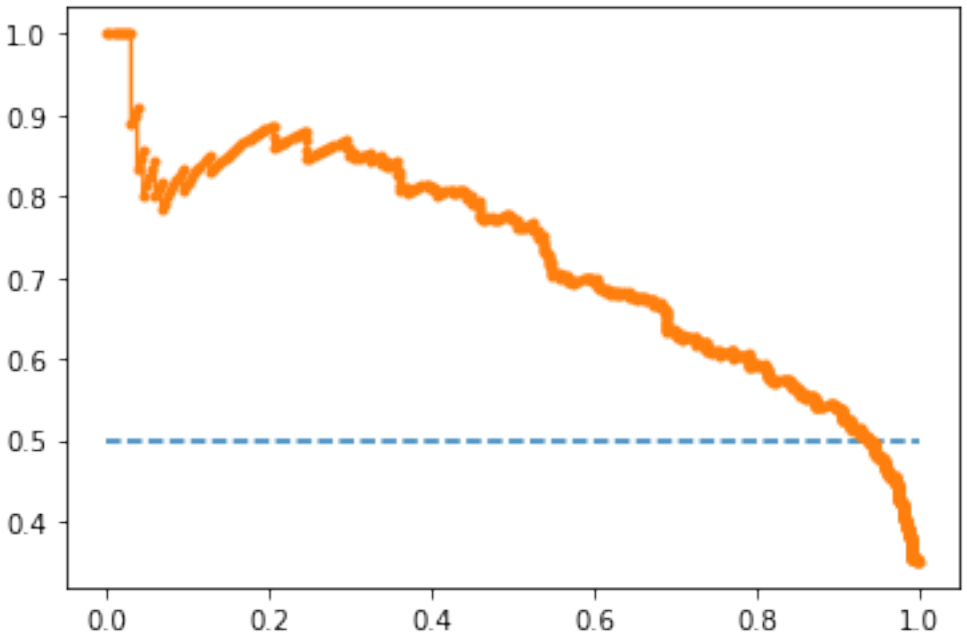
[61]:
```
#Precision Recall Curve for Logistic Regression

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
```

[61]: [<matplotlib.lines.Line2D at 0x7f4800734290>]



[ ]:

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