ML LAB 7

Implement Naïve Bayes algorithm in a given business environment and comment on its efficiency and performance.

In [1]:
```
import pandas as pd
import numpy as np
import seaborn as sns
from matplotlib import pyplot as plt
%matplotlib inline
from sklearn.preprocessing import PolynomialFeatures, StandardScaler
from warnings import filterwarnings
filterwarnings('ignore')
```

In [2]:
```
data = pd.read_csv('C:/Users/user/Downloads/archive (2)/drug200.csv')
```

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

Out[3]:

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
0	23	F	HIGH	HIGH	25.355	DrugY
1	47	M	LOW	HIGH	13.093	drugC
2	47	M	LOW	HIGH	10.114	drugC
3	28	F	NORMAL	HIGH	7.798	drugX
4	61	F	LOW	HIGH	18.043	DrugY

In [4]:
```
data.isnull().sum()
```

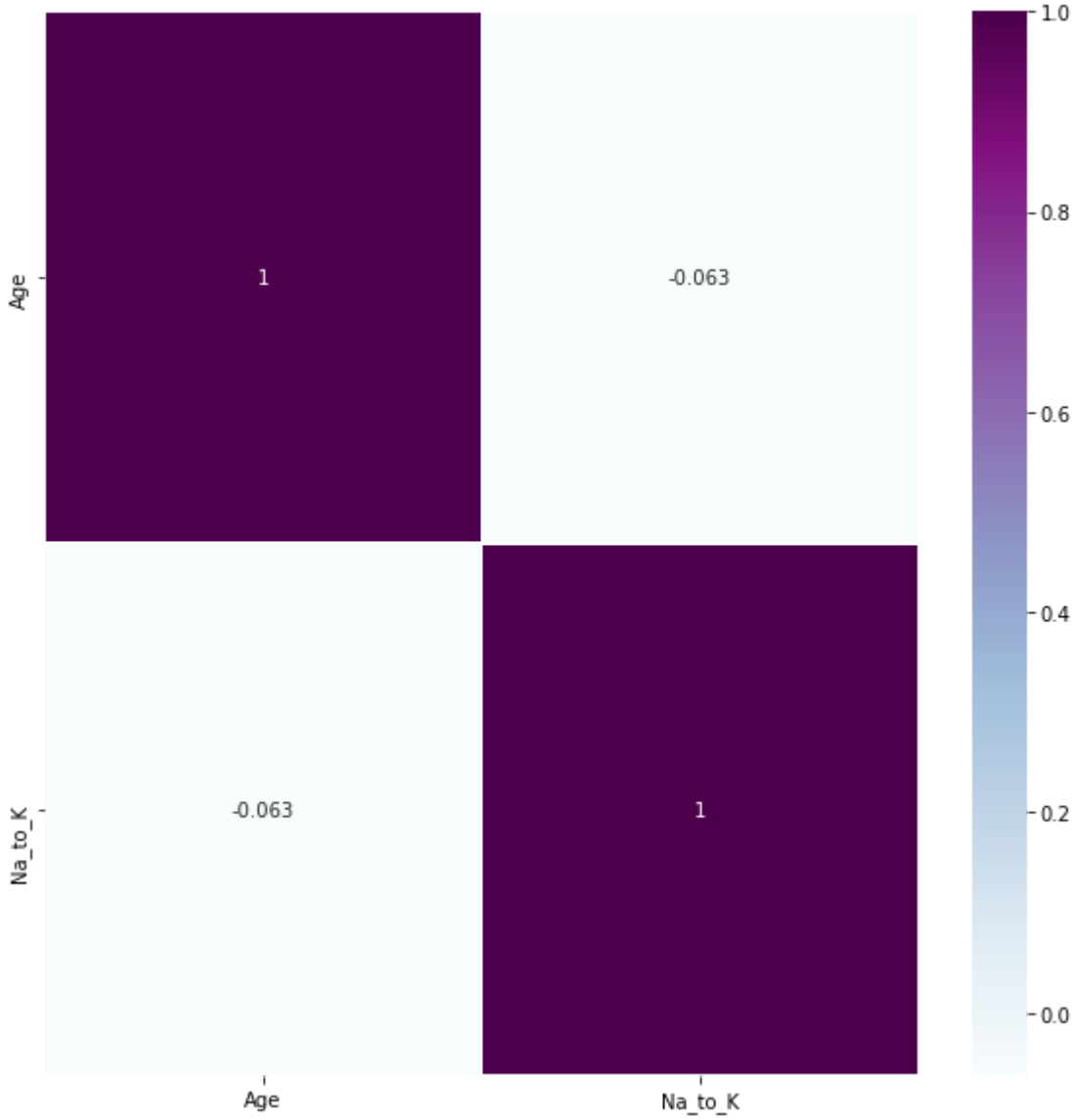
Out[4]:
```
Age            0
Sex            0
BP             0
Cholesterol    0
Na_to_K        0
Drug           0
dtype: int64
```

In [5]:
```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 200 entries, 0 to 199
Data columns (total 6 columns):
 #   Column       Non-Null Count  Dtype  
---  ------       --------------  -----  
 0   Age          200 non-null    int64  
 1   Sex          200 non-null    object 
 2   BP           200 non-null    object 
 3   Cholesterol  200 non-null    object 
 4   Na_to_K      200 non-null    float64
 5   Drug         200 non-null    object 
dtypes: float64(1), int64(1), object(4)
memory usage: 9.5+ KB
```

there is no missing values in the date we have 6 coulmns and 200 rows

In [6]:
```
fig, ax = plt.subplots(figsize  = (10, 10))
sns.heatmap(data.corr(), cmap = 'BuPu', cbar = True, linewidth = 0.5, annot = Tru
plt.show()
```

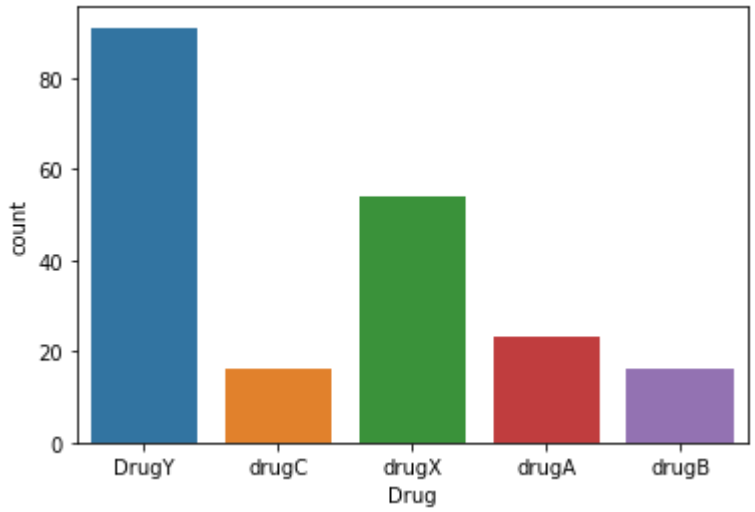


In [7]:
```
data['Drug'].value_counts()
```

Out[7]:
```
DrugY    91
drugX    54
drugA    23
drugC    16
drugB    16
Name: Drug, dtype: int64
```

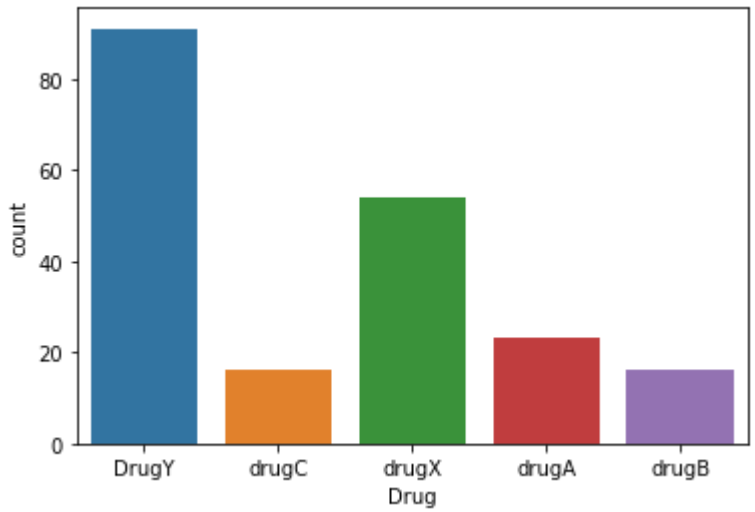
In [8]:
```
sns.countplot(x = 'Drug', data= data)
```

Out[8]:
```
<AxesSubplot:xlabel='Drug', ylabel='count'>
```



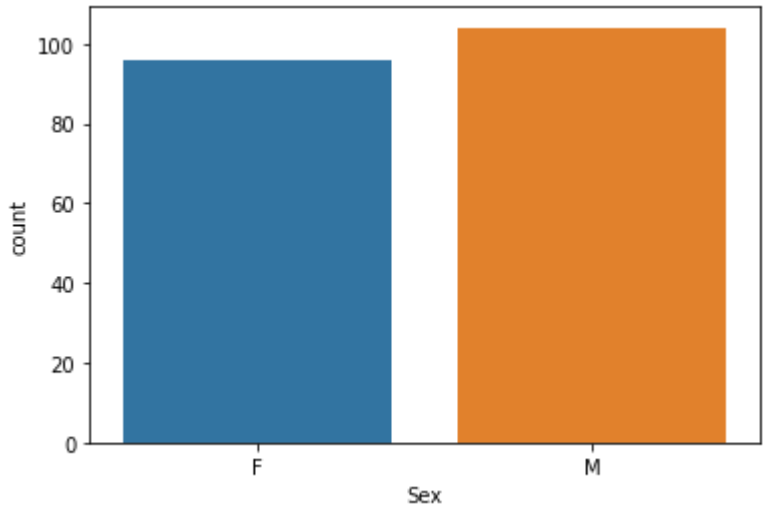
In [9]:
```
sns.countplot(x = 'Drug', data= data)
```

Out[9]:
```
<AxesSubplot:xlabel='Drug', ylabel='count'>
```



In [10]:
```
sns.countplot(x = 'Sex', data= data)
```

Out[10]:
```
<AxesSubplot:xlabel='Sex', ylabel='count'>
```

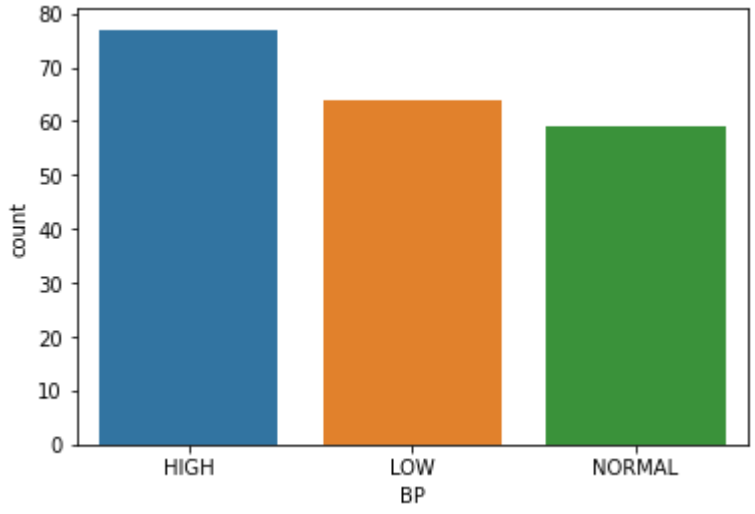


In [11]:
```
data['BP'].value_counts()
```

Out[11]:
```
HIGH      77
LOW       64
NORMAL    59
Name: BP, dtype: int64
```

In [12]:
```
sns.countplot(x = 'BP', data= data)
```

Out[12]:
```
<AxesSubplot:xlabel='BP', ylabel='count'>
```

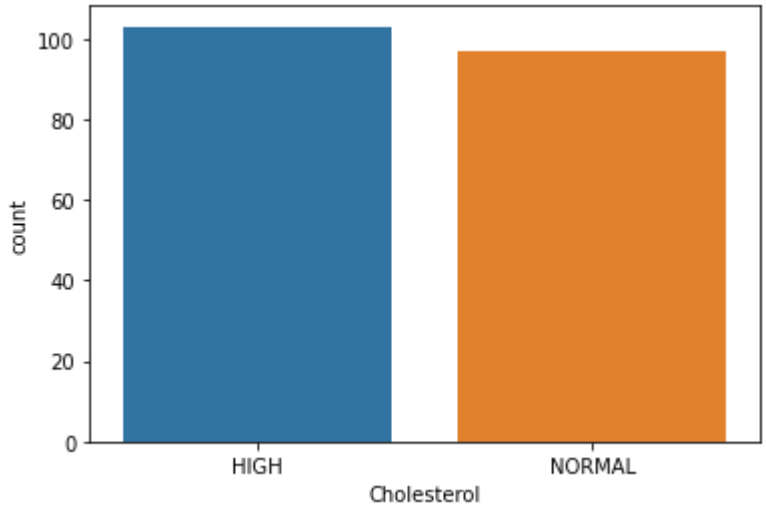


In [13]:
```
data['Cholesterol'].value_counts()
```

Out[13]:
```
HIGH      103
NORMAL     97
Name: Cholesterol, dtype: int64
```

In [14]:
```
sns.countplot(x = 'Cholesterol', data= data)
```

Out[14]:
```
<AxesSubplot:xlabel='Cholesterol', ylabel='count'>
```

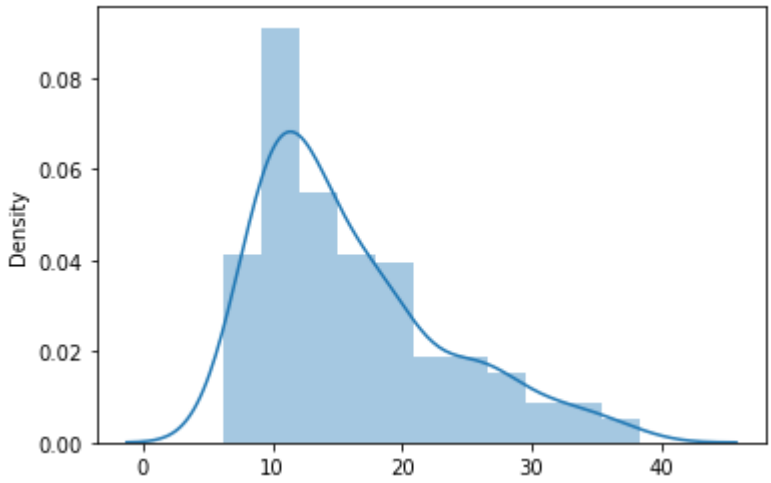


In [15]:
```
data['Na_to_K'].describe()
```

Out[15]:
```
count    200.000000
mean      16.084485
std        7.223956
min        6.269000
25%       10.445500
50%       13.936500
75%       19.380000
max       38.247000
Name: Na_to_K, dtype: float64
```

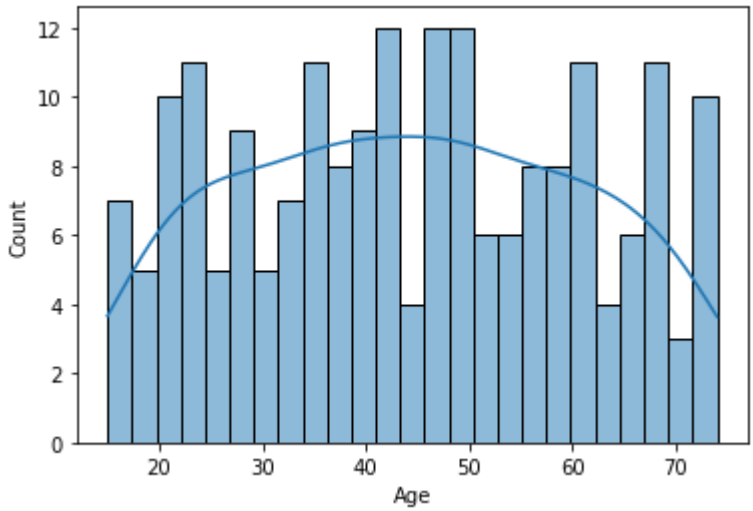
In [16]:
```
sns.distplot(x = data['Na_to_K'])
```

Out[16]:
```
<AxesSubplot:ylabel='Density'>
```



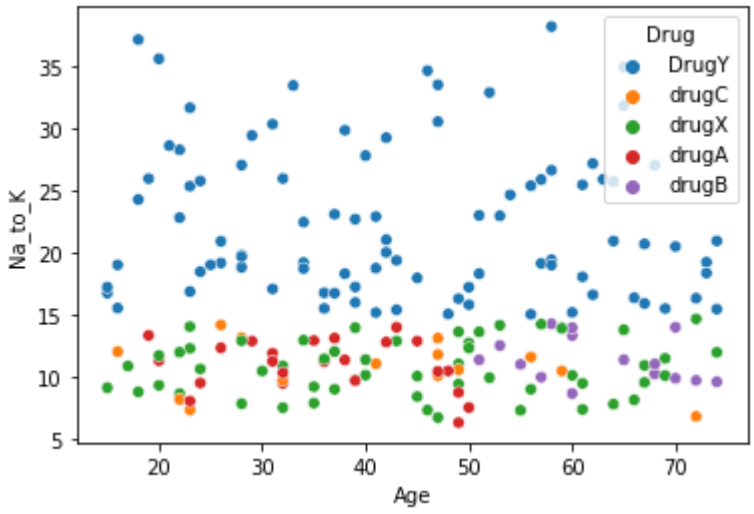
In [17]:
```
sns.histplot(x = 'Age', kde=True, bins = 25, data = data)
```

Out[17]:
```
<AxesSubplot:xlabel='Age', ylabel='Count'>
```



In [18]:
```
sns.scatterplot(x = 'Age', y = 'Na_to_K', data = data, hue = 'Drug')
```

Out[18]:
```
<AxesSubplot:xlabel='Age', ylabel='Na_to_K'>
```



In the last fig we find all the items have more than 15 Na_to_K have DrugY type

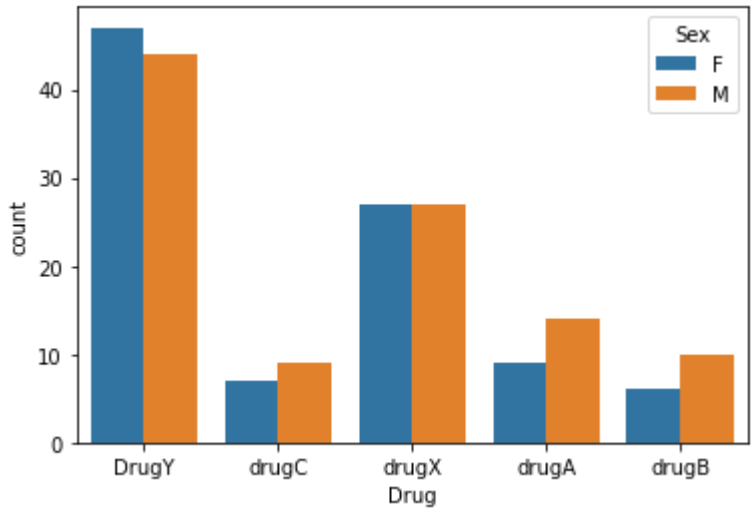
In the next We will find out the number of each Drug type per Sex

In [19]:
```
data_sex_drug = data.groupby(['Drug','Sex']).size().reset_index(name = 'count')
print(data_sex_drug)
```

```
    Drug Sex  count
0  DrugY   F     47
1  DrugY   M     44
2  drugA   F      9
3  drugA   M     14
4  drugB   F      6
5  drugB   M     10
6  drugC   F      7
7  drugC   M      9
8  drugX   F     27
9  drugX   M     27
```

In [20]:
```
sns.countplot(x = 'Drug', data= data, hue = 'Sex')
```

Out[20]: <AxesSubplot:xlabel='Drug', ylabel='count'>

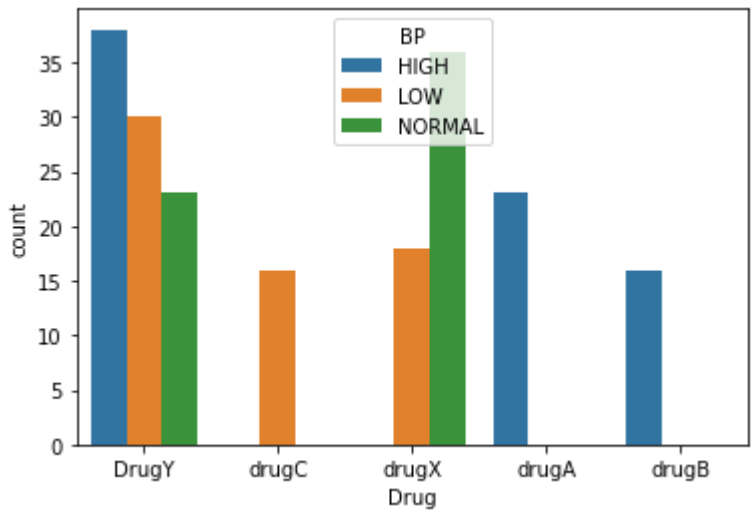


In [21]:
```
data_BP_drug = data.groupby(['Drug','BP']).size().reset_index(name = 'count')
print(data_BP_drug)
```

```
    Drug      BP  count
0  DrugY    HIGH     38
1  DrugY     LOW     30
2  DrugY  NORMAL     23
3  drugA    HIGH     23
4  drugB    HIGH     16
5  drugC     LOW     16
6  drugX     LOW     18
7  drugX  NORMAL     36
```

In [22]:
```
sns.countplot(x = 'Drug', data= data, hue = 'BP')
```

Out[22]: <AxesSubplot:xlabel='Drug', ylabel='count'>

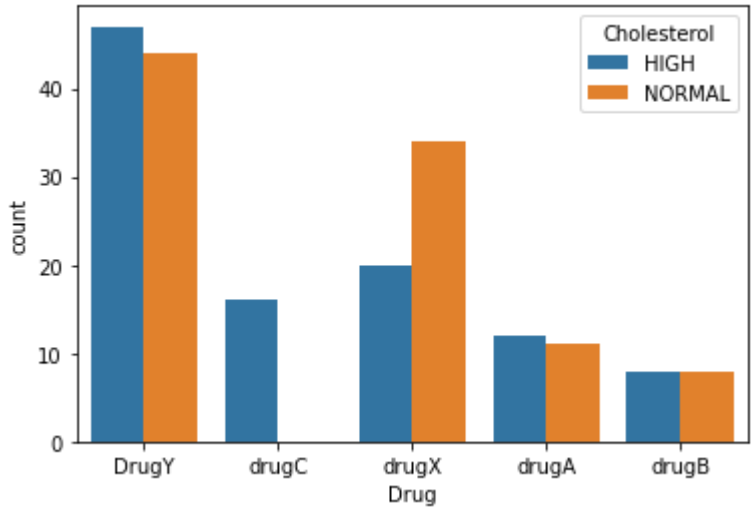


In [23]:
```
data_Cholesterol_drug = data.groupby(['Drug','Cholesterol']).size().reset_index(n
print(data_Cholesterol_drug)
```

```
    Drug Cholesterol  count
0  DrugY        HIGH     47
1  DrugY      NORMAL     44
2  drugA        HIGH     12
3  drugA      NORMAL     11
4  drugB        HIGH      8
5  drugB      NORMAL      8
6  drugC        HIGH     16
7  drugX        HIGH     20
8  drugX      NORMAL     34
```

In [24]:
```
sns.countplot(x = 'Drug', data= data, hue = 'Cholesterol')
```

Out[24]: <AxesSubplot:xlabel='Drug', ylabel='count'>



In [25]:
```
data['Sex'] = data['Sex'].map({'M': 1, 'F': 0})
data['Cholesterol'] = data['Cholesterol'].map({'HIGH' : 1, 'NORMAL' : 0})
data['Drug'] = data['Drug'].map({'DrugY':1, 'drugC':2, 'drugX':3, 'drugA':4, 'dru
data.head()
```

Out[25]:

	Age	Sex	BP	Cholesterol	Na_to_K	Drug
0	23	0	HIGH	1	25.355	1
1	47	1	LOW	1	13.093	2
2	47	1	LOW	1	10.114	2
3	28	0	NORMAL	1	7.798	3
4	61	0	LOW	1	18.043	1

In [26]:
```
data.shape
```

Out[26]: (200, 6)

In [27]:
```
data = pd.get_dummies(data)
data.head()
```

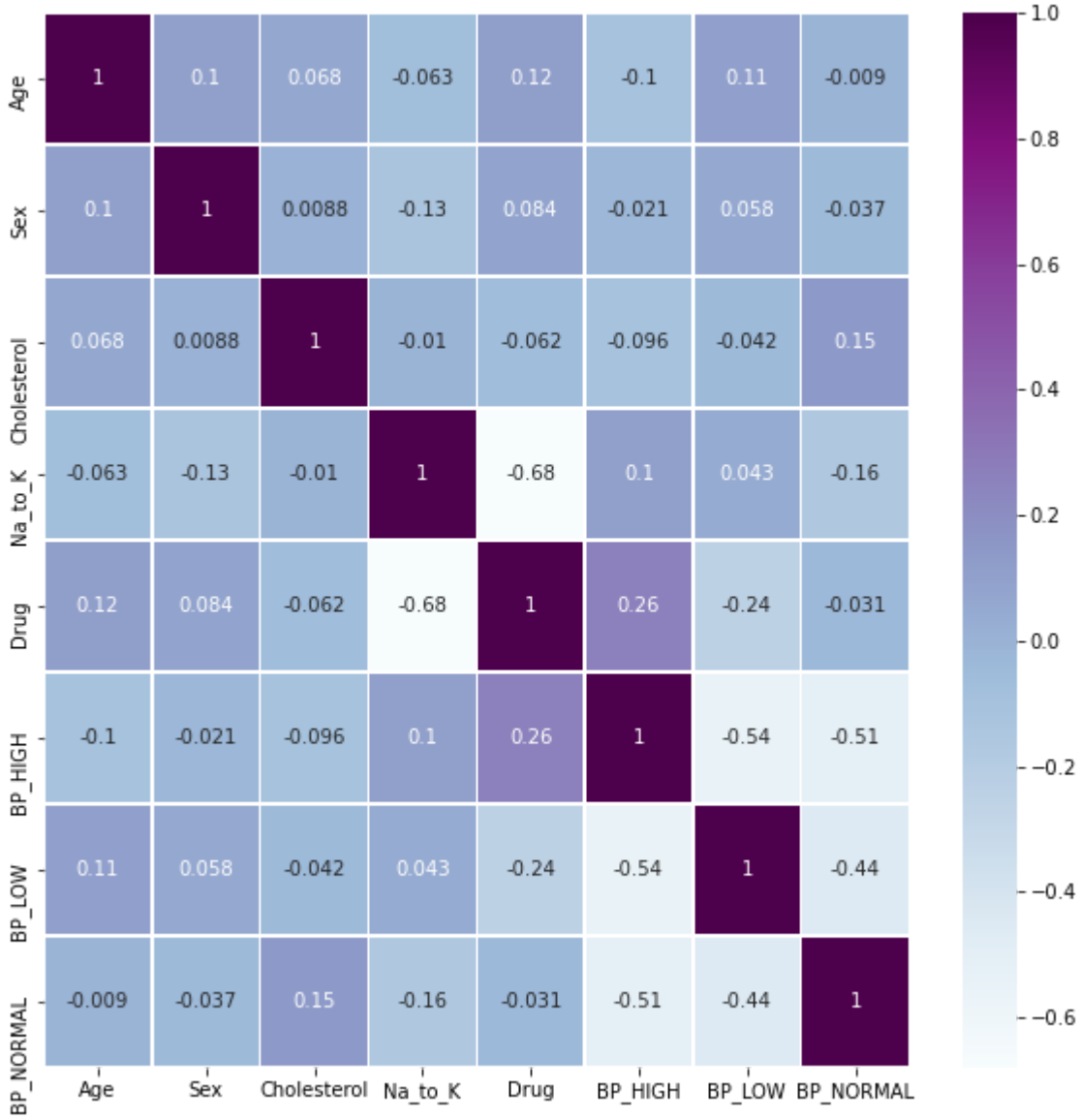
Out[27]:

	Age	Sex	Cholesterol	Na_to_K	Drug	BP_HIGH	BP_LOW	BP_NORMAL
0	23	0	1	25.355	1	1	0	0
1	47	1	1	13.093	2	0	1	0
2	47	1	1	10.114	2	0	1	0
3	28	0	1	7.798	3	0	0	1
4	61	0	1	18.043	1	0	1	0

In [28]:
```
data.shape
```

Out[28]:
```
(200, 8)
```

In [29]:
```
fig, ax = plt.subplots(figsize  = (10, 10))
sns.heatmap(data.corr(), cmap = 'BuPu', cbar = True, linewidth = 0.5, annot = Tru
plt.show()
```



In [30]:
```
X = data.drop('Drug', axis = 1).values
y = data['Drug'].values.reshape((-1,1))
```

In [31]:
```
from sklearn.model_selection import train_test_split
```

In [32]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size = 0.2, random
print('x train shape {}'.format(X_train.shape))
print('x test shape  {}'.format(X_test.shape))
print('y train shape {}'.format(y_train.shape))
print('y test shape  {}'.format(y_test.shape))
```

```
x train shape (160, 7)
x test shape  (40, 7)
y train shape (160, 1)
y test shape  (40, 1)
```

In [33]:
```
from sklearn.naive_bayes import GaussianNB
```

In [34]:
```
# classificador logreg
GNB = GaussianNB()

# Fitting with train data
model = GNB.fit(X_train, y_train)
```

In [37]:
```
# Printing the Training Score
print("Training score data: ")
print(model.score(X_train, y_train))
```

```
Training score data:
0.7625
```

In [38]:
```
y_pred = model.predict(X_test)

print('\nAccuracy of Naive Bayes classifier on test set: {:.2f}'.format(accuracy_
```

```
Accuracy of Naive Bayes classifier on test set: 0.75
```

In [39]:
```
from sklearn.metrics import confusion_matrix, accuracy_score, classification_repo
```

In [41]:
```
print(confusion_matrix(y_test, y_pred))
print(classification_report(y_test, y_pred))
```

```
[[ 7  4  4  2  0]
 [ 0  4  0  0  0]
 [ 0  0 13  0  0]
 [ 0  0  0  4  0]
 [ 0  0  0  0  2]]
              precision    recall  f1-score   support

           1       1.00      0.41      0.58        17
           2       0.50      1.00      0.67         4
           3       0.76      1.00      0.87        13
           4       0.67      1.00      0.80         4
           5       1.00      1.00      1.00         2

    accuracy                           0.75        40
   macro avg       0.79      0.88      0.78        40
weighted avg       0.84      0.75      0.73        40
```

Interpretation:

Of the entire test set, 84% of the drugs were predicted correctly.

In [ ]:
```
```