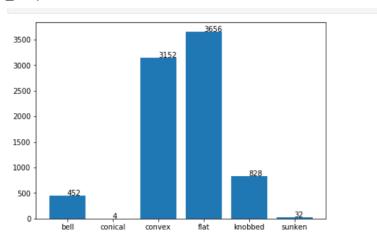
2.data visualization (hw1_1.py,hw1_2.py):

hw1_1.py 因為要畫圖過多,所以有 warning,但是圖都有畫出來, 在我的電腦上跑也只須等個幾秒就好。

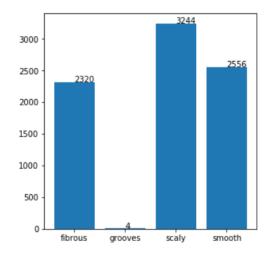
Mushroom dataset:

Value frequency of every feature:

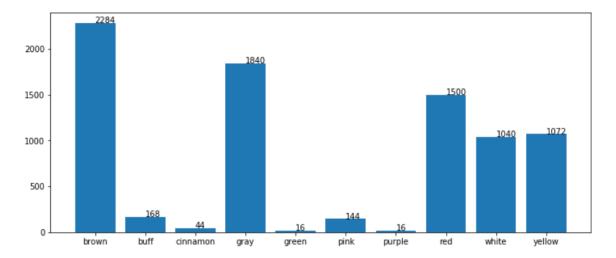
Cap_shape



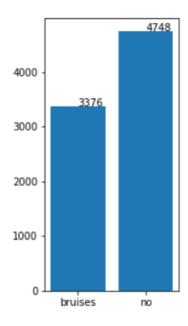
Cap_surface:



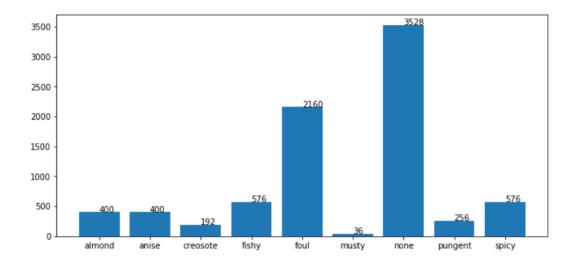
Cap_color:



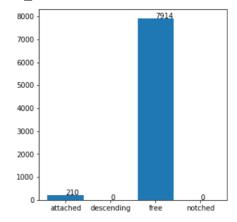
Bruises:



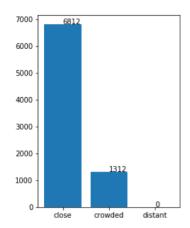
Odor:



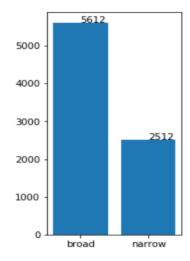
Gill_attachment:



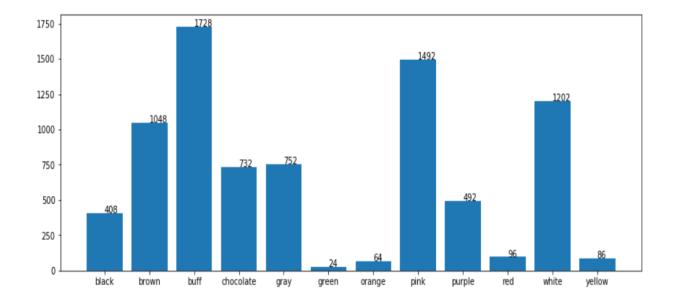
gill-spacing:



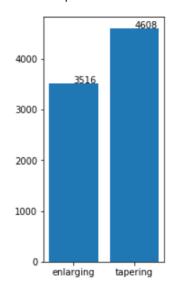
gill-size:



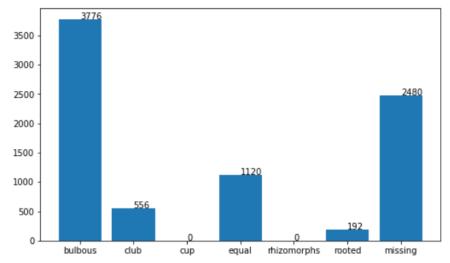
gill-color:



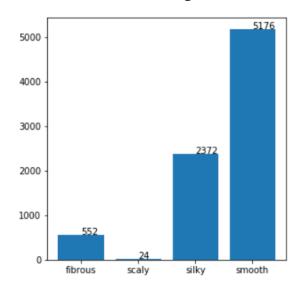
stalk-shape:



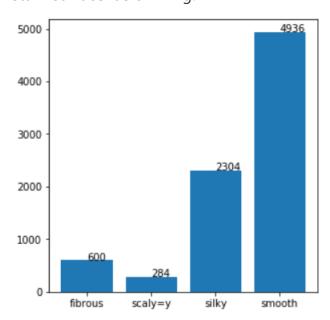
stalk-root:



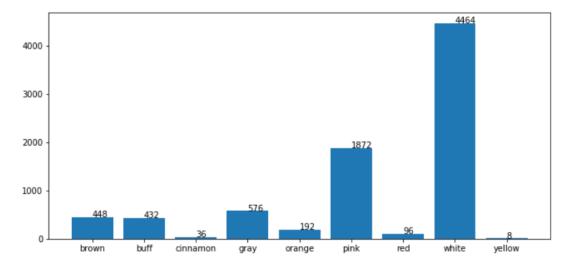
stalk-surface-above-ring:



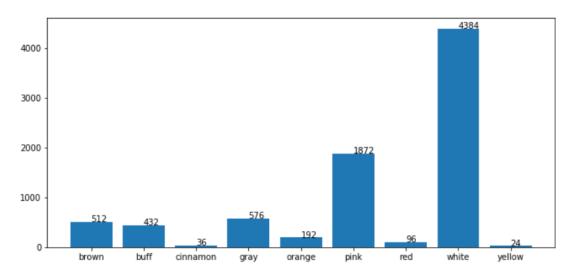
stalk-surface-below-ring:



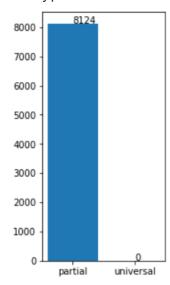
stalk-color-above-ring:



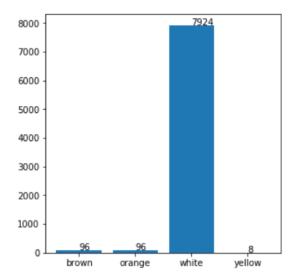
stalk-color-below-ring:



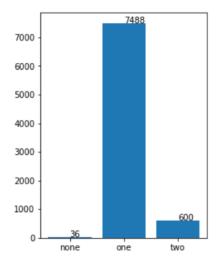
veil-type:



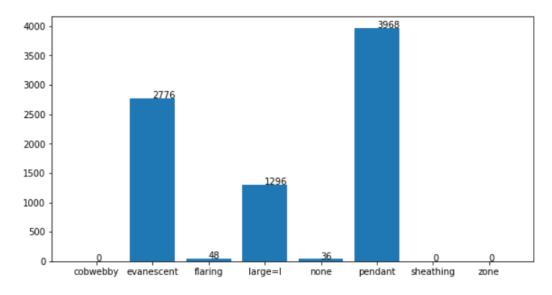
veil-color:



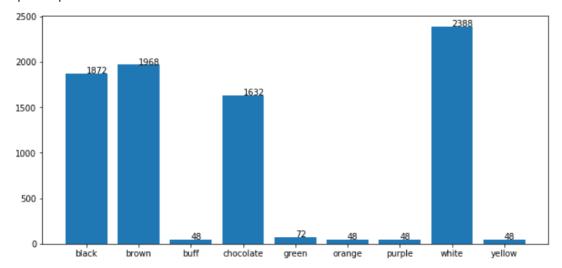
ring-number:



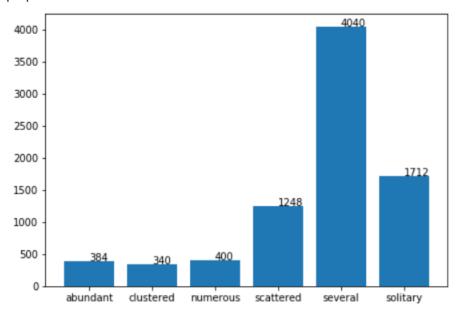
ring-type:



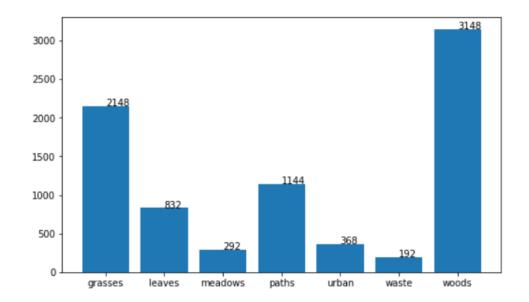
spore-print-color:



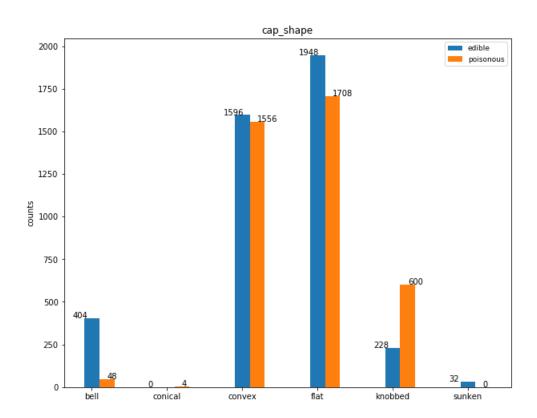
population:

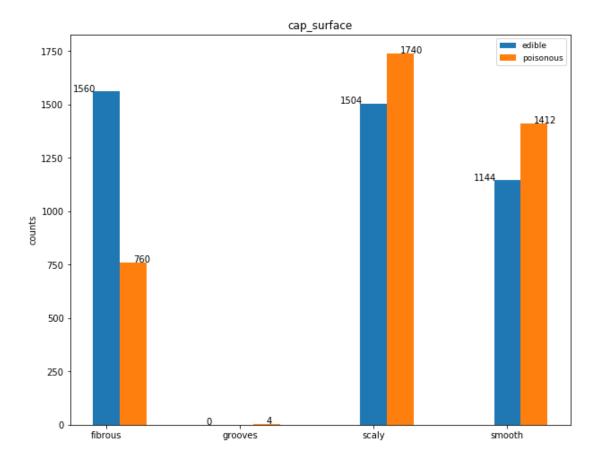


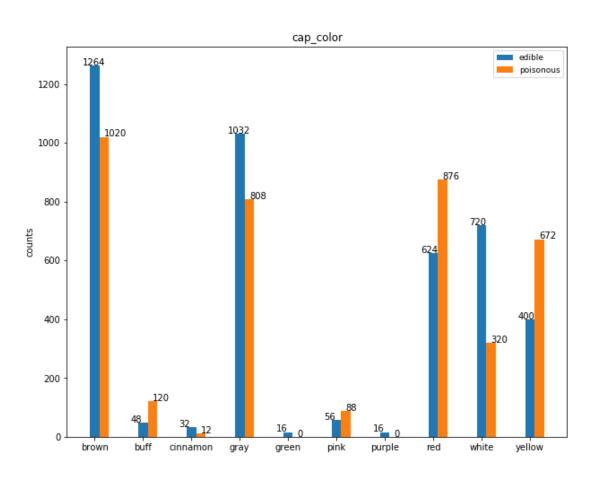
habitat:

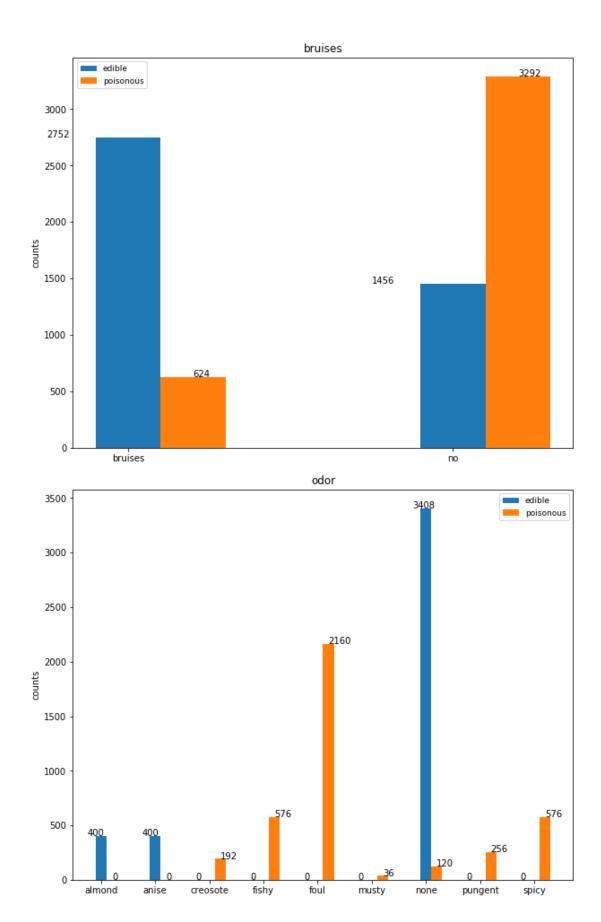


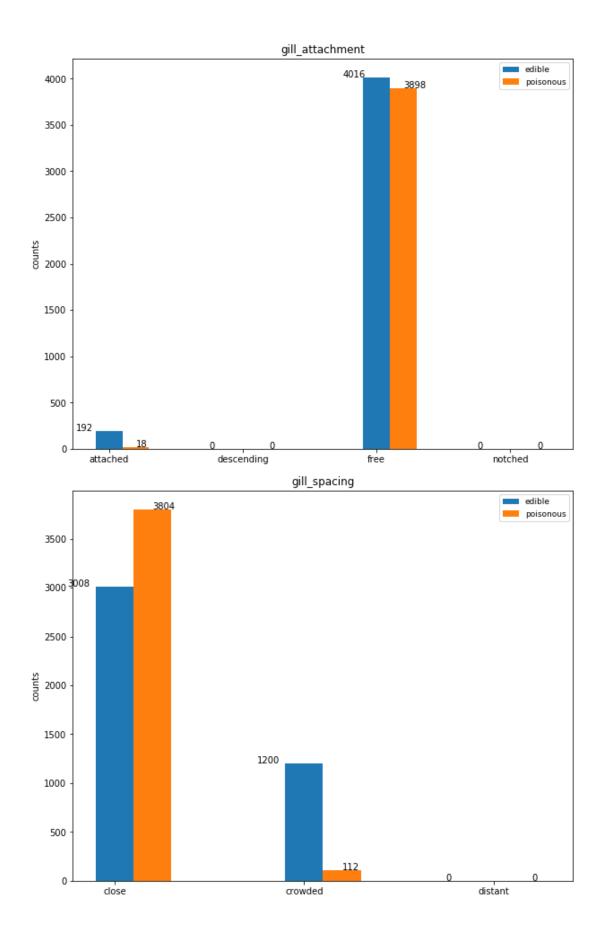
Mushroom :split data based on their labels and show the data distribution again:

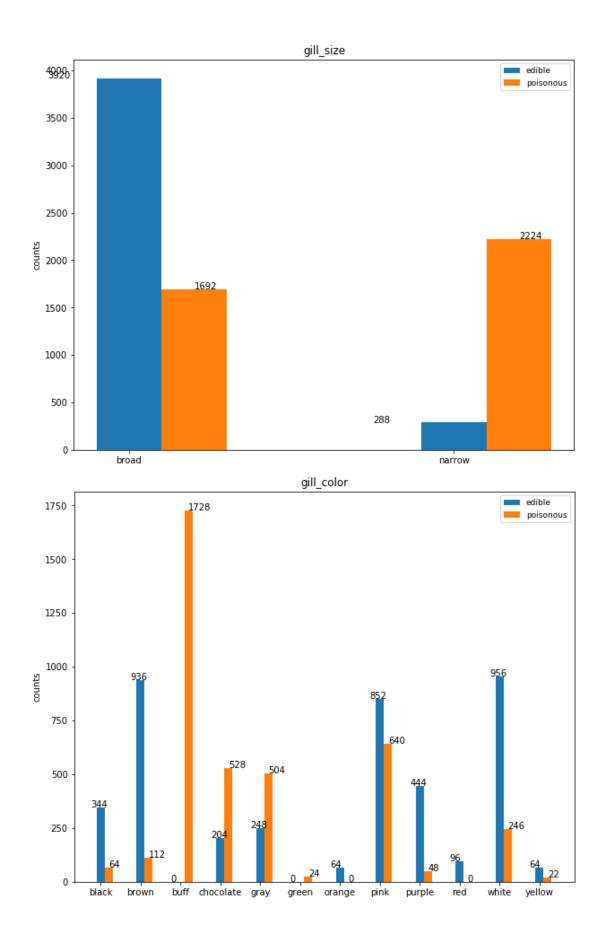


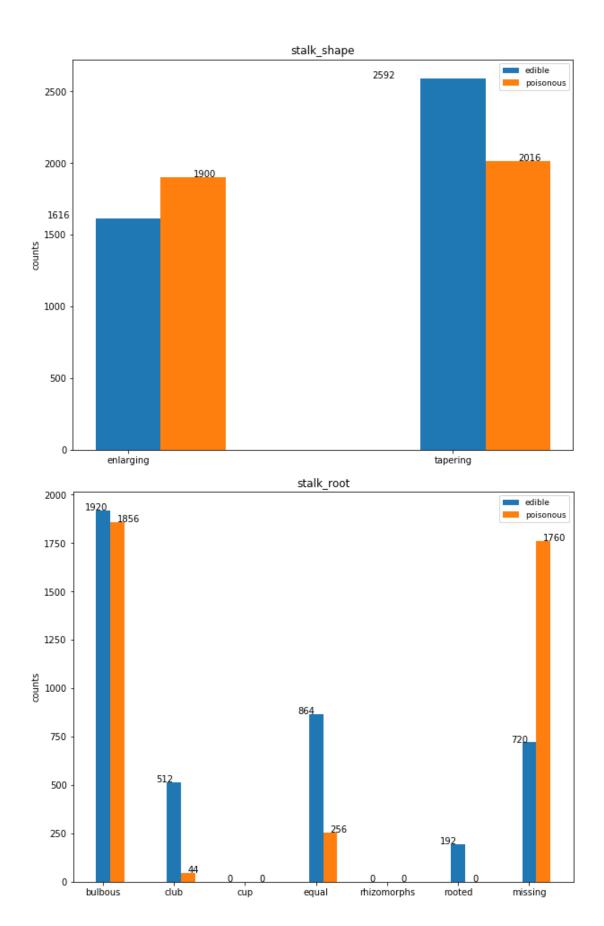


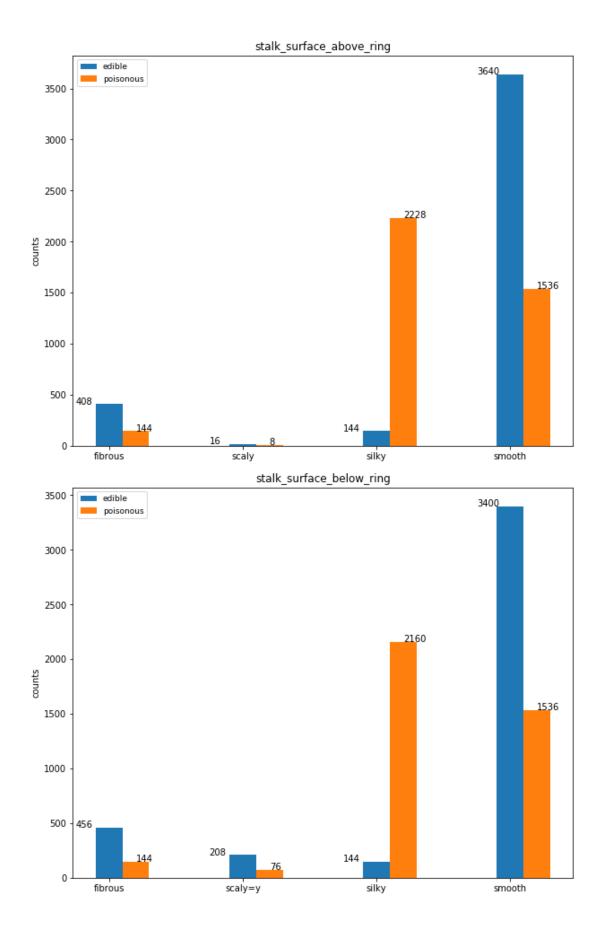


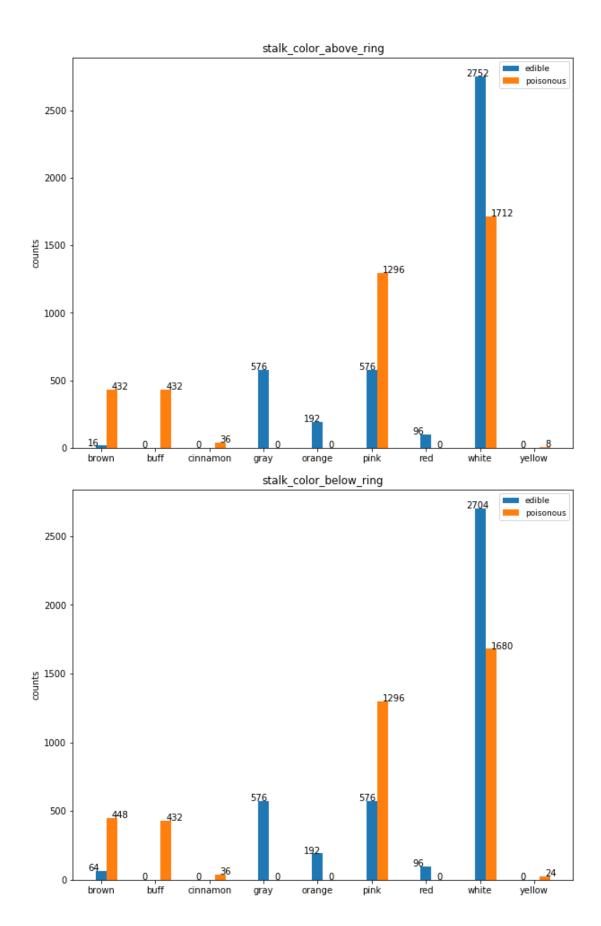


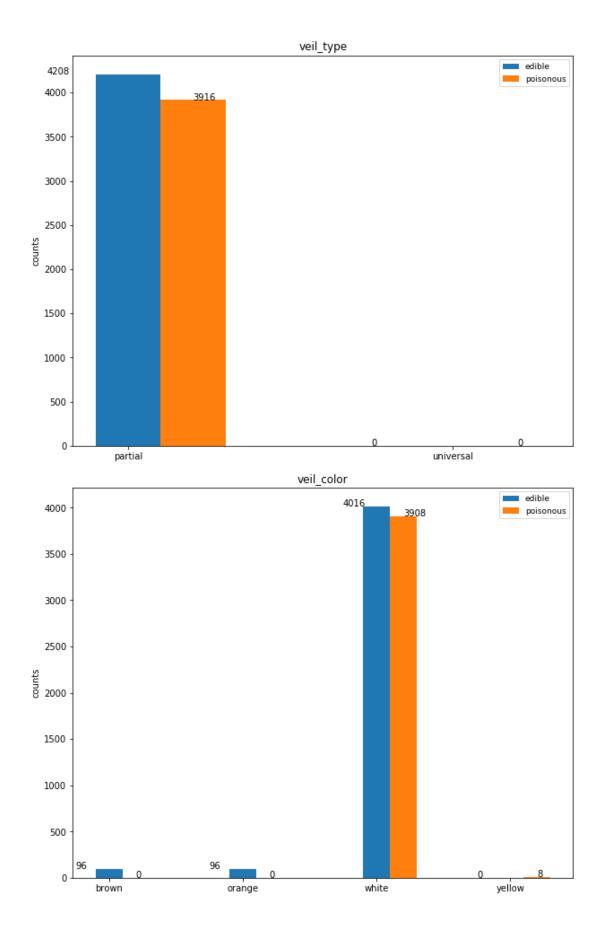


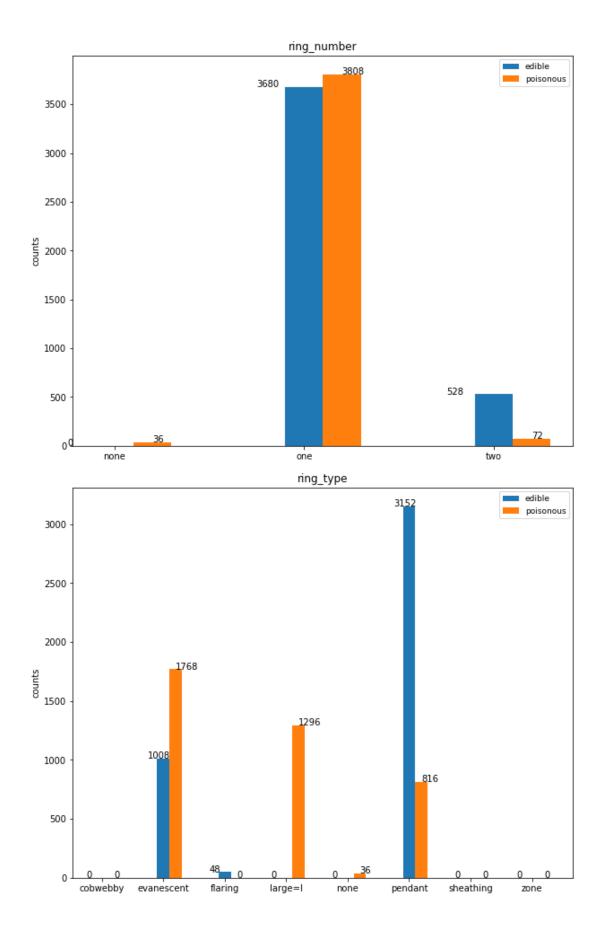


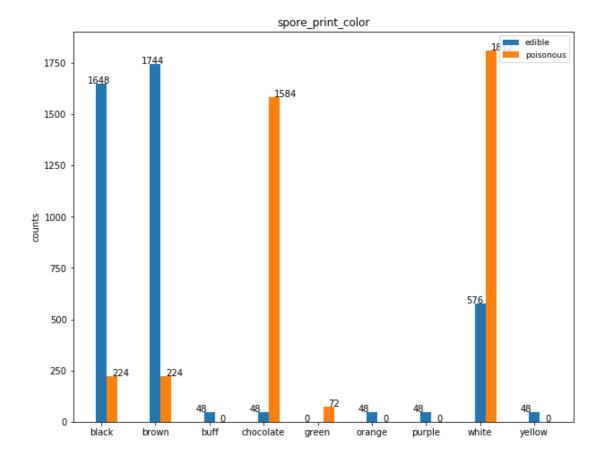


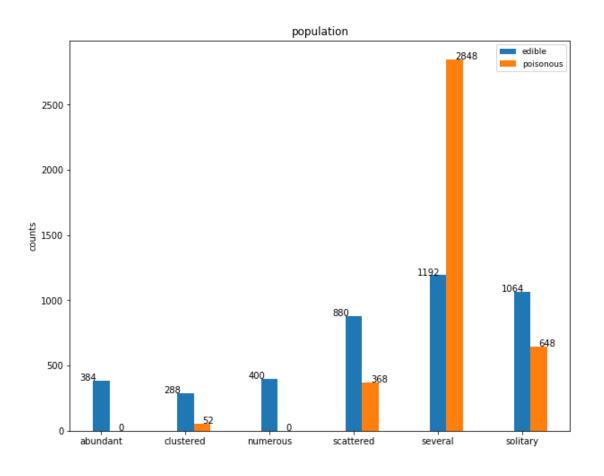


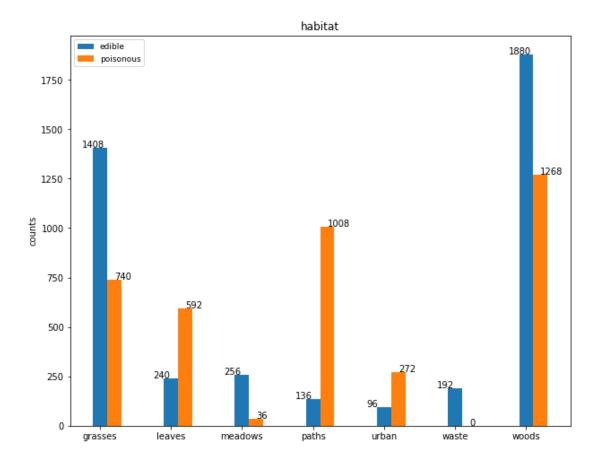






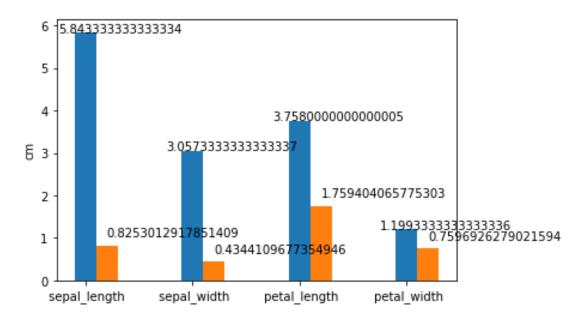




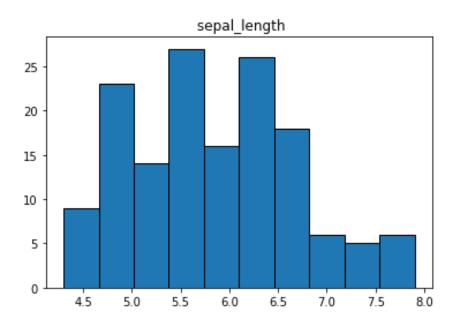


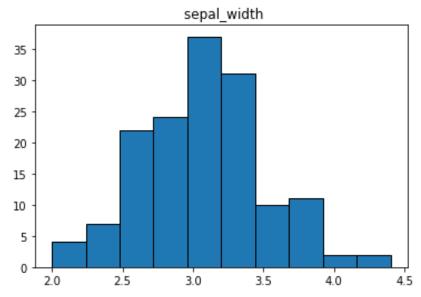
Iris dataset:

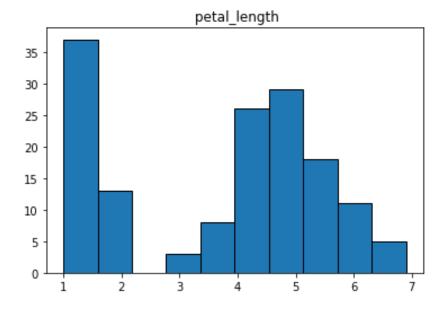
Blue: average orange: standard deviation

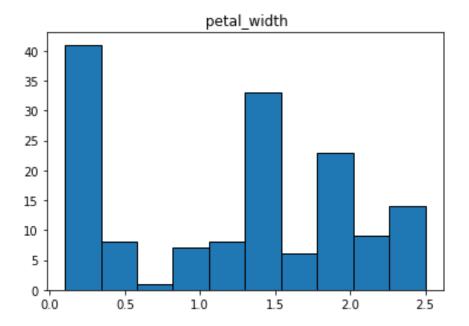


Value frequency of each feature:







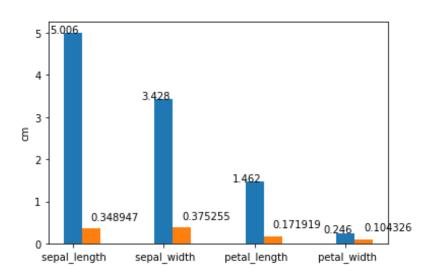


Iris dataset with split data based on their labels:

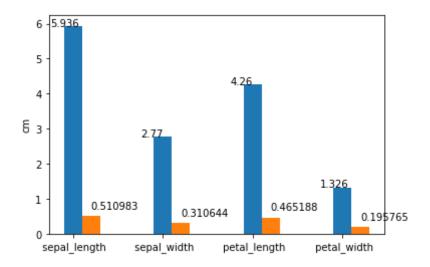
average, standard deviation:

Blue: average orange: standard deviation

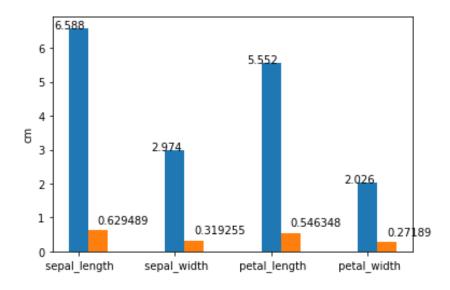
Iris-setosa:



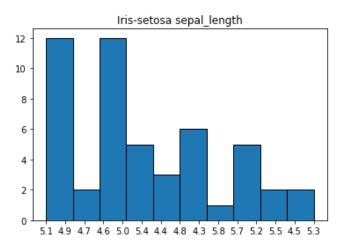
Iris-versicolor:

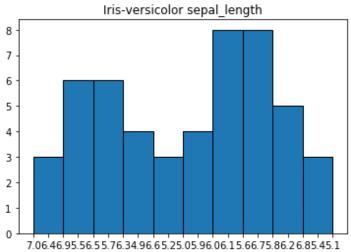


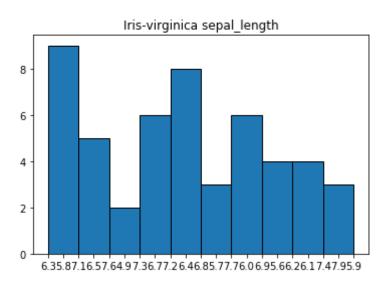
Iris-virginica

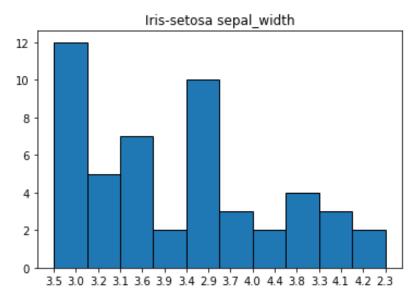


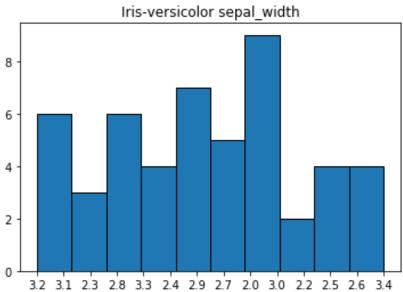
Each label's frequency:

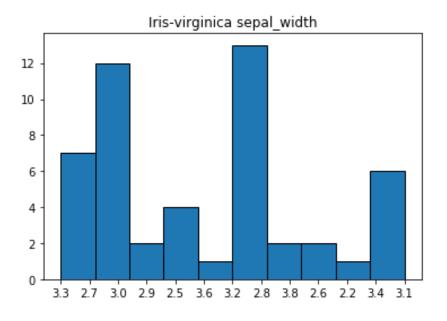


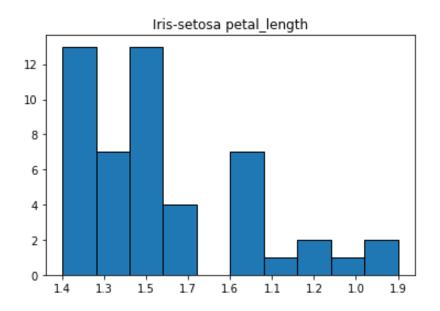


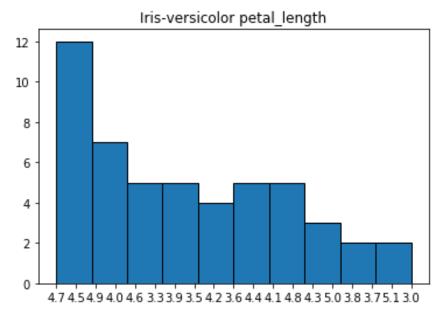


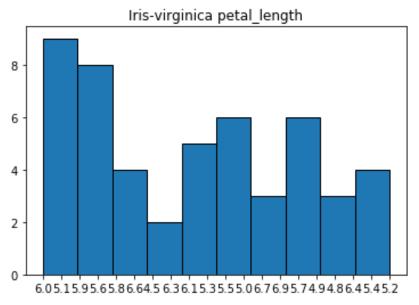


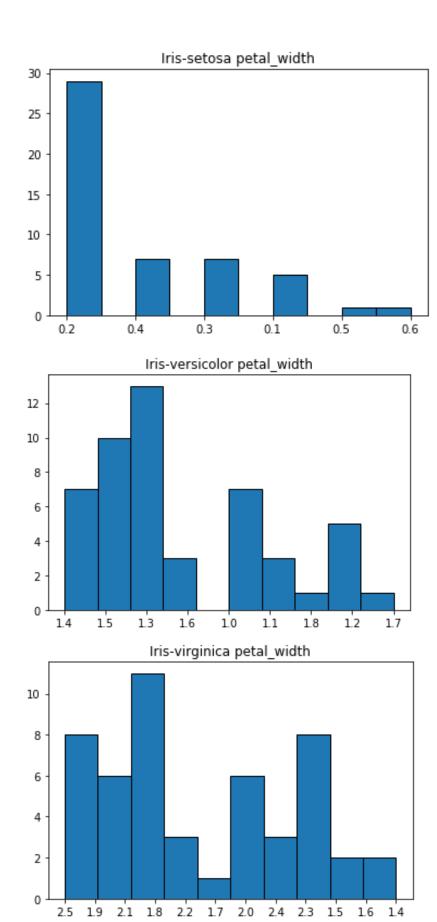












3. Data preprocessing:

Drop feature:

don't use stalk_root to bulid classfier in my code because it has missing value.

Shuffle the data:

Use random.shuffle() in python to shuffle the data.

3.Data Preprocessing+4.Model Construction +5.Train-Test-Split in code +6.**Results** hw1_3.py,hw1_4.py.

6 result:

Mushroom:

```
Holdout validation without laplace
   confusion matrix:
    1269 1
    17 1150
   Classification accuracy: 0.9926138695116947
   Sensitivity: 0.9992125984251968
   Precision: 0.9867807153965785
   Holdout validation with laplace
   confusion matrix:
    1269 79
    17 1072
   Classification accuracy: 0.9606073040623717
   Sensitivity: 0.9413946587537092
   Precision: 0.9867807153965785
   K-fold cross-validation without laplace
   confusion matrix:
    1394.666666666667 1.0
    8.0 1304.3333333333333
   Classification accuracy: 0.9966765140324964
   Sensitivity: 0.9992809104502295
   Precision: 0.9943115660075713
   K-fold cross-validation with laplace
   confusion matrix:
    1394.0 103.33333333333333
    Classification accuracy: 0.9586410635155097
   Sensitivity: 0.9310220479762409
   Precision: 0.9938374076386761
]:
```

Iris:

Above is Holdout validation with the ratio 7:3

Below is K-fold cross-validation with K=3

```
confusion matrix:
     13 0 0
     0 16 1
     0 2 13
    Classification accuracy: 0.9333333333333333
    setosa_sensitivity: 1.0
    versicolor_sensitivity: 0.9411764705882353
    virginica_sensitivity: 0.8666666666666667
    setosa precession: 1.0
    virginica_precession: 0.9285714285714286
    confusion matrix:
     16.6666666666668 0.0 0.0
     Classification accuracy: 0.6733333333333335
    setosa sensitivity: 1.0
    versicolor_sensitivity: 0.9400000000000001
    virginica_sensitivity: 0.5
    setosa_precession: 1.0
    versicolor_precession: 0.9215686274509803
    virginica_precession: 0.5714285714285715
[]:
```

7. Comparison & Conclusion:

如果有做 laplace smoothing 準確度會下降,但是可以處理 train data feature 中有項目為 0 的情況,K-fold cross-validation 跟 Holdout validation 起來多了小數點,因為它是多次平均綜合,感覺 結果比較讓人信服。