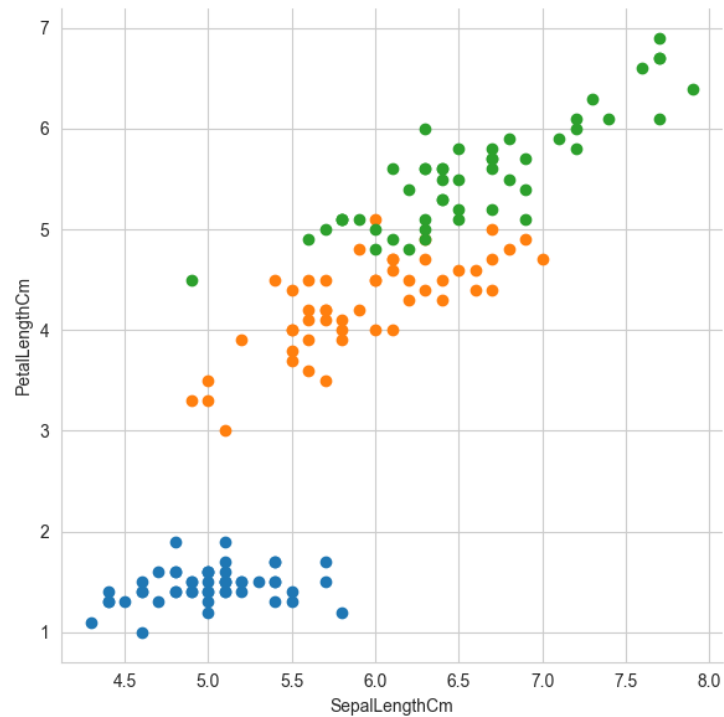


[[14 0 0 2 0] [0 3 1 0 1] [3 1 3 1 1] [0 0 2 4 0] [1 1 1 0 1]]				
	precision	recall	f1-score	support
1	0.78	0.88	0.82	16
2	0.60	0.60	0.60	5
3	0.43	0.33	0.38	9
4	0.57	0.67	0.62	6
5	0.33	0.25	0.29	4
accuracy			0.62	40
macro avg	0.54	0.55	0.54	40
weighted avg	0.60	0.62	0.61	40

	SepalLengthCm	SepalWidthCm	PetalLengthCm	PetalWidthCm
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2
3	4.6	3.1	1.5	0.2
4	5.0	3.6	1.4	0.2
0	Setosa			
1	Setosa			
2	Setosa			
3	Setosa			
4	Setosa			
Name: Species, dtype: object				

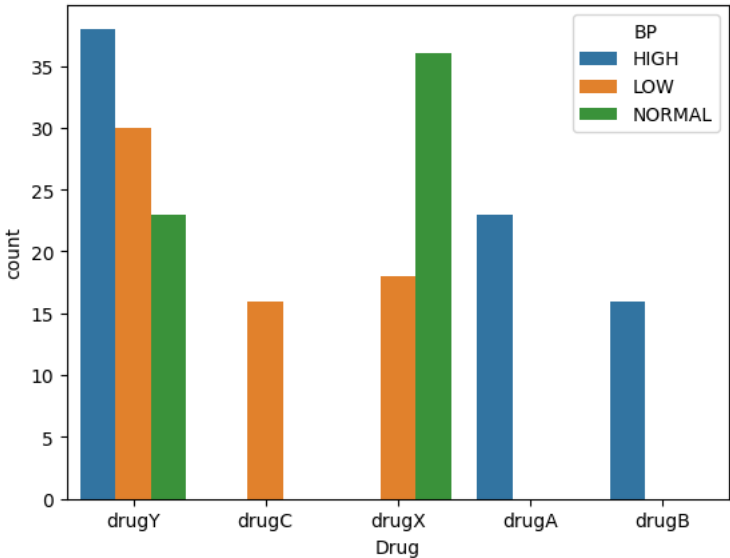
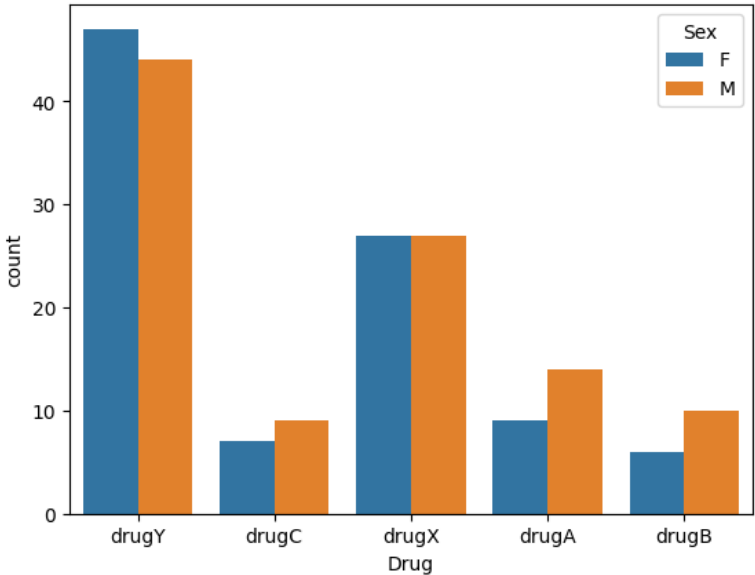
Eigenvectors				
[[0.52106591 -0.37741762 -0.71956635 0.26128628] [-0.26934744 -0.92329566 0.24438178 -0.12350962] [0.5804131 -0.02449161 0.14212637 -0.80144925] [0.56485654 -0.06694199 0.63427274 0.52359713]]				
Eigenvalues				
[2.91849782 0.91403047 0.14675688 0.02071484]				



[[-0.90068117 1.01900435 -1.34022653 -1.3154443] [-1.14301691 -0.13197948 -1.34022653 -1.3154443] [-1.38535265 0.32841405 -1.39706395 -1.3154443] [-1.50652052 0.09821729 -1.2833891 -1.3154443] [-1.02184904 1.24920112 -1.34022653 -1.3154443]]				
150				

[-4.73695157e-16 -7.81597009e-16 -4.26325641e-16 -4.73695157e-16]				
Covariance matrix				
[[1. -0.11756978 0.87175378 0.81794113] [-0.11756978 1. -0.4284401 -0.36612593] [0.87175378 -0.4284401 1. 0.96286543] [0.81794113 -0.36612593 0.96286543 1.]]				

	PC1	PC2	species
0	-2.264703	-0.480027	Setosa
1	-2.080961	0.674134	Setosa
2	-2.364229	0.341908	Setosa
3	-2.299384	0.597395	Setosa
4	-2.389842	-0.646835	Setosa



```
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
```

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

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

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

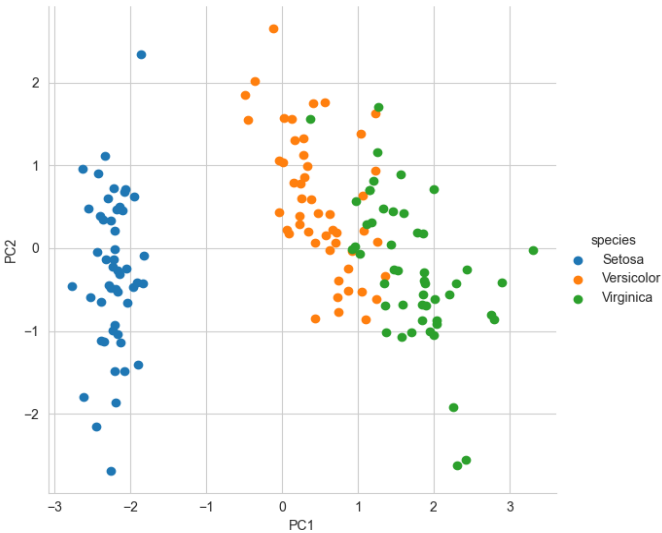
	Age	Sex	Cholesterol	Na_to_K	Drug	BP_HIGH	BP_LOW	BP_NORMAL
0	23	0	1	25.355	1	1	0	0
1	47	1	1	13.093	2	0	1	0
2	47	1	1	10.114	2	0	1	0
3	28	0	1	7.798	3	0	0	1
4	61	0	1	18.043	1	0	1	0

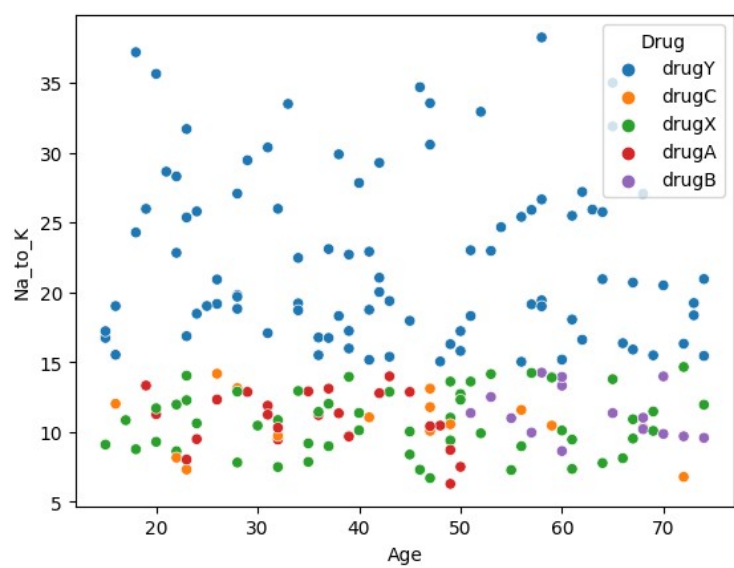
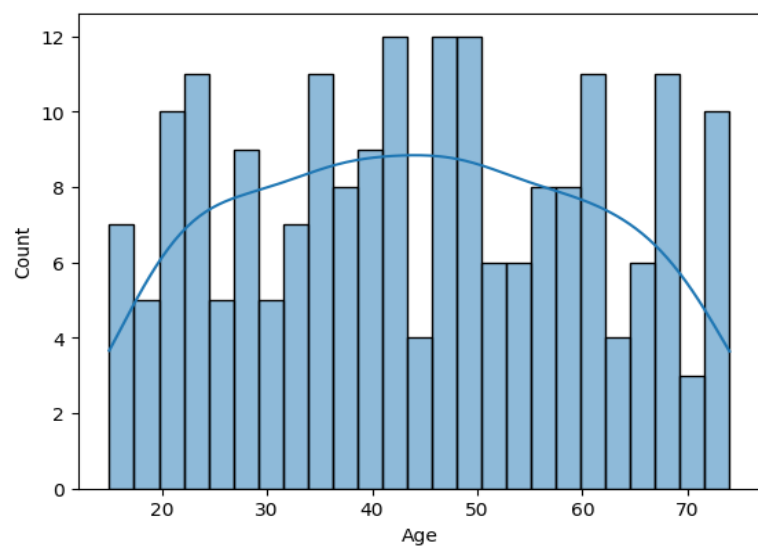
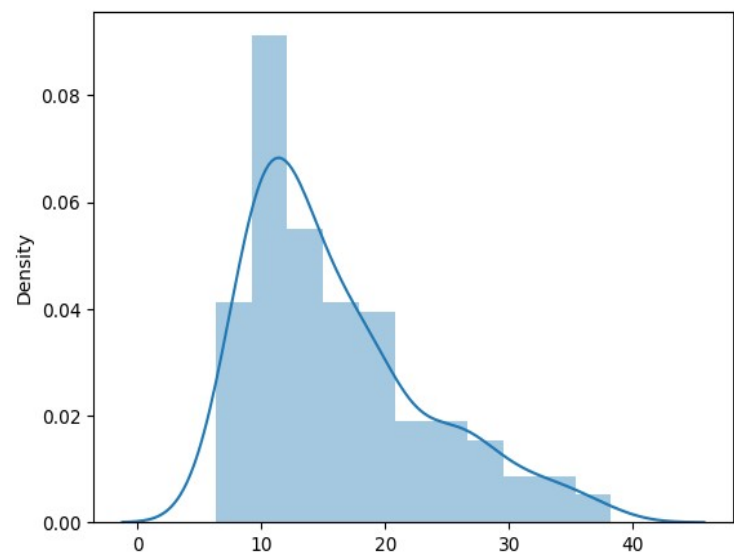
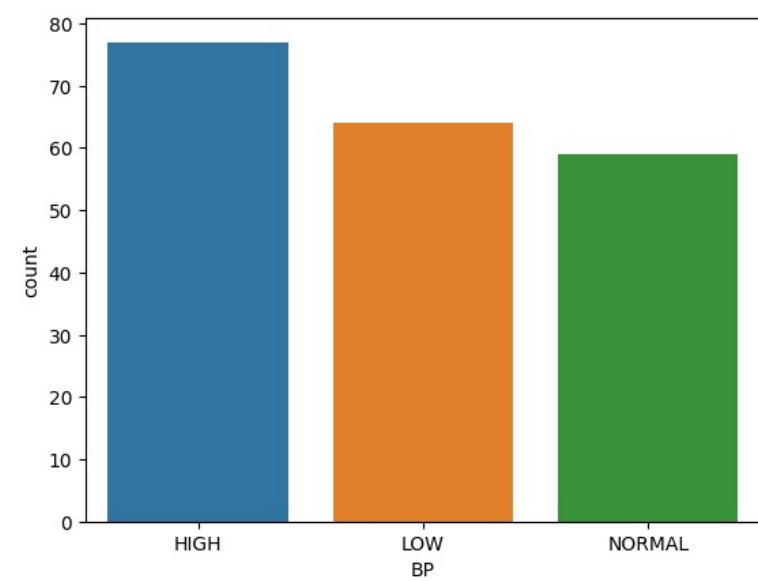
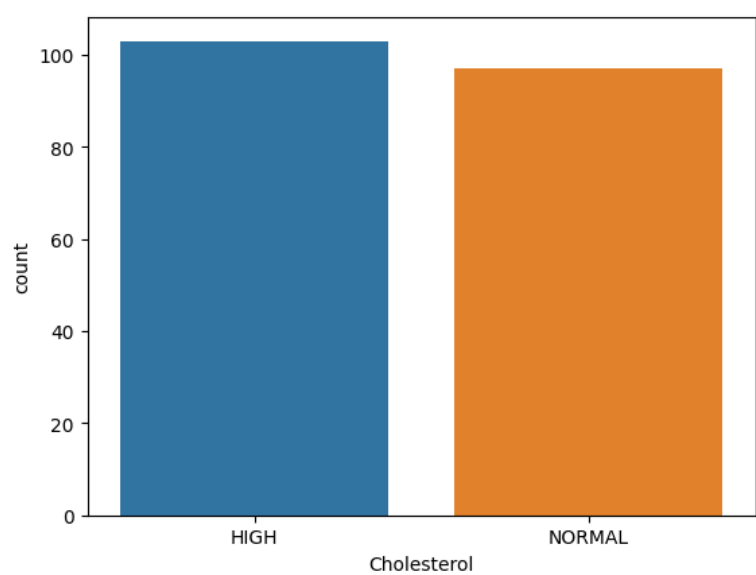
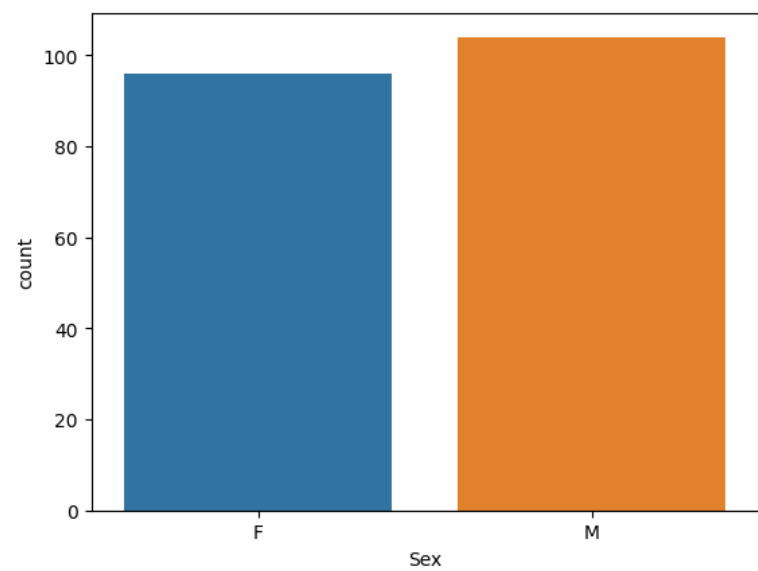
(200, 6)

(200, 8)

86.875
62.5

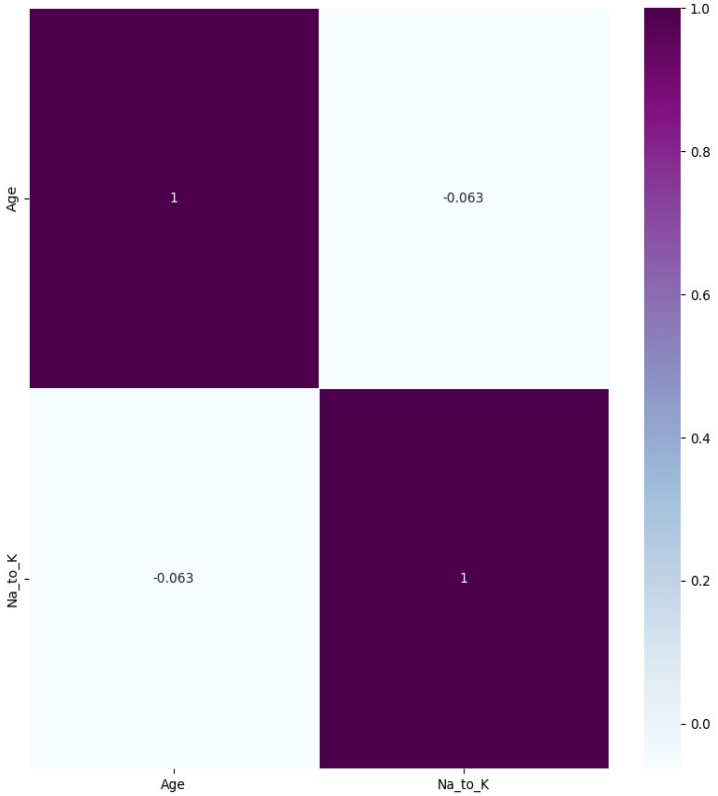
```
x train shape (160, 7)
x test shape (40, 7)
y train shape (160, 1)
y test shape (40, 1)
```





	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

```
<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
```



```
drugY    91
drugX    54
drugA    23
drugC    16
drugB    16
Name: Drug, dtype: int64
```

```
Age      0
Sex      0
BP       0
Cholesterol  0
Na_to_K  0
Drug     0
dtype: int64
```

```
HIGH    103
NORMAL   97
Name: Cholesterol, dtype: int64
```

```
HIGH    77
LOW     64
NORMAL  59
Name: BP, dtype: int64
```

