Project_3_Weihua_PAN

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IE 7300: Statistical learning for Engineering

Project check point #3

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Percentage of Effort Contributed by Student : 100% Signature of Student : Weihua Pan Submission Date: 11/28/2023

[1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt

pd.set_option('display.max_columns',30)
```

1 a) Problem Statement

1.1 Clearly define the problem statement

Problem statement : To determine whether some features of Mushroom,such as `cap diameter`, `cap shape` and `cap color`,can be used to predict its edibility.

1.2 State your hypothesis

Hypothesis : Mushrooms with specify feature characteristic are more likely to be edible or poisonous.

2 Dataset

2.1 Present the dataset and include a data dictionary

[2]:
```
df = pd.read_csv("MushroomDataset/secondary_data.csv",sep=";")
df.info()
df.head()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 61069 entries, 0 to 61068
```

```
Data columns (total 21 columns):
 #   Column                Non-Null Count  Dtype
---  ------                --------------  -----
 0   class                 61069 non-null  object
 1   cap-diameter          61069 non-null  float64
 2   cap-shape             61069 non-null  object
 3   cap-surface           46949 non-null  object
 4   cap-color             61069 non-null  object
 5   does-bruise-or-bleed  61069 non-null  object
 6   gill-attachment       51185 non-null  object
 7   gill-spacing          36006 non-null  object
 8   gill-color            61069 non-null  object
 9   stem-height           61069 non-null  float64
 10  stem-width            61069 non-null  float64
 11  stem-root             9531 non-null   object
 12  stem-surface          22945 non-null  object
 13  stem-color            61069 non-null  object
 14  veil-type             3177 non-null   object
 15  veil-color            7413 non-null   object
 16  has-ring              61069 non-null  object
 17  ring-type             58598 non-null  object
 18  spore-print-color     6354 non-null   object
 19  habitat               61069 non-null  object
 20  season                61069 non-null  object
dtypes: float64(3), object(18)
memory usage: 9.8+ MB
```

[2]:

```
  class  cap-diameter cap-shape cap-surface cap-color does-bruise-or-bleed  \
0     p         15.26         x           g         o                    f
1     p         16.60         x           g         o                    f
2     p         14.07         x           g         o                    f
3     p         14.17         f           h         e                    f
4     p         14.64         x           h         o                    f

  gill-attachment gill-spacing gill-color  stem-height  stem-width stem-root  \
0               e          NaN          w        16.95       17.09         s
1               e          NaN          w        17.99       18.19         s
2               e          NaN          w        17.80       17.74         s
3               e          NaN          w        15.77       15.98         s
4               e          NaN          w        16.53       17.20         s

  stem-surface stem-color veil-type veil-color has-ring ring-type  \
0            y          w         u          w        t         g
1            y          w         u          w        t         g
2            y          w         u          w        t         g
3            y          w         u          w        t         p
4            y          w         u          w        t         p
```

```
  spore-print-color habitat season
0               NaN       d      w
1               NaN       d      u
2               NaN       d      w
3               NaN       d      w
4               NaN       d      w
```

The dataset contains 61069 rows and 21 columns. The target variable is class (e or p).

[3]:
```python
df.select_dtypes(include='object')
```

[3]:
```
      class cap-shape cap-surface cap-color does-bruise-or-bleed  \
0         p         x           g         o                    f
1         p         x           g         o                    f
2         p         x           g         o                    f
3         p         f           h         e                    f
4         p         x           h         o                    f
…       …         …           …         …                    …
61064     p         s           s         y                    f
61065     p         f           s         y                    f
61066     p         s           s         y                    f
61067     p         f           s         y                    f
61068     p         s           s         y                    f

      gill-attachment gill-spacing gill-color stem-root stem-surface  \
0                   e          NaN          w         s            y
1                   e          NaN          w         s            y
2                   e          NaN          w         s            y
3                   e          NaN          w         s            y
4                   e          NaN          w         s            y
…                   …            …          …         …            …
61064               f            f          f       NaN          NaN
61065               f            f          f       NaN          NaN
61066               f            f          f       NaN          NaN
61067               f            f          f       NaN          NaN
61068               f            f          f       NaN          NaN

      stem-color veil-type veil-color has-ring ring-type spore-print-color  \
0              w         u          w        t         g               NaN
1              w         u          w        t         g               NaN
2              w         u          w        t         g               NaN
3              w         u          w        t         p               NaN
4              w         u          w        t         p               NaN
…            …         …          …        …         …                 …
61064          y       NaN        NaN        f         f               NaN
61065          y       NaN        NaN        f         f               NaN
```

```
61066          y       NaN        NaN       f         f                NaN
61067          y       NaN        NaN       f         f                NaN
61068          y       NaN        NaN       f         f                NaN

      habitat season
0           d      w
1           d      u
2           d      w
3           d      w
4           d      w
…         …     …
61064       d      a
61065       d      a
61066       d      u
61067       d      u
61068       d      u

[61069 rows x 18 columns]
```

17 of them are categorical feature :['cap-shape', 'cap-surface', 'cap-color', 'does-bruise-or-bleed', 'gill-attachment', 'gill-spacing', 'gill-color', 'stem-root', 'stem-surface', 'stem-color', 'veil-type', 'veil-color', 'has-ring', 'ring-type', 'spore-print-color', 'habitat', 'season'] I will do one-hot-encode later.

[4]:
```
df.select_dtypes(include='number')
```

[4]:
```
       cap-diameter  stem-height  stem-width
0             15.26        16.95       17.09
1             16.60        17.99       18.19
2             14.07        17.80       17.74
3             14.17        15.77       15.98
4             14.64        16.53       17.20
…               …           …         …
61064          1.18         3.93        6.22
61065          1.27         3.18        5.43
61066          1.27         3.86        6.37
61067          1.24         3.56        5.44
61068          1.17         3.25        5.45

[61069 rows x 3 columns]
```

3 of them are numerical: ['cap-diameter', 'stem-height', 'stem-width'].

2.1.1 Dataset Dictionary

Target variable: `class` divided in edible=e and poisonous=p n: nominal, m: metrical 1. cap-diameter (m): float number in cm 2. cap-shape (n): * bell=b, * conical=c, * convex=x, * flat=f, * sunken=s, * spherical=p, * others=o 3. cap-surface (n): * fibrous=i, * grooves=g, * scaly=y, * smooth=s, * shiny=h, * leathery=l, * silky=k, * sticky=t, * wrinkled=w, * fleshy=e 4. cap-color (n): * brown=n, * buff=b, * gray=g, * green=r, * pink=p, * purple=u, * red=e, * white=w, * yellow=y, * blue=l, * orange=o, * black=k 5. does-bruise-bleed (n): * bruises-or-bleeding=t, * no=f 6. gill-attachment (n): * adnate=a, * adnexed=x, * decurrent=d, * free=e, * sinuate=s, * pores=p, * none=f, * unknown=? 7. gill-spacing (n): * close=c, * distant=d, * none=f 8. gill-color (n): * see cap-color + * none=f 9. stem-height (m): float number in cm 10. stem-width (m): float number in mm 11. stem-root (n): * bulbous=b, * swollen=s, * club=c, * cup=u, * equal=e, * rhizomorphs=z, * rooted=r 12. stem-surface (n): see cap-surface + none=f 13. stem-color (n): see cap-color + none=f 14. veil-type (n): partial=p, universal=u 15. veil-color (n): see cap-color + none=f 16. has-ring (n): * ring=t, * none=f 17. ring-type (n): * cobwebby=c, * evanescent=e, * flaring=r, * grooved=g, * large=l, * pendant=p, * sheathing=s, * zone=z, * scaly=y, * movable=m, * none=f, * unknown=? 18. spore-print-color (n): see cap color 19. habitat (n): * grasses=g, * leaves=l, * meadows=m, * paths=p, * heaths=h, * urban=u, * waste=w, * woods=d 20. season (n): * spring=s, * summer=u, * autumn=a, * winter=w

Most of the columns are categorical, so I need to do one-hot-encoding for these categorical data in order to train a model

2.2 Explain how this dataset supports your hypothesis

[5]:
```
# split mushrooms df into poison and edible df.
poison = df[df['class']=='p']
edible = df[df['class']=='e']
```

[6]:
```
print(poison.shape)
print(edible.shape)
```

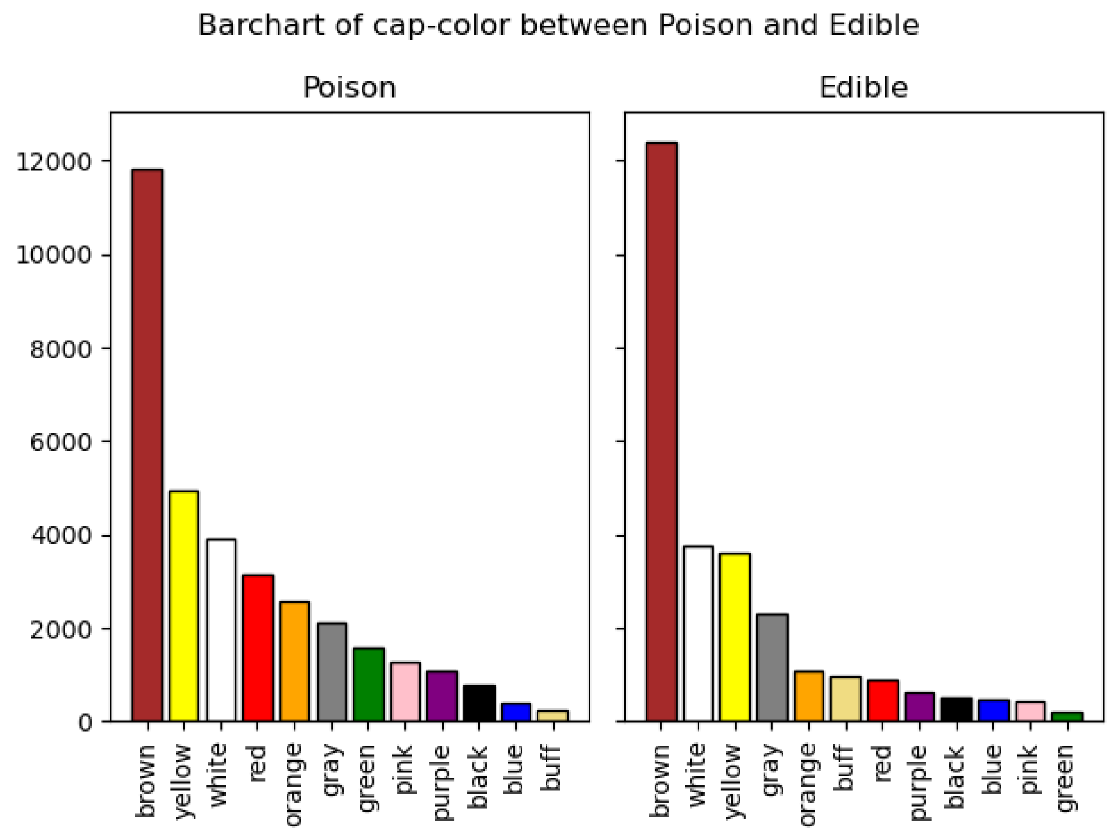
```
(33888, 21)
(27181, 21)
```

[7]:
```
p_color = poison['cap-color'].value_counts().index
p_counts = poison['cap-color'].value_counts().values
e_color = edible['cap-color'].value_counts().index
e_counts = edible['cap-color'].value_counts().values
```

[8]:
```
color_code = {"n":"brown",
             "b":"#f0dc82", #buff
             "g":"gray",
             "r":"green",
             "p":"pink",
             "u":"purple",
             "e":"red",
             "w":"white",
             "y":"yellow",
             "l":"blue",
             "o":"orange",
             "k":"black"}
```

[9]:
```
color_map = {"n":"brown",
             "b":"buff", #buff
             "g":"gray",
             "r":"green",
             "p":"pink",
             "u":"purple",
             "e":"red",
             "w":"white",
             "y":"yellow",
             "l":"blue",
             "o":"orange",
             "k":"black"}
```

[10]:
```
import warnings
warnings.filterwarnings('ignore')

fig,ax = plt.subplots(1,2,sharey=True)

ax[0].bar([color_map[c] for c in p_color],p_counts,color=[color_code[code] for␣
 ↪code in p_color],
          edgecolor='black')
ax[0].set_title('Poison')

#
ax[1].bar([color_map[c] for c in e_color],e_counts,color=[color_code[code] for␣
 ↪code in e_color],
          edgecolor='black')
ax[1].set_title('Edible')

# rotate xlabels
ax[0].set_xticklabels([color_map[c] for c in p_color],rotation=90)
ax[1].set_xticklabels([color_map[c] for c in e_color],rotation=90)

fig.suptitle("Barchart of cap-color between Poison and Edible")
plt.tight_layout()
plt.show()
```



Using `cap-color` and other features, we are able to find some pattern to classify base on these features. For example, From the above plot, We can see most green and red mushroom are poisonous. In addition, the most common color is brown for both poison and edible mushrooms, Therefore, it might be tough to use brown to classify whether a mushroom is poisonous or edible.

3 Exploratory Data Analysis(EDA)

3.1 Descriptive Statistics

[11]:
```
df.describe()
```

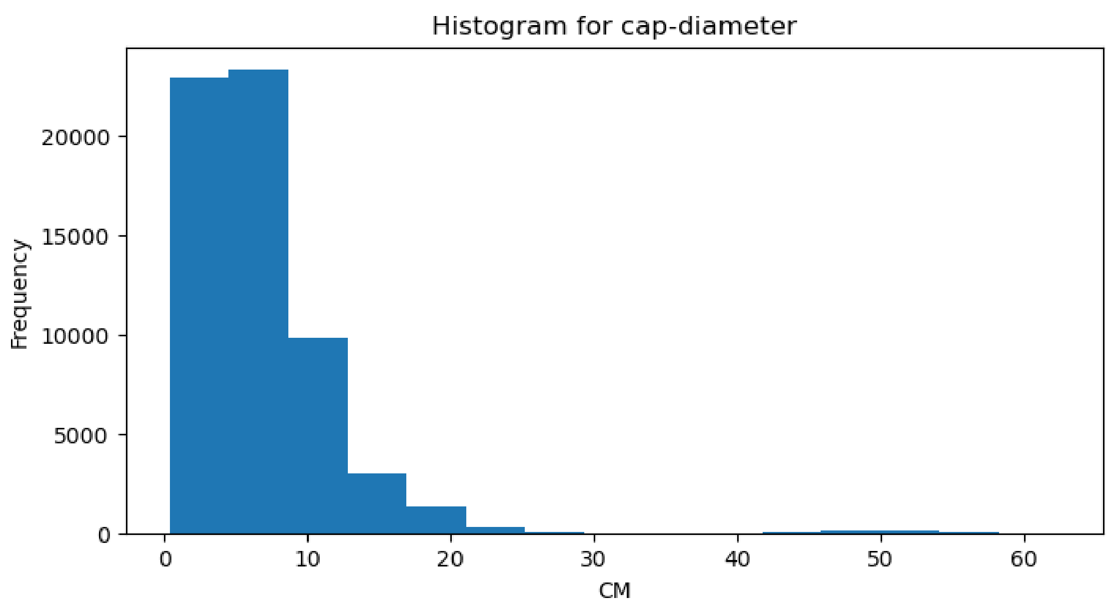
[11]:

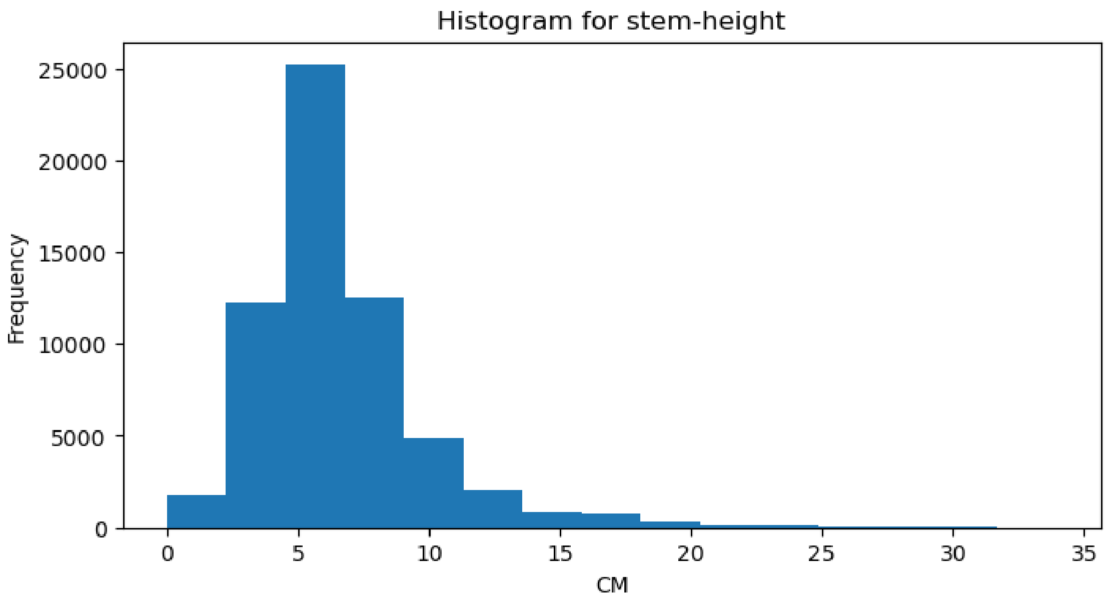
	cap-diameter	stem-height	stem-width
count	61069.000000	61069.000000	61069.000000
mean	6.733854	6.581538	12.149410
std	5.264845	3.370017	10.035955
min	0.380000	0.000000	0.000000
25%	3.480000	4.640000	5.210000
50%	5.860000	5.950000	10.190000
75%	8.540000	7.740000	16.570000
max	62.340000	33.920000	103.910000

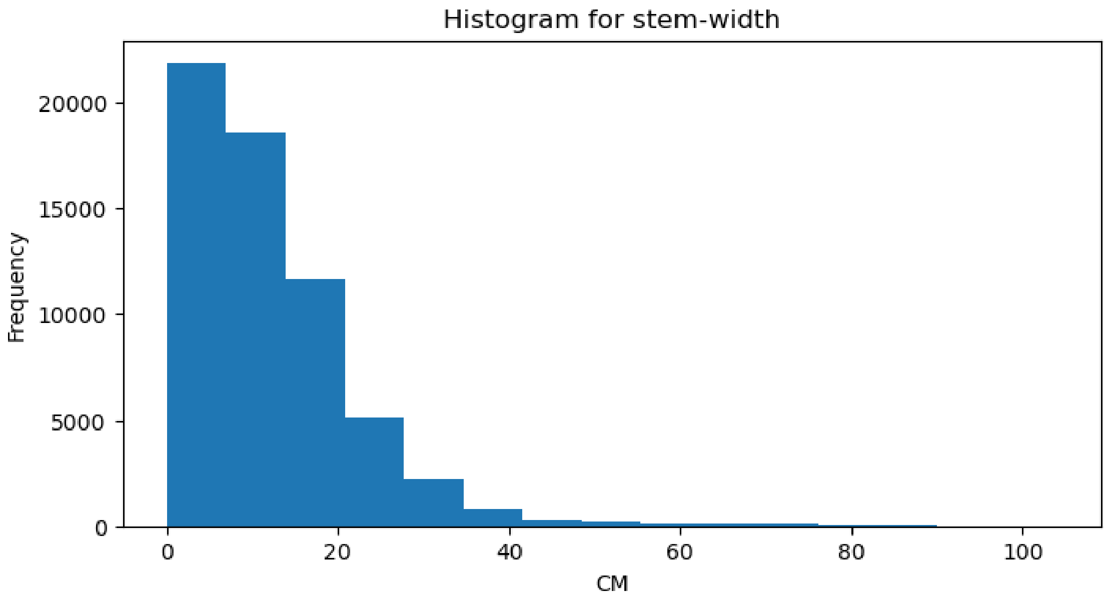
Only 3 columns are numerical. 1. cap-diameter: * min: 0.38 cm * max: 62.34 cm * mean 6.7 cm 2. stem-height: * min: 0 cm * max: 33.92 cm * mean 6.58 cm 3. stem-width: * min: 0 cm * max: 103.91 cm * mean: 10.03 cm

Base on the basic statistic, I can take a guess `cap-diameter` and `stem-height` are in right skewed, and `stem-width` is about normal by mean and 50% quartile. And they all have some outliers. I will consider whether remove them later.

[12]:
```
# draw histogram for all numerical columns
numerical_columns = df.select_dtypes(include='number')

for column in numerical_columns:
    fig, ax = plt.subplots(figsize=(8, 4))
    df[column].plot(kind='hist', title=f"Histogram for {column}", ax=ax,bins=15)
    ax.set_xlabel("CM")
    plt.show()
```



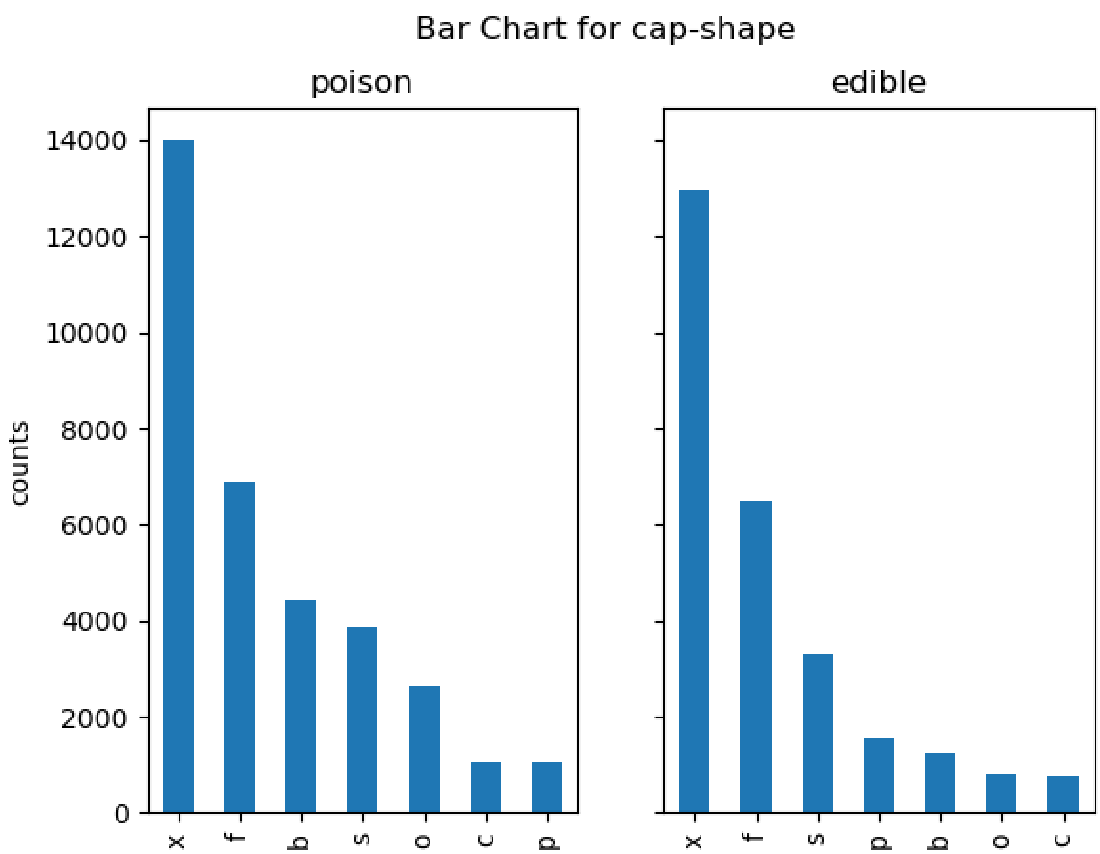


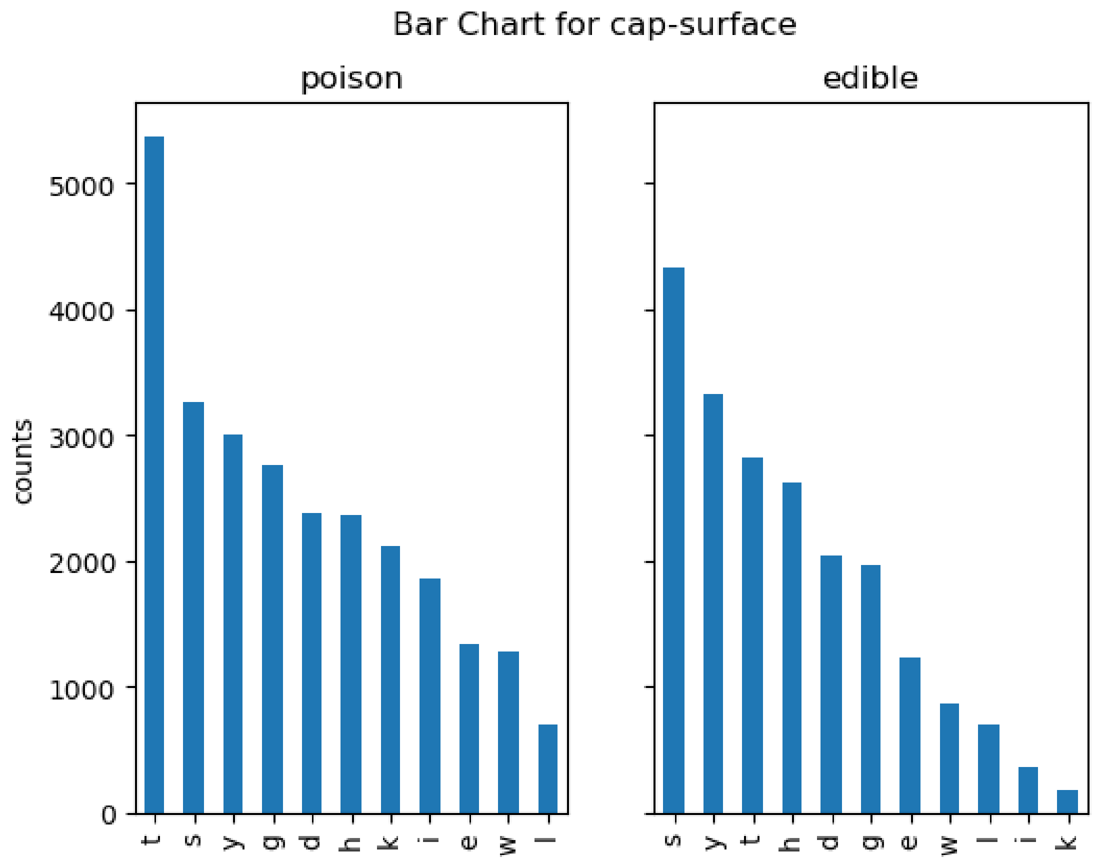


By the histogram plot, we can see `cap-diameter` and `stem-width` are right skewed. And only `stem-height` is normal distributive.

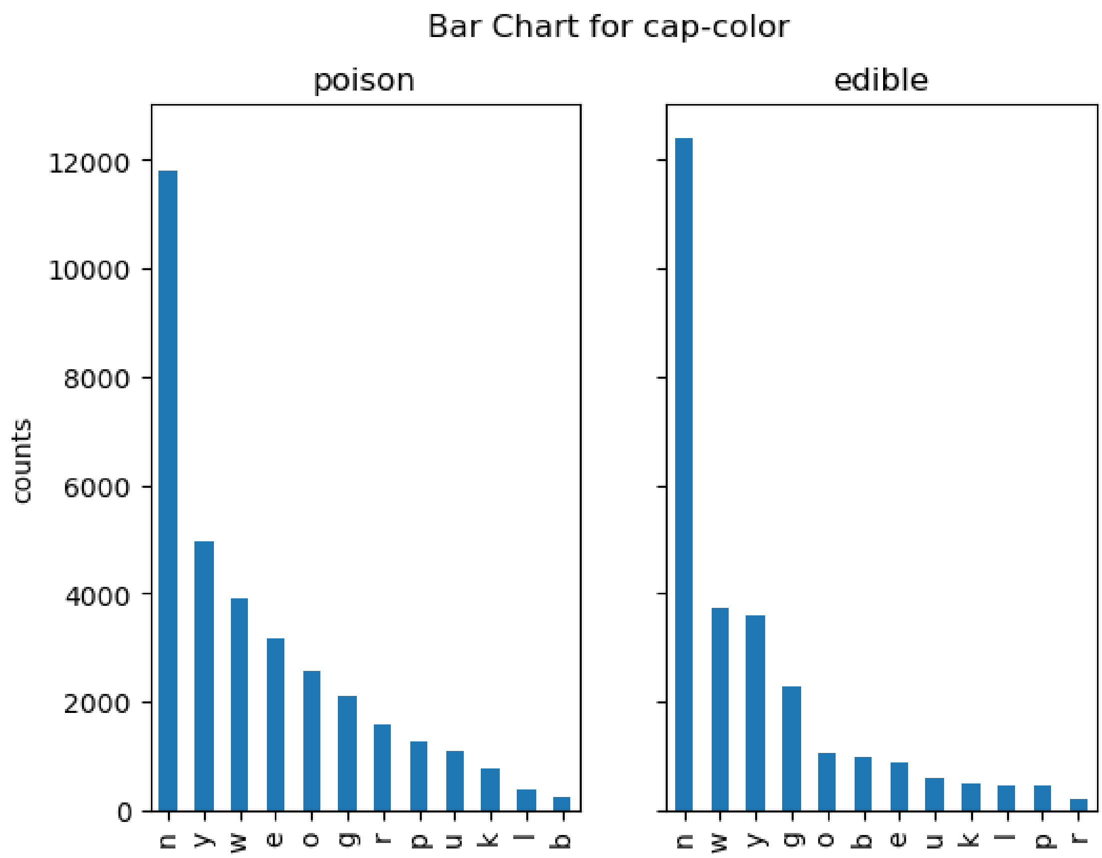
3.2 Bar chart among 2 target variables

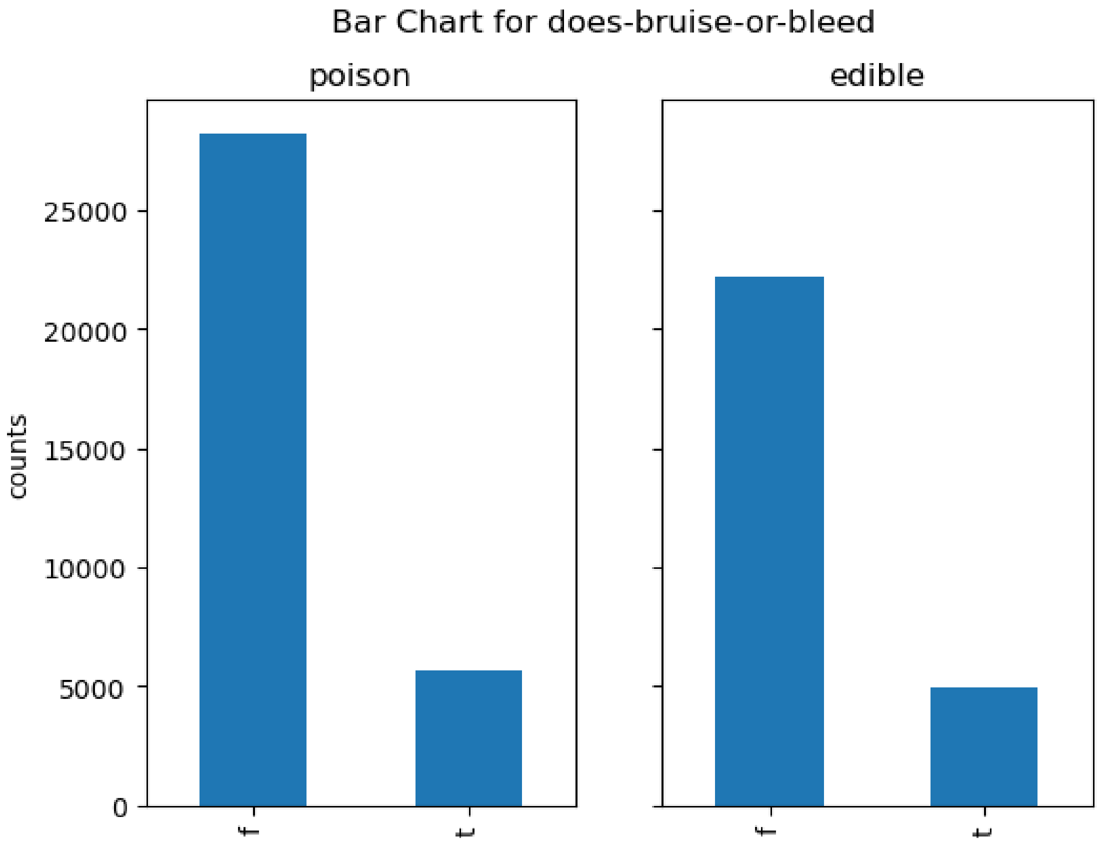
[13]:
```
object_columns = df.select_dtypes(include=['object']).columns[1:]

for column in object_columns:
    # Count the occurrences of each category
    poison_C = poison[column].value_counts()
    edible_C = edible[column].value_counts()

    # Create a subplot chart
    fig,ax = plt.subplots(1,2,sharey=True)

    poison_C.plot(kind='bar',ax=ax[0],title='poison',ylabel='counts')
    edible_C.plot(kind='bar',ax=ax[1],title='edible')



    fig.suptitle(f'Bar Chart for {column}')

    # Show the plot
    plt.show()
```

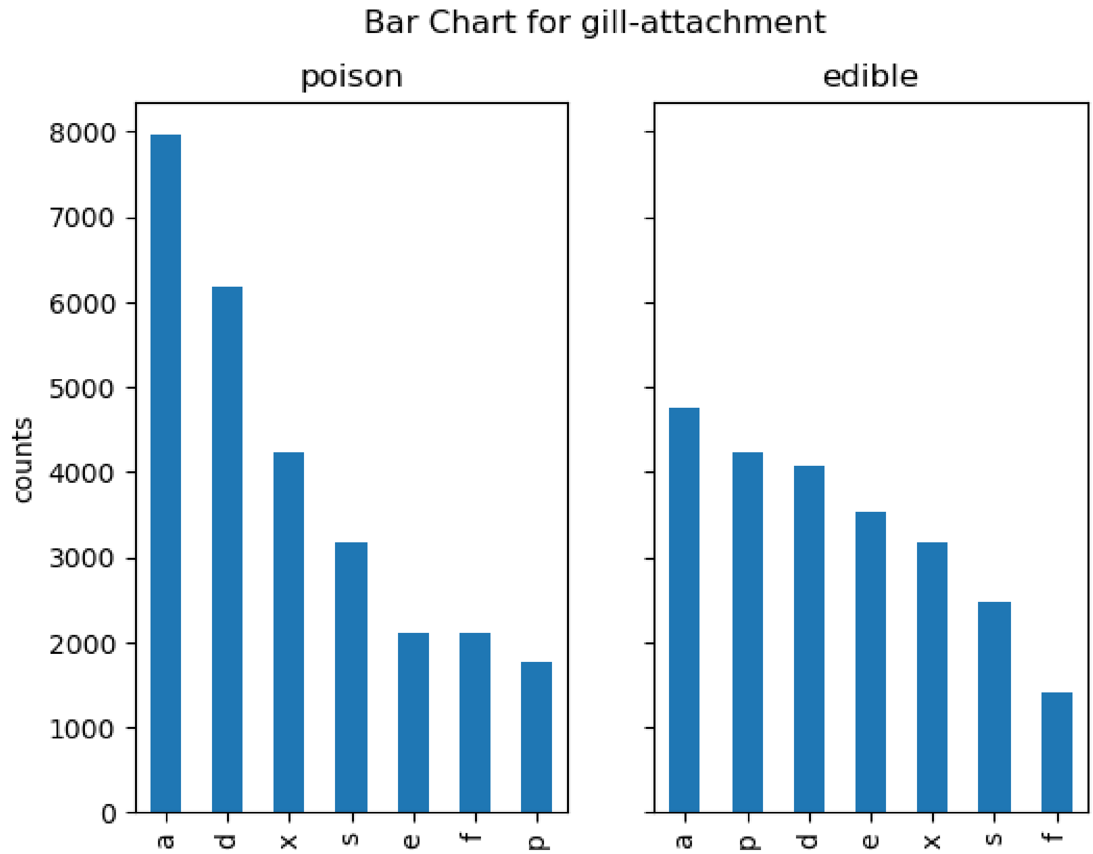


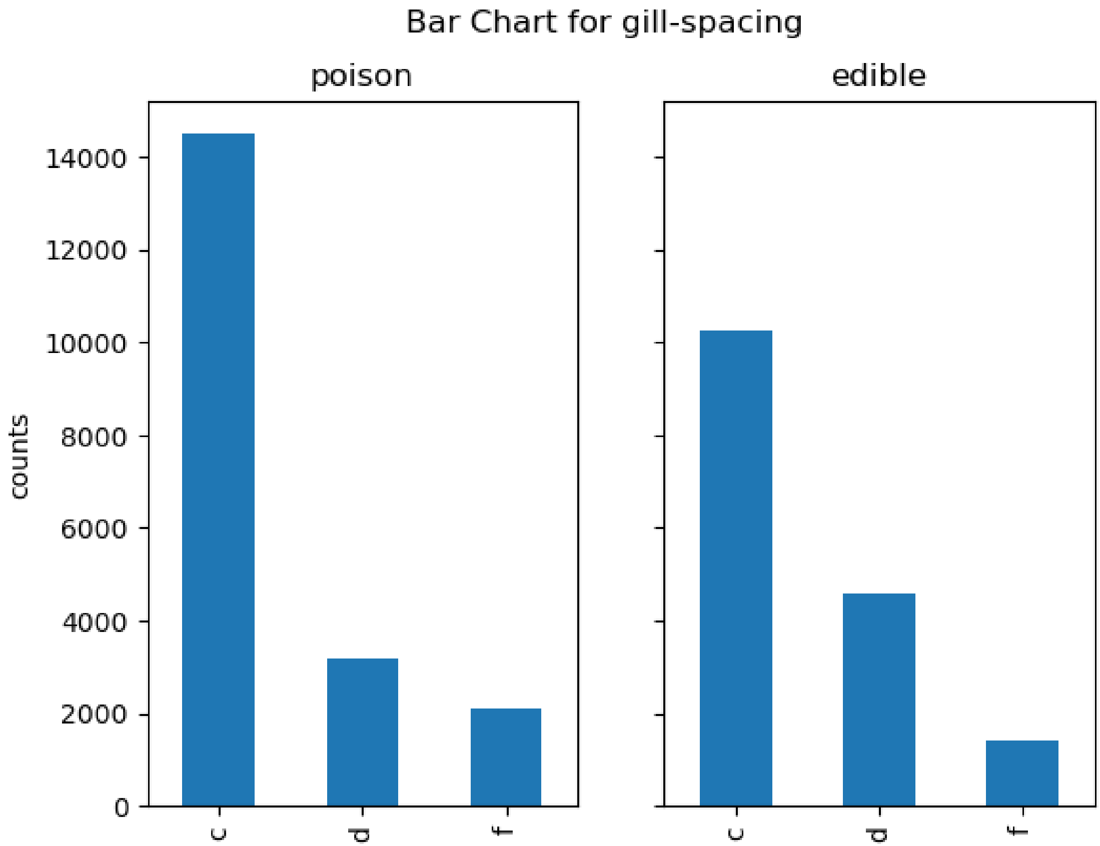


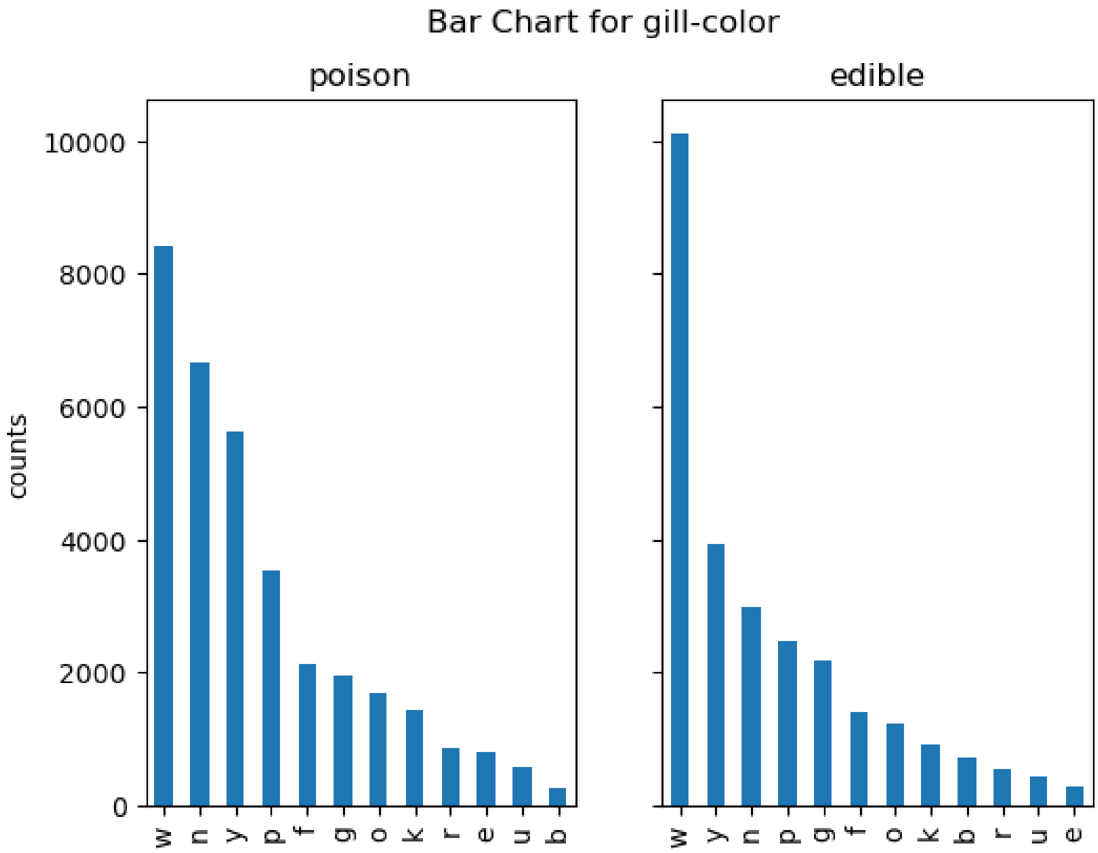
Bar Chart for cap-surface
poison
edible
counts
0
1000
2000
3000
4000
5000
t
s
y
g
d
h
k
i
e
w
l
s
y
t
h
d
g
e
w
l
i
k


Bar Chart for cap-color
poison
edible
counts
0
2000
4000
6000
8000
10000
12000
n y w e o g r p u k l b
n w y g o b e u k l p r

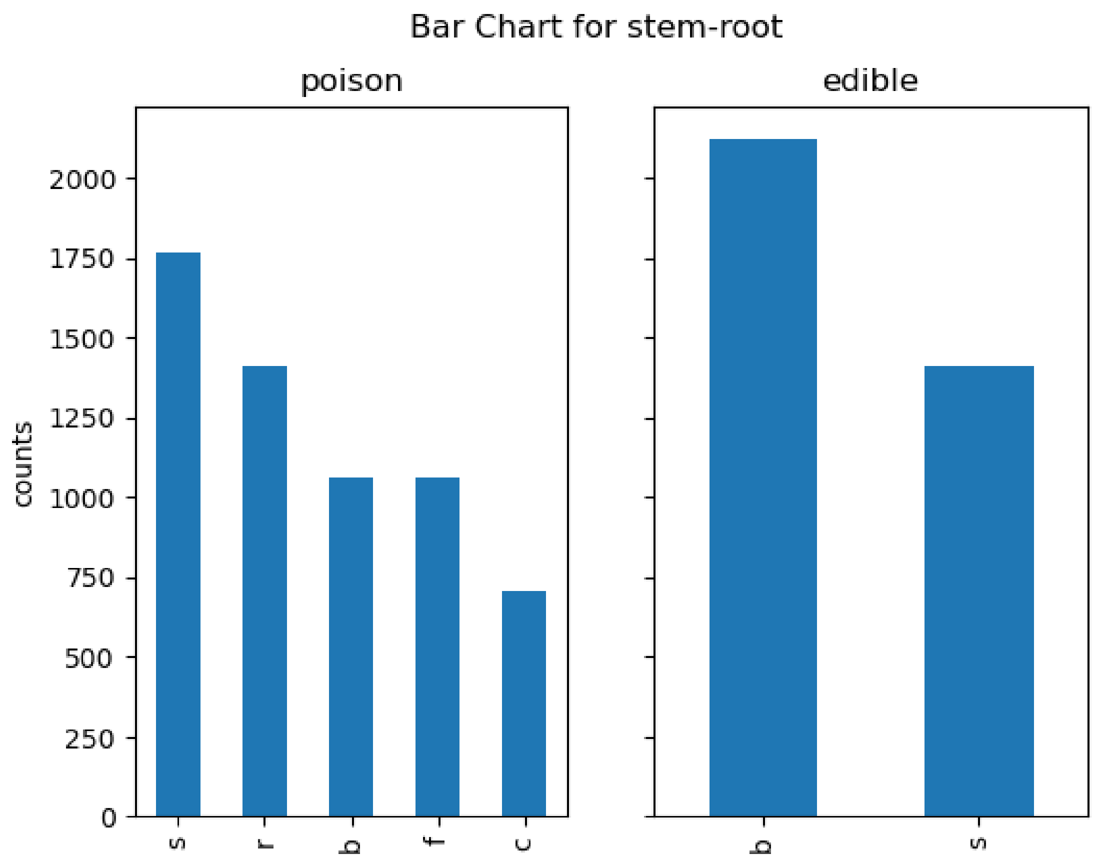

Bar Chart for does-bruise-or-bleed
poison
edible
counts
0
5000
10000
15000
20000
25000
f
t
f
t


Bar Chart for gill-attachment
poison
edible
counts
8000
7000
6000
5000
4000
3000
2000
1000
0
a
d
x
s
e
f
p
a
p
d
e
x
s
f

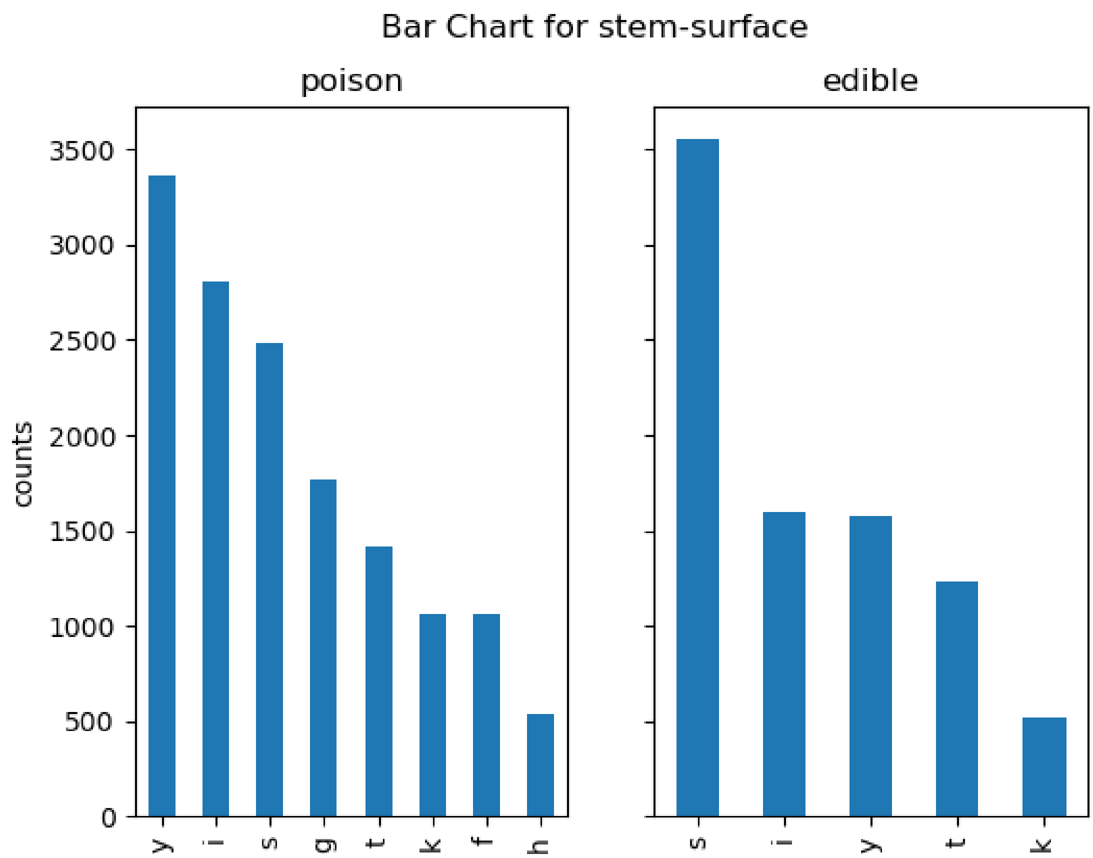

Bar Chart for gill-spacing
poison
edible
counts
14000
12000
10000
8000
6000
4000
2000
0
c
d
f
c
d
f

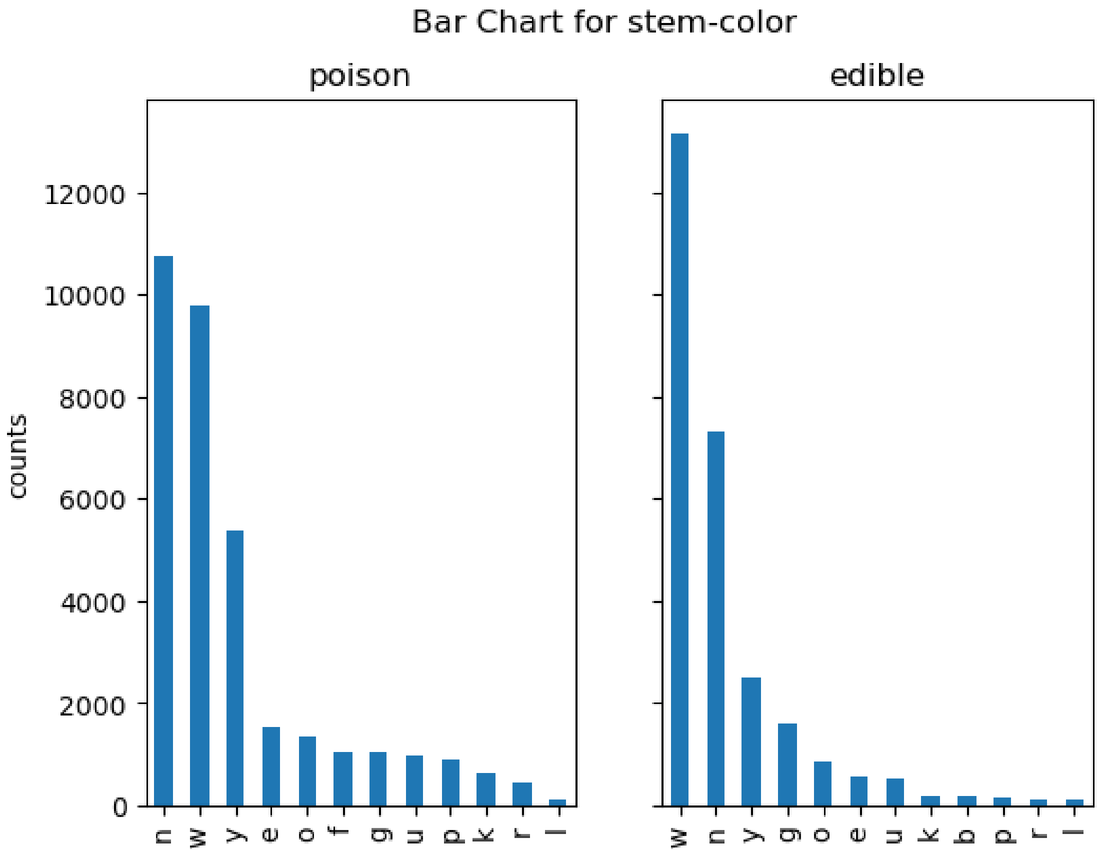


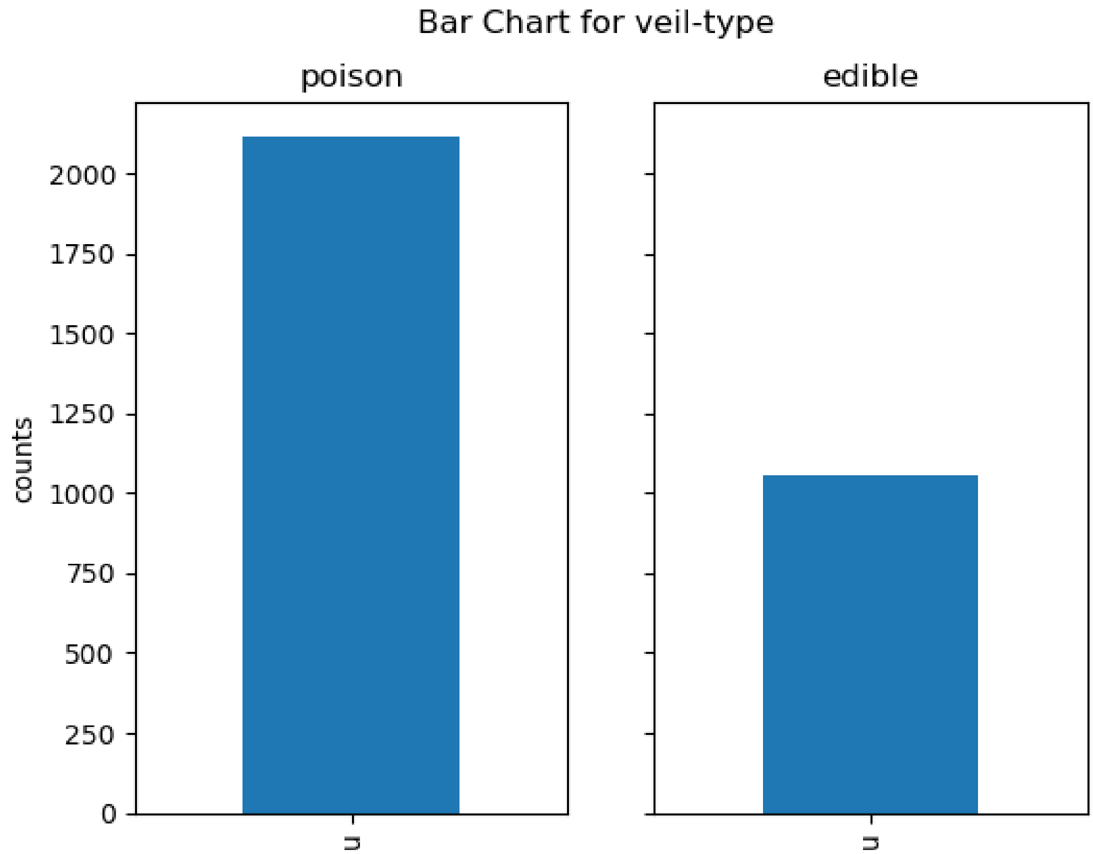
Bar Chart for gill-color
poison
edible
counts
10000
8000
6000
4000
2000
0
w
n
y
p
f
g
o
k
r
e
u
b
w
y
n
p
g
f
o
k
b
r
u
e



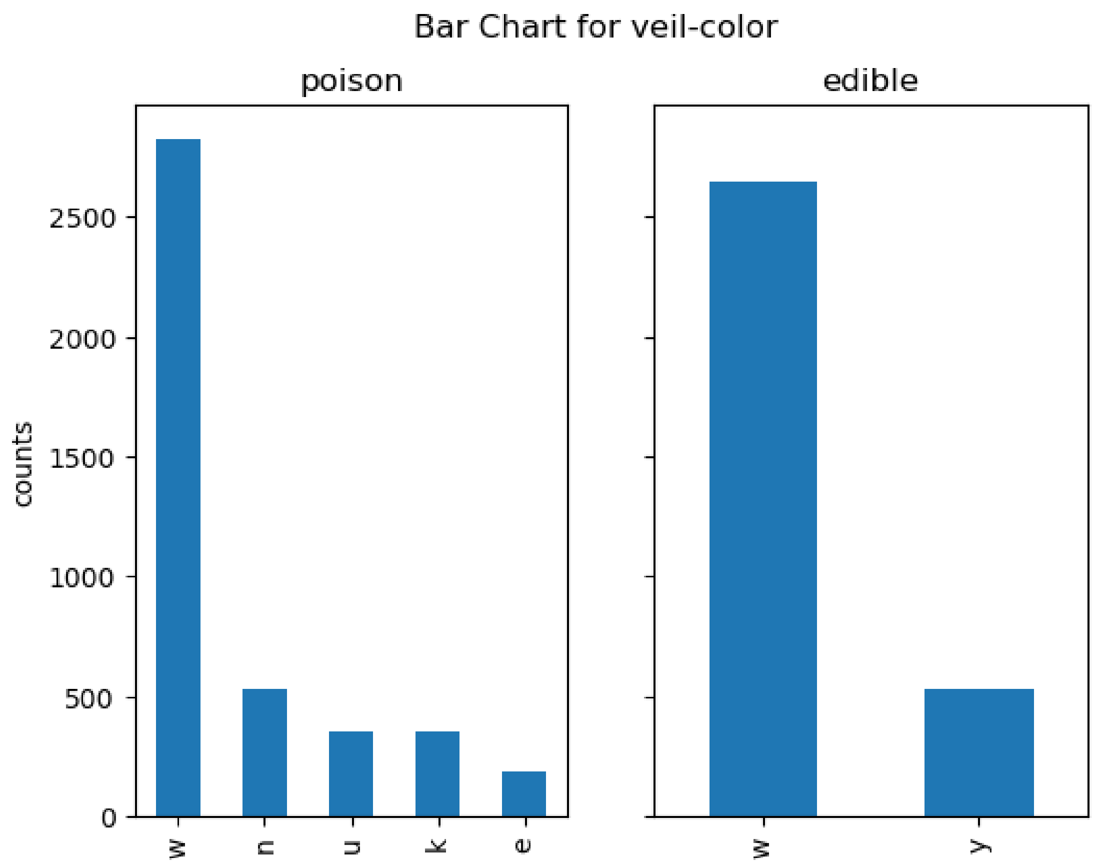
Bar Chart for stem-root
poison
edible
counts
0
250
500
750
1000
1250
1500
1750
2000
s
r
b
f
c
b
s

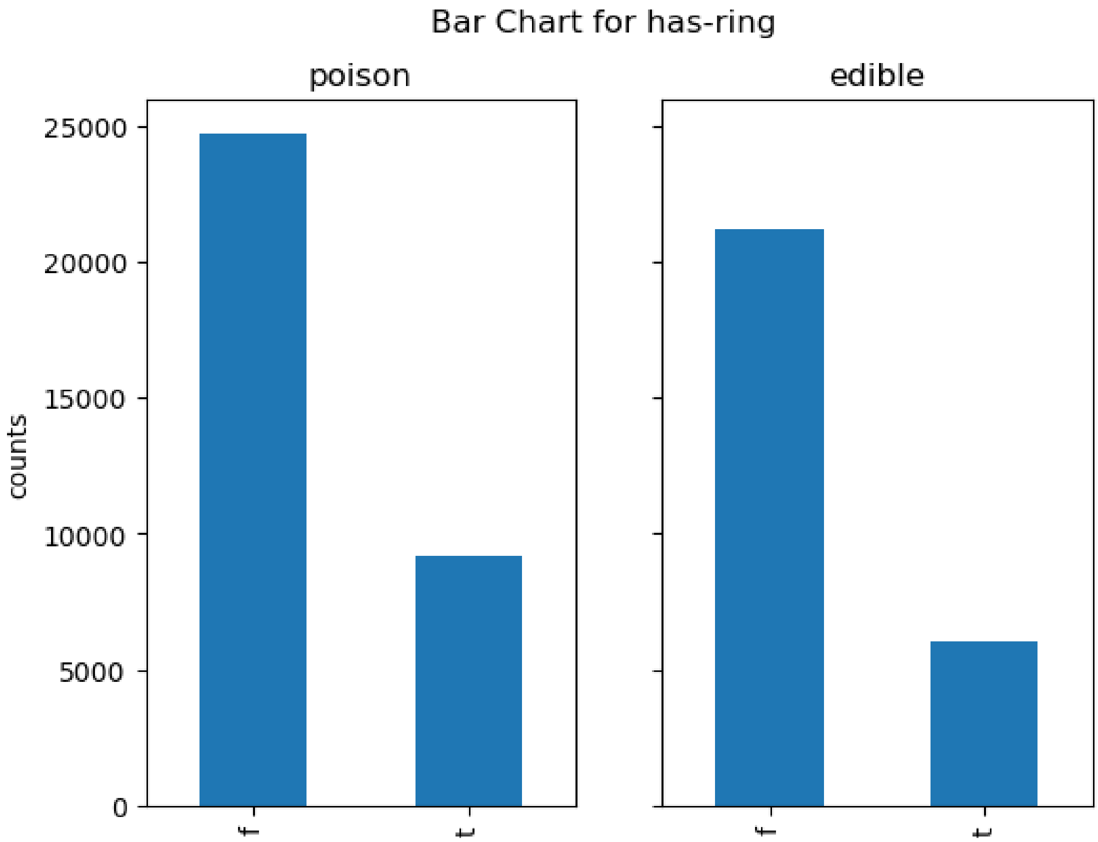

Bar Chart for stem-surface
poison
edible
counts
3500
3000
2500
2000
1500
1000
500
0
y
i
s
g
t
k
f
h
s
i
y
t
k

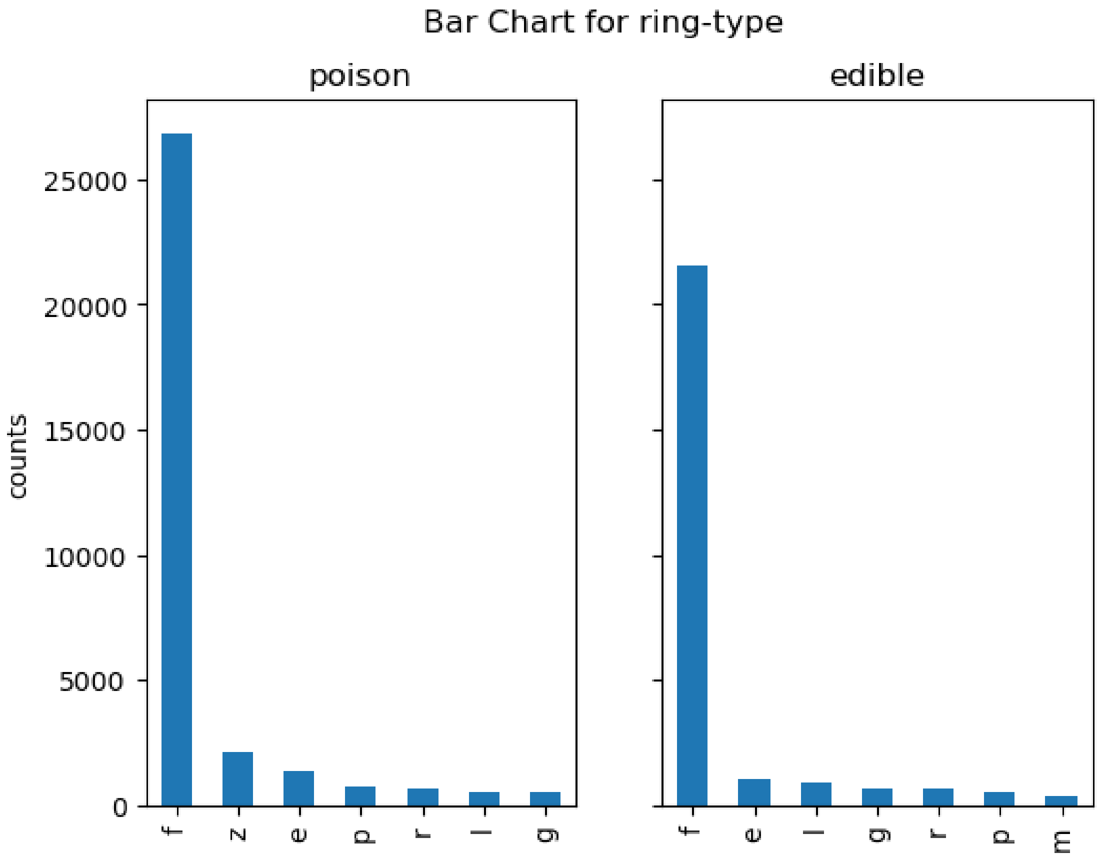

Bar Chart for stem-color
poison
edible
counts
12000
10000
8000
6000
4000
2000
0
n
w
y
e
o
f
g
u
p
k
r
l
w
n
y
g
o
e
u
k
b
p
r
l

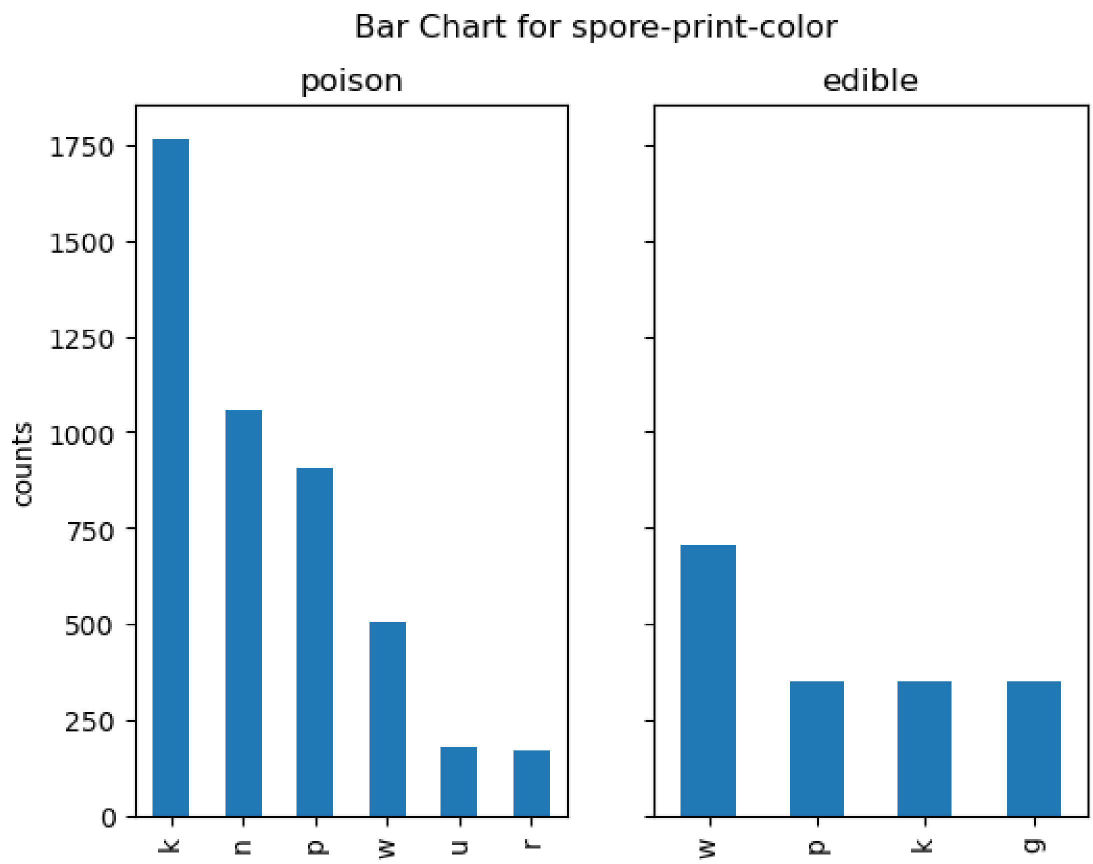


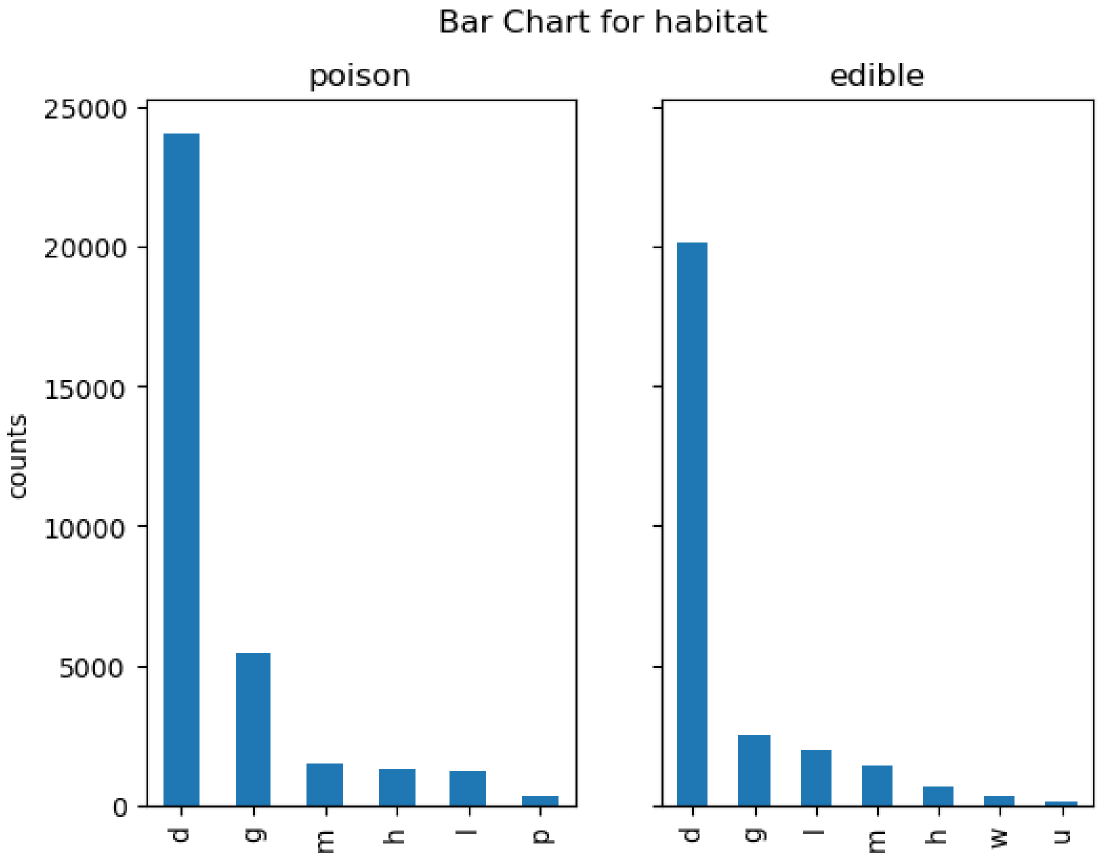
Bar Chart for veil-type
poison
edible
counts
0
250
500
750
1000
1250
1500
1750
2000
u
u

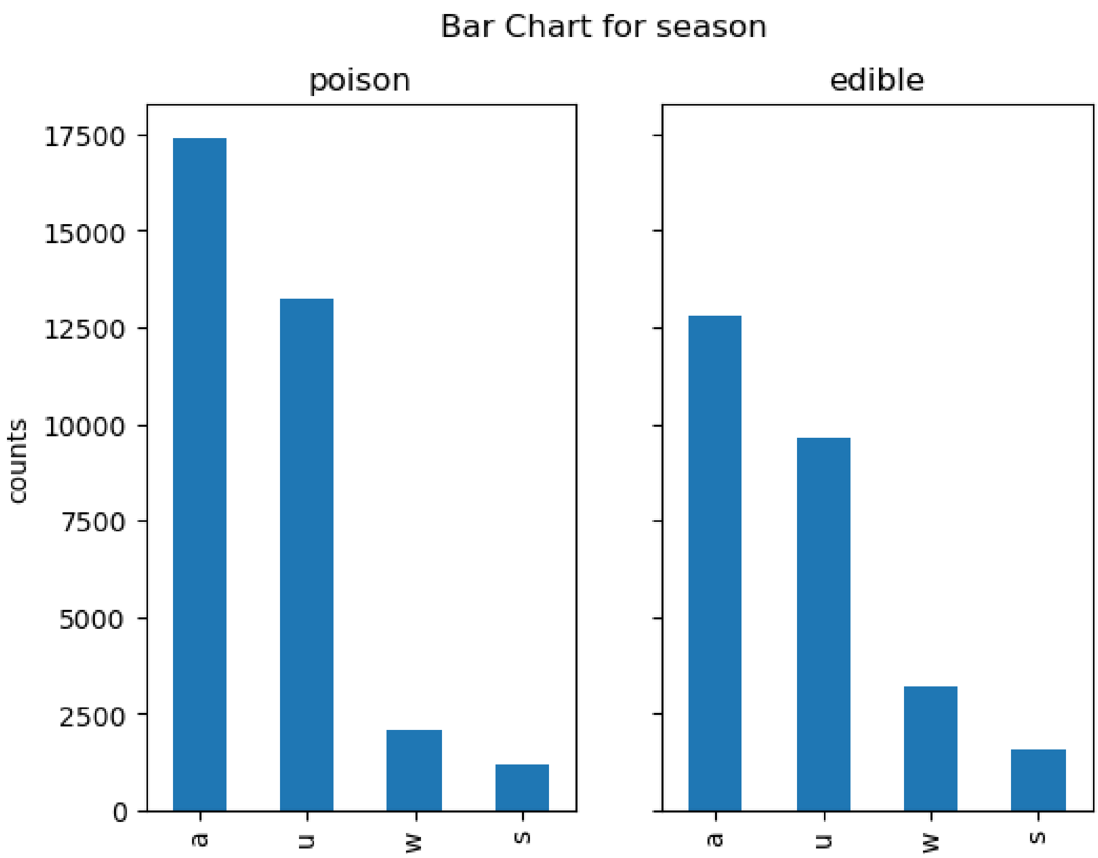

Bar Chart for veil-color
poison
edible
counts
2500
2000
1500
1000
500
0
w
n
u
k
e
w
y


Bar Chart for has-ring
poison
edible
counts
25000
20000
15000
10000
5000
0
f
t
f
t


Bar Chart for ring-type
poison
edible
counts
25000
20000
15000
10000
5000
0
f
z
e
p
r
l
g
f
e
l
g
r
p
m


Bar Chart for spore-print-color
poison
edible
counts
1750
1500
1250
1000
750
500
250
0
k
n
p
w
u
r
w
p
k
g


Bar Chart for habitat
poison
edible
counts
25000
20000
15000
10000
5000
0
d
g
m
h
l
p
d
g
l
m
h
w
u



By the above bar charts, we can find some pattern to classify poisonous mushroom by categorical features. For example, In `season` bar chart, we can see most poisonous mushrooms live in autumn and summer. And we can find pattern in `veil-color` as well. We can easily classify the mushrooms with yellow veil is edible since there is no poisonous mushroom with yell veil. All the `veil-type` are universal, other than that are missing values.

3.3 Missing values

[14]:
```
NA_dict = dict()
for column in df.columns[1:]:
    NA_dict[column] = df[column].isna().sum()

NA_dict
```

[14]:
```
{'cap-diameter': 0,
 'cap-shape': 0,
 'cap-surface': 14120,
 'cap-color': 0,
 'does-bruise-or-bleed': 0,
 'gill-attachment': 9884,
```

```
 'gill-spacing': 25063,
 'gill-color': 0,
 'stem-height': 0,
 'stem-width': 0,
 'stem-root': 51538,
 'stem-surface': 38124,
 'stem-color': 0,
 'veil-type': 57892,
 'veil-color': 53656,
 'has-ring': 0,
 'ring-type': 2471,
 'spore-print-color': 54715,
 'habitat': 0,
 'season': 0}
```

`cap-surface`,`gill-attachment`,`gill-spacing`,`stem-root`,`stem-surface`,`veil-type`,`veil-color`,`ring-type`,`spo` have missing values. And all of them are categorical. All the missing values here might means unknown or not applicable. I decide to impute them using "?", since I have no idea how these missing values appear and cannot apply imputation strategy like mode or k_nearest. We can let the model to decide and find pattern when they meet the missing values "?".

[15]:
```python
df= df.fillna('?')
```

3.4 Feature engineering

[16]:
```python
y = df.iloc[:,0]
X = df.iloc[:,1:]
X = pd.get_dummies(X) # encode categorical data by one-hot-encoding
X = X.astype(float) # convert true and false to 1 and 0
X
```

[16]:
```
       cap-diameter  stem-height  stem-width  cap-shape_b  cap-shape_c  \
0             15.26        16.95       17.09          0.0          0.0
1             16.60        17.99       18.19          0.0          0.0
2             14.07        17.80       17.74          0.0          0.0
3             14.17        15.77       15.98          0.0          0.0
4             14.64        16.53       17.20          0.0          0.0
…               …            …          …            …           …
61064          1.18         3.93        6.22          0.0          0.0
61065          1.27         3.18        5.43          0.0          0.0
61066          1.27         3.86        6.37          0.0          0.0
61067          1.24         3.56        5.44          0.0          0.0
61068          1.17         3.25        5.45          0.0          0.0

       cap-shape_f  cap-shape_o  cap-shape_p  cap-shape_s  cap-shape_x  \
0              0.0          0.0          0.0          0.0          1.0
1              0.0          0.0          0.0          0.0          1.0
```

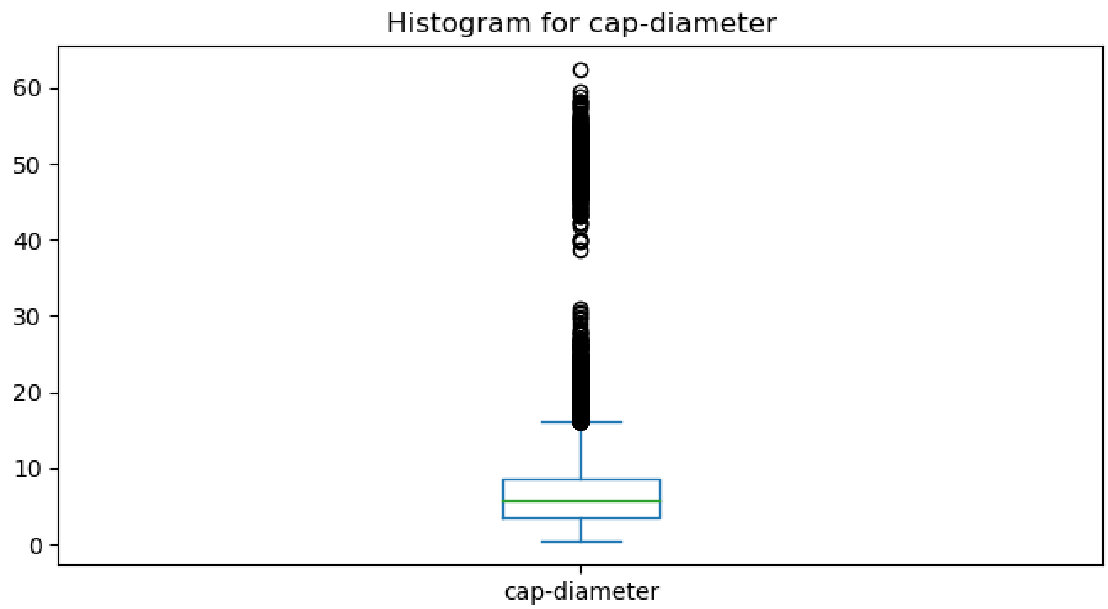
```
2            0.0          0.0          0.0          0.0          1.0
3            1.0          0.0          0.0          0.0          0.0
4            0.0          0.0          0.0          0.0          1.0
…          …          …          …          …          …
61064        0.0          0.0          0.0          1.0          0.0
61065        1.0          0.0          0.0          0.0          0.0
61066        0.0          0.0          0.0          1.0          0.0
61067        1.0          0.0          0.0          0.0          0.0
61068        0.0          0.0          0.0          1.0          0.0

       cap-surface_?  cap-surface_d  cap-surface_e  cap-surface_g  \
0                0.0            0.0            0.0            1.0
1                0.0            0.0            0.0            1.0
2                0.0            0.0            0.0            1.0
3                0.0            0.0            0.0            0.0
4                0.0            0.0            0.0            0.0
…              …            …            …            …
61064            0.0            0.0            0.0            0.0
61065            0.0            0.0            0.0            0.0
61066            0.0            0.0            0.0            0.0
61067            0.0            0.0            0.0            0.0
61068            0.0            0.0            0.0            0.0

       cap-surface_h  …  spore-print-color_r  spore-print-color_u  \
0                0.0  …                  0.0                  0.0
1                0.0  …                  0.0                  0.0
2                0.0  …                  0.0                  0.0
3                1.0  …                  0.0                  0.0
4                1.0  …                  0.0                  0.0
…              …  …                …                  …
61064            0.0  …                  0.0                  0.0
61065            0.0  …                  0.0                  0.0
61066            0.0  …                  0.0                  0.0
61067            0.0  …                  0.0                  0.0
61068            0.0  …                  0.0                  0.0

       spore-print-color_w  habitat_d  habitat_g  habitat_h  habitat_l  \
0                      0.0        1.0        0.0        0.0        0.0
1                      0.0        1.0        0.0        0.0        0.0
2                      0.0        1.0        0.0        0.0        0.0
3                      0.0        1.0        0.0        0.0        0.0
4                      0.0        1.0        0.0        0.0        0.0
…                    …        …        …        …        …
61064                  0.0        1.0        0.0        0.0        0.0
61065                  0.0        1.0        0.0        0.0        0.0
61066                  0.0        1.0        0.0        0.0        0.0
61067                  0.0        1.0        0.0        0.0        0.0
```

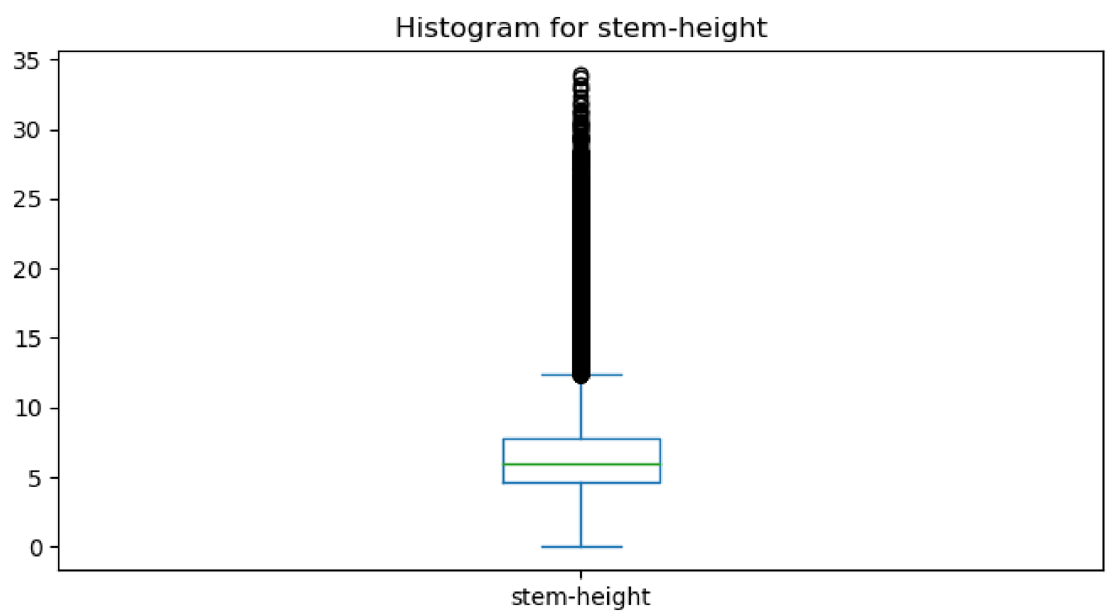
```
61068                   0.0         1.0        0.0         0.0         0.0

       habitat_m  habitat_p  habitat_u  habitat_w  season_a  season_s  \
0            0.0        0.0        0.0        0.0       0.0       0.0
1            0.0        0.0        0.0        0.0       0.0       0.0
2            0.0        0.0        0.0        0.0       0.0       0.0
3            0.0        0.0        0.0        0.0       0.0       0.0
4            0.0        0.0        0.0        0.0       0.0       0.0
…          …        …        …        …        …       …
61064        0.0        0.0        0.0        0.0       1.0       0.0
61065        0.0        0.0        0.0        0.0       1.0       0.0
61066        0.0        0.0        0.0        0.0       0.0       0.0
61067        0.0        0.0        0.0        0.0       0.0       0.0
61068        0.0        0.0        0.0        0.0       0.0       0.0

       season_u  season_w
0           0.0       1.0
1           1.0       0.0
2           0.0       1.0
3           0.0       1.0
4           0.0       1.0
…         …       …
61064       0.0       0.0
61065       0.0       0.0
61066       1.0       0.0
61067       1.0       0.0
61068       1.0       0.0

[61069 rows x 128 columns]
```

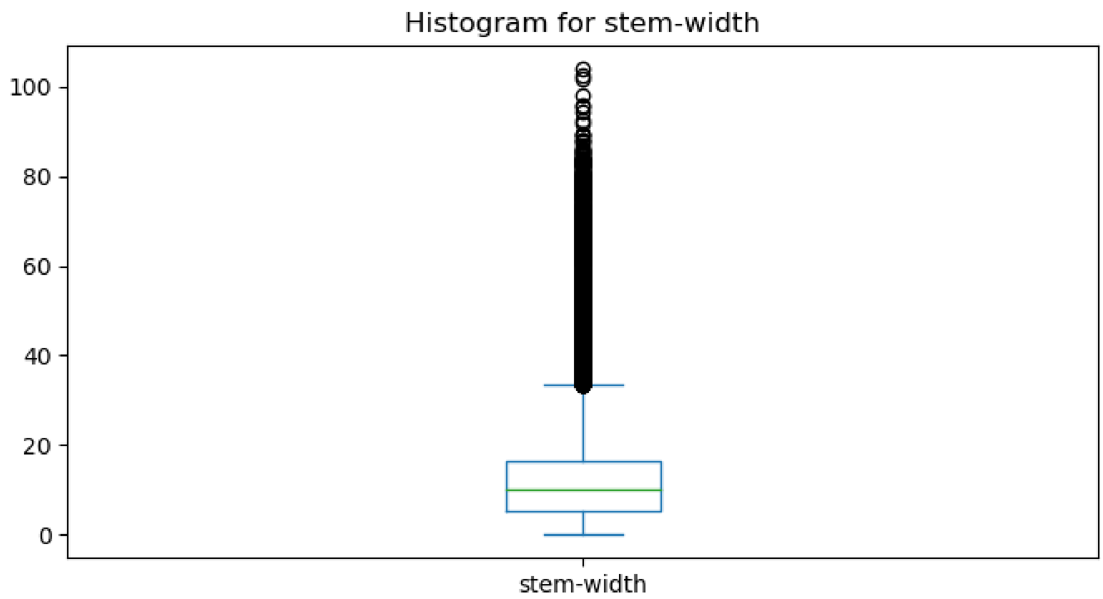
Most columns are categorical, so we need to one-hot-encode the categorical columns. Therefore the models can fit the dataset easier.

3.5 Outlier detection

[17]:
```
for column in numerical_columns:
    fig, ax = plt.subplots(figsize=(8, 4))
    df[column].plot(kind='box', title=f"Histogram for {column}", ax=ax)
    plt.show()
```


Histogram for cap-diameter
60
50
40
30
20
10
0
cap-diameter


Histogram for stem-height
35
30
25
20
15
10
5
0
stem-height



By the box plot, we can see there are a lot of outlier in the positive side for all numerical columns.

[18]:
```
outliers_dict = dict()

for column in numerical_columns:
    # Calculate the first quartile (Q1) and third quartile (Q3)
    Q1 = df[column].quantile(0.25)
    Q3 = df[column].quantile(0.75)

    # Calculate the interquartile range (IQR)
    IQR = Q3 - Q1

    # Define the lower and upper bounds for outliers
    lower_bound = Q1 - 1.5 * IQR
    upper_bound = Q3 + 1.5 * IQR

    # Identify outliers
    outliers = df[(df[column] < lower_bound) | (df[column] > upper_bound)].loc[:
 ↪,column]

    outliers_dict[column] = outliers.count()
```

[19]:
```
outliers_dict
```

[19]:
```
{'cap-diameter': 2400, 'stem-height': 3169, 'stem-width': 1967}
```

Since the amount of outliers is small compare with the total rows, I will not remove any outliers.

And I will use ensemble model. They are able to handle the outliers.

4 Model Training and Evaluation

The models I will use is logistic regression, Decision Tree, and KNN * Logistic Regression: simple model, suitable for binary classification especially when the dataset have linear pattern * Decision Tree: model that is capable for regression and classification. This model is able to find the important features easily, and capture the non-linear pattern which logistic regression cannot. * KNN: simple model that can capture nonlinear pattern, but it require to compute the distance for all data points which would are complex when the dataset is large.

All of these models are easy to understand and easy to implement, and these models are representor of Gradient_based, Tree-based and Distance-based models.

[20]:
```
from sklearn.model_selection import train_test_split
train_X,test_X,train_y,test_y = train_test_split(X,y,test_size=0.
 ↪2,random_state=42)
```

4.1 Logistic Regression

[21]:
```
# import numpy as np
# import pandas as pd

# class MyLogisticRegression:

#     def __init__(self, epochs = 10000, threshold=1e-3,
#                  regularization=None,alpha=0.01) -> None:

#         # Initialize parameters and flags for the model.
#         self.epochs = epochs
#         self.threshold = threshold
#         self.regularization = regularization
#         self.alpha = alpha


#     def train(self, X, y, batch_size=64, lr=1e-3, seed=11, verbose=False):
#         """
#         Train the model using stochastic gradient descent.
#         """
#         # Set seed for reproducibility.
#         np.random.seed(seed)

#         # Define the unique classes and their corresponding indices.
#         self.classes = np.unique(y)
#         self.class_labels = {c: i for i, c in enumerate(self.classes)}

#         # Add bias term to the features.
```

```
#         X = self.add_bias(X)

#         # Convert labels into one-hot encoded format.
#         y = self.one_hot(y)

#         # Initialize weights matrix with zeros.
#         self.loss = []
#         self.weights = np.zeros(shape=(len(self.classes), X.shape[1]))

#         # Start the training process.
#         self.fit_data(X, y, batch_size, lr, verbose)
#         return self



#     def fit_data(self, X, y, batch_size, lr, verbose):
#         """
#         Fit the data using stochastic gradient descent.
#         """
#         i = 0
#         while (not self.epochs or i < self.epochs):
#             # Compute and store the cross-entropy loss.
#             self.loss.append(self.cross_entropy(y, self.predict_(X)))

#             # Randomly select a batch of data.
#             idx = np.random.choice(X.shape[0], batch_size)
#             X_batch, y_batch = X[idx], y[idx]

#             # Calculate the error between predicted and true values.
#             error = y_batch - self.predict_(X_batch)

#             # Update the weights based on the error and learning rate.
#             update = lr * np.dot(error.T, X_batch)

#             # Apply regularization if specified.
#             if self.regularization == 'Ridge':
#                 update += self.alpha * self.weights
#             elif self.regularization == 'Lasso':
#                 update += self.alpha * np.sign(self.weights)
#             elif self.regularization == 'Elastic Net':
#                 update_w += self.alpha * (self.weights + np.sign(self.
↪weights))

#             self.weights += update

#             # Stop training if updates are smaller than a threshold.
#             if np.abs(update).max() < self.threshold:
```

```
#                 break

#             # Print training accuracy every 1000 iterations if verbose is␣
↪True.
#             if i % 1000 == 0 and verbose:
#                 print(' Training Accuracy at {} iterations is {}'.format(i,␣
↪self.evaluate_(X, y)))
#             i += 1

#     def predict(self, X):
#         return self.predict_(self.add_bias(X))

#     def predict_(self, X):
#         pre_vals = np.dot(X, self.weights.T).reshape(-1,len(self.classes))
#         return self.softmax(pre_vals)

#     def softmax(self, z):
#         return np.exp(z) / np.sum(np.exp(z), axis=1).reshape(-1,1)

#     def predict_classes(self, X):
#         self.probs_ = self.predict(X)
#         return np.vectorize(lambda c: self.classes[c])(np.argmax(self.probs_,␣
↪axis=1))

#     def add_bias(self,X):
#         return np.insert(X, 0, 1, axis=1)

#     def one_hot(self, y):
#         return np.eye(len(self.classes))[np.vectorize(lambda c: self.
↪class_labels[c])(y).reshape(-1)]

#     def score(self, X, y):
#         '''
#         Accuracy metric
#         '''
#         return round(np.mean(self.predict_classes(X).reshape(-1,1) == y),3)

#     def evaluate_(self, X, y):
#         return np.mean(np.argmax(self.predict_(X), axis=1) == np.argmax(y,␣
↪axis=1))

#     def cross_entropy(self, y, probs):
#         return -1 * np.mean(y * np.log(probs))

#     def confusion_matrix(self, actual, predicted,norm=False):
#         """
```

```
#         Compute the confusion matrix for the given actual and predicted
 ↪outputs.

#         Args:
#         - actual (array-like): Actual outputs (ground truth).
#         - predicted (array-like): Predicted outputs from the model.

#         Returns:
#         - matrix (np.ndarray): N x N confusion matrix, where N is the number
 ↪of unique classes.
#         """

#         # Create an empty matrix
#         matrix = np.zeros((len(self.classes), len(self.classes)), dtype=float)

#         # Fill the matrix
#         for i, true_class in enumerate(self.classes):
#             for j, pred_class in enumerate(self.classes):
#                 matrix[i, j] = np.sum((actual == true_class) & (predicted ==
 ↪pred_class))

#         if norm:
#             for i in range(len(self.classes)):
#                 total = np.sum(matrix[i])
#                 for j in range(len(self.classes)):
#                     matrix[i,j] = round(matrix[i,j] / total,2)

#         matrix_df = pd.DataFrame(matrix, index=self.classes, columns=self.
 ↪classes)
#         return matrix_df
```

[22]:
```
from LogisticRegression import MyLogisticRegression
lm = MyLogisticRegression()
lm.train(train_X.values,train_y.values)
```

[22]: <LogisticRegression.MyLogisticRegression at 0x133453650>

4.1.1 Training set evaluation

[24]:
```
pred_train_y = lm.predict_classes(train_X.values)
lm.confusion_matrix(train_y,pred_train_y)
```

[24]:

	e	p
e	20183.0	1624.0
p	7378.0	19670.0

logistic regression can classify e much better than p, but the overall performance is great. We treat e as positive and p as negative, then if we misclassify e to p, we call it type 1 error(false positive). And misclassify p as e, we call it type 2 error(false negative). Type 2 is bad for this case, because people eat the poisonous mushrooms which were classified as edible. Therefore, we should increase the overall accuracy or decrease the type 2 error.

[ ]:
```
print(f'accuracy: {np.mean(pred_train_y == train_y)}')
```

```
accuracy: 0.8157404564527684
```

Logistic regression perform great in training set, acquire 81.5% accuracy.

4.1.2 Test set evaluation

[ ]:
```
pred_test_y = lm.predict_classes(test_X)
lm.confusion_matrix(test_y,pred_test_y)
```

[ ]:

	e	p
e	4934.0	440.0
p	1865.0	4975.0

[ ]:
```
print(f'accuracy: {np.mean(pred_test_y == test_y)}')
```

```
accuracy: 0.8112821352546259
```

The logistic model seems perform about the same in test dataset. It acquires 81.1% accuracy which is just 0.4% lower than the accuracy in test dataset.

4.1.3 Important features

[ ]:
```
pd.set_option('display.max_columns', None)
pd.DataFrame(lm.weights,index=[0,1],columns=X.columns.insert(0,'bias'))
```

[ ]:

	bias	cap-diameter	stem-height	stem-width	cap-shape_b	cap-shape_c
0	-1.465632	0.165223	0.0796	0.092808	-1.341672	-0.191079
1	1.465632	-0.165223	-0.0796	-0.092808	1.341672	0.191079

	cap-shape_f	cap-shape_o	cap-shape_p	cap-shape_s	cap-shape_x
0	0.104998	-0.926183	0.137476	0.482723	0.268105
1	-0.104998	0.926183	-0.137476	-0.482723	-0.268105

	cap-surface_?	cap-surface_d	cap-surface_e	cap-surface_g	cap-surface_h
0	0.229483	0.241876	-0.66786	0.811854	0.623892
1	-0.229483	-0.241876	0.66786	-0.811854	-0.623892

	cap-surface_i	cap-surface_k	cap-surface_l	cap-surface_s	cap-surface_t
0	-1.622021	-3.011944	1.189832	0.574294	-0.686148
1	1.622021	3.011944	-1.189832	-0.574294	0.686148

```
   cap-surface_w  cap-surface_y  cap-color_b  cap-color_e  cap-color_g  \
0       0.068476       0.782634     1.066569    -1.446941      0.35109   
1      -0.068476      -0.782634    -1.066569     1.446941     -0.35109   

   cap-color_k  cap-color_l  cap-color_n  cap-color_o  cap-color_p  \
0    -0.618687     1.166477     0.849755    -0.035764    -0.606174   
1     0.618687    -1.166477    -0.849755     0.035764     0.606174   

   cap-color_r  cap-color_u  cap-color_w  cap-color_y  does-bruise-or-bleed_f  \
0    -2.086839    -0.480523     0.090853     0.284552               -0.827921   
1     2.086839     0.480523    -0.090853    -0.284552                0.827921   

   does-bruise-or-bleed_t  gill-attachment_?  gill-attachment_a  \
0               -0.637711          -0.801695          -0.893634   
1                0.637711           0.801695           0.893634   

   gill-attachment_d  gill-attachment_e  gill-attachment_f  gill-attachment_p  \
0          -2.158874           1.088682          -0.047301           2.981584   
1           2.158874          -1.088682           0.047301          -2.981584   

   gill-attachment_s  gill-attachment_x  gill-spacing_?  gill-spacing_c  \
0          -0.306381          -1.328013       -1.006156        -0.38982   
1           0.306381           1.328013        1.006156         0.38982   

   gill-spacing_d  gill-spacing_f  gill-color_b  gill-color_e  gill-color_f  \
0       -0.022356       -0.047301      1.247254     -0.938048     -0.047301   
1        0.022356        0.047301     -1.247254      0.938048      0.047301   

   gill-color_g  gill-color_k  gill-color_n  gill-color_o  gill-color_p  \
0       0.14095     -0.856506     -0.848034      0.174075       0.24918   
1      -0.14095      0.856506      0.848034     -0.174075      -0.24918   

   gill-color_r  gill-color_u  gill-color_w  gill-color_y  stem-root_?  \
0      0.215163      0.012258       0.46076     -1.275383     2.445175   
1     -0.215163     -0.012258      -0.46076      1.275383    -2.445175   

   stem-root_b  stem-root_c  stem-root_f  stem-root_r  stem-root_s  \
0     2.774851    -3.522699    -0.151454    -2.844927    -0.166577   
1    -2.774851     3.522699     0.151454     2.844927     0.166577   

   stem-surface_?  stem-surface_f  stem-surface_g  stem-surface_h  \
0        1.212086       -0.151454       -3.119523       -1.049839   
1       -1.212086        0.151454        3.119523        1.049839   

   stem-surface_i  stem-surface_k  stem-surface_s  stem-surface_t  \
0       -0.006051       -0.816623        1.511848        2.198119   
1        0.006051        0.816623       -1.511848       -2.198119   
```

```
   stem-surface_y  stem-color_b  stem-color_e  stem-color_f  stem-color_g  \
0       -1.244194      0.460045     -1.315729     -0.151454      1.145737
1        1.244194     -0.460045      1.315729      0.151454     -1.145737

   stem-color_k  stem-color_l  stem-color_n  stem-color_o  stem-color_p  \
0     -0.975333      0.560633     -0.059773      0.901764      -1.59306
1      0.975333     -0.560633      0.059773     -0.901764       1.59306

   stem-color_r  stem-color_u  stem-color_w  stem-color_y  veil-type_?  \
0     -0.379744     -0.795127      1.315065     -0.578656     1.196461
1      0.379744      0.795127     -1.315065      0.578656    -1.196461

   veil-type_u  veil-color_?  veil-color_e  veil-color_k  veil-color_n  \
0    -2.662093     -0.688759     -0.540438     -0.184157     -1.108955
1     2.662093      0.688759      0.540438      0.184157      1.108955

   veil-color_u  veil-color_w  veil-color_y  has-ring_f  has-ring_t  \
0     -1.147823      0.706619      1.497881    0.278252   -1.743884
1      1.147823     -0.706619     -1.497881   -0.278252    1.743884

   ring-type_?  ring-type_e  ring-type_f  ring-type_g  ring-type_l  \
0      0.88374    -1.047384    -1.160445     0.750416     0.387372
1     -0.88374     1.047384     1.160445    -0.750416    -0.387372

   ring-type_m  ring-type_p  ring-type_r  ring-type_z  spore-print-color_?  \
0     1.548294    -0.894767      1.08723    -3.020089            -0.029702
1    -1.548294     0.894767     -1.08723     3.020089             0.029702

   spore-print-color_g  spore-print-color_k  spore-print-color_n  \
0             1.168732            -1.231195            -1.083105
1            -1.168732             1.231195             1.083105

   spore-print-color_p  spore-print-color_r  spore-print-color_u  \
0            -1.023482             -0.08949            -0.186547
1             1.023482              0.08949             0.186547

   spore-print-color_w  habitat_d  habitat_g  habitat_h  habitat_l  habitat_m  \
0             1.009156  -0.585411  -0.645654  -0.198758  -0.226998    0.24723
1            -1.009156   0.585411   0.645654   0.198758   0.226998   -0.24723

   habitat_p  habitat_u  habitat_w  season_a  season_s  season_u  season_w
0  -0.693242   0.133146   0.504056 -0.962381  0.229055 -1.014429  0.282124
1   0.693242  -0.133146  -0.504056  0.962381 -0.229055  1.014429 -0.282124
```

- cap-surface_g: 0.81
- cap-color_l: 1.16

- ring-type_m: 1.54

These are the important features. The important feature in logistic regression would have higher weight

4.2 Decision Tree

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

# class Node():
#     def __init__(self, feature_index=None, threshold=None, left=None,␣
↪right=None, var_red=None, info_gain=None, value=None):
#         ''' constructor '''

#         # for decision node
#         self.feature_index = feature_index
#         self.threshold = threshold # threshold for splitting data
#         self.left = left
#         self.right = right
#         self.var_red = var_red # index for regressor, choose the highest␣
↪feature to split
#         self.info_gain = info_gain # index for classifier, choose the highest␣
↪to split

#         # for leaf node
#         self.value = value



# # ========Regression==========================================================
# class DecisionTreeRegressor():
#     def __init__(self, min_samples_split=2, max_depth=2):
#         ''' constructor '''

#         # initialize the root of the tree
#         self.root = None

#         # stopping conditions
#         self.min_samples_split = min_samples_split # min elements need to␣
↪split
#         self.max_depth = max_depth # max depth for tree

#     def build_tree(self, dataset, curr_depth=0):
#         ''' recursive function to build the tree '''

#         X, Y = dataset[:,:-1], dataset[:,-1]
#         num_samples, num_features = np.shape(X)
```

```
#         best_split = {}
#         # split until stopping conditions are met
#         if num_samples>=self.min_samples_split and curr_depth<=self.max_depth:
#             # find the best split
#             best_split = self.get_best_split(dataset, num_samples,␣
↪num_features)
#             # check if information gain is positive
#             if best_split["var_red"]>0:
#                 # recur left
#                 left_subtree = self.build_tree(best_split["dataset_left"],␣
↪curr_depth+1)
#                 # recur right
#                 right_subtree = self.build_tree(best_split["dataset_right"],␣
↪curr_depth+1)
#                 # return decision node
#                 return Node(best_split["feature_index"],␣
↪best_split["threshold"],
#                             left_subtree, right_subtree,␣
↪best_split["var_red"])

#         # compute leaf node
#         leaf_value = self.calculate_leaf_value(Y)
#         # return leaf node
#         return Node(value=leaf_value)

#     def get_best_split(self, dataset, num_samples, num_features):
#         '''
#         function to find the best split

#         Returns:
#             Dict: A dict that contains information for best split
#         '''

#         # dictionary to store the best split
#         best_split = {}
#         max_var_red = -float("inf")
#         # loop over all the features
#         for feature_index in range(num_features):
#             feature_values = dataset[:, feature_index]
#             possible_thresholds = np.unique(feature_values)
#             # loop over all the feature values present in the data
#             for threshold in possible_thresholds:
#                 # get current split
#                 dataset_left, dataset_right = self.split(dataset,␣
↪feature_index, threshold)
#                 # check if childs are not null
```

```
#                 if len(dataset_left)>0 and len(dataset_right)>0:
#                     y, left_y, right_y = dataset[:, -1], dataset_left[:, -1],␣
↪dataset_right[:, -1]
#                     # compute information gain
#                     curr_var_red = self.variance_reduction(y, left_y, right_y)
#                     # update the best split if needed
#                     # if curr is higher, update everything
#                     if curr_var_red>max_var_red:
#                         best_split["feature_index"] = feature_index
#                         best_split["threshold"] = threshold
#                         best_split["dataset_left"] = dataset_left
#                         best_split["dataset_right"] = dataset_right
#                         best_split["var_red"] = curr_var_red
#                         max_var_red = curr_var_red

#         # return best split
#         return best_split

#     def split(self, dataset, feature_index, threshold):
#         ''' function to split the data using a feature and threshold

#         Returns:
#             Tuple: dataset_left, dataset_right
#         '''

#         dataset_left = np.array([row for row in dataset if␣
↪row[feature_index]<=threshold])
#         dataset_right = np.array([row for row in dataset if␣
↪row[feature_index]>threshold])
#         return dataset_left, dataset_right

#     def variance_reduction(self, parent, l_child, r_child):
#         ''' function to compute variance reduction

#         Returns:
#             float: measure the information gain for a certain split
#         '''

#         weight_l = len(l_child) / len(parent)
#         weight_r = len(r_child) / len(parent)
#         reduction = np.var(parent) - (weight_l * np.var(l_child) + weight_r *␣
↪np.var(r_child))
#         return reduction

#     def calculate_leaf_value(self, Y):
#         ''' function to compute leaf node using mean
```

```
#         Returns:
#             float: mean value for given node value
#         '''

#         val = np.mean(Y)
#         return val

#     def print_tree(self, tree=None, indent=" "):
#         ''' function to print the tree '''

#         if not tree:
#             tree = self.root

#         if tree.value is not None:
#             print(tree.value)

#         else:
#             print("X_"+str(tree.feature_index), "<=", tree.threshold, "?",␣
 ↪tree.var_red)
#             print("%sleft:" % (indent), end="")
#             self.print_tree(tree.left, indent + indent)
#             print("%sright:" % (indent), end="")
#             self.print_tree(tree.right, indent + indent)

#     def pretty_print(self,node=None,depth=0,prefix="Root: "):
#         '''Print tree in pretty format using post order traversal'''

#         if node is None:
#             node = self.root

#         indent = "  " * depth * 4

#         if node.value is not None:
#             print(f"{indent}{prefix}Leaf => Value: {round(node.value,2)} |␣
 ↪depth: {depth}")
#         else:
#             self.pretty_print(node.right, depth + 1, prefix="R--> ")
#             print(f"{indent}{prefix} X_{node.feature_index} <= {round(node.
 ↪threshold,2)} | depth: {depth}")
#             self.pretty_print(node.left, depth + 1, prefix="L--> ")

#     def fit(self, X, Y):
#         ''' function to train the tree '''

#         dataset = np.concatenate((X, Y), axis=1)
#         self.root = self.build_tree(dataset)
```

```
#     def make_prediction(self, x, tree):
#         ''' function to predict new dataset '''

#         if tree.value!=None: return tree.value
#         feature_val = x[tree.feature_index]
#         if feature_val<=tree.threshold:
#             return self.make_prediction(x, tree.left)
#         else:
#             return self.make_prediction(x, tree.right)

#     def predict(self, X):
#         ''' function to predict a single data point '''

#         preditions = [self.make_prediction(x, self.root) for x in X]
#         return preditions

#     def mse(self,y_true, y_pred,verbose=False):
#         ''' Calculate Mean Square Error'''

#         res = np.mean((y_true - y_pred)**2)
#         if verbose:
#             print(f"MSE: {res}")
#         return res

#     def r2(self,y_true,y_pred,verbose=False):
#         ''' Calculate r2 score for regressor, range form -inf to 1, higher␣
↪means better
#         '''
#         y_mean = np.mean(y_true)

#         # Calculate total sum of squares
#         SST = np.sum((y_true - y_mean) ** 2)

#         # Calculate residual sum of squares
#         SSR = np.sum((y_true - y_pred) ** 2)

#         # Calculate R^2 score
#         r2 = 1 - (SSR / SST)

#         return r2


# # =======Regression=====================================================
```

```
# #␣
↪========Classification==========================================================
# class DecisionTreeClassifier():
#     def __init__(self, min_samples_split=2, max_depth=2):
#         ''' constructor '''

#         # initialize the root of the tree
#         self.root = None

#         # stopping conditions
#         self.min_samples_split = min_samples_split
#         self.max_depth = max_depth

#     def build_tree(self, dataset, curr_depth=0):
#         ''' recursive function to build the tree '''

#         X, Y = dataset[:,:-1], dataset[:,-1]
#         num_samples, num_features = np.shape(X)

#         # split until stopping conditions are met
#         if num_samples>=self.min_samples_split and curr_depth<=self.max_depth:
#             # find the best split
#             best_split = self.get_best_split(dataset, num_samples,␣
↪num_features)
#             # check if information gain is positive
#             if best_split["info_gain"]>0:
#                 # recur left
#                 left_subtree = self.build_tree(best_split["dataset_left"],␣
↪curr_depth+1)
#                 # recur right
#                 right_subtree = self.build_tree(best_split["dataset_right"],␣
↪curr_depth+1)
#                 # return decision node
#                 return Node(best_split["feature_index"],␣
↪best_split["threshold"],
#                             left_subtree,␣
↪right_subtree,info_gain=best_split["info_gain"])

#         # compute leaf node
#         leaf_value = self.calculate_leaf_value(Y)
#         # return leaf node
#         return Node(value=leaf_value)

#     def get_best_split(self, dataset, num_samples, num_features):
#         ''' function to find the best split '''
```

```
#         # dictionary to store the best split
#         best_split = {}
#         max_info_gain = -float("inf")

#         # loop over all the features
#         for feature_index in range(num_features):
#             feature_values = dataset[:, feature_index]
#             possible_thresholds = np.unique(feature_values)
#             # loop over all the feature values present in the data
#             for threshold in possible_thresholds:
#                 # get current split
#                 dataset_left, dataset_right = self.split(dataset,␣
↪feature_index, threshold)
#                 # check if childs are not null
#                 if len(dataset_left)>0 and len(dataset_right)>0:
#                     y, left_y, right_y = dataset[:, -1], dataset_left[:, -1],␣
↪dataset_right[:, -1]
#                     # compute information gain
#                     curr_info_gain = self.information_gain(y, left_y,␣
↪right_y, "gini")
#                     # update the best split if needed
#                     if curr_info_gain>max_info_gain:
#                         best_split["feature_index"] = feature_index
#                         best_split["threshold"] = threshold
#                         best_split["dataset_left"] = dataset_left
#                         best_split["dataset_right"] = dataset_right
#                         best_split["info_gain"] = curr_info_gain
#                         max_info_gain = curr_info_gain

#         # return best split
#         return best_split

#     def split(self, dataset, feature_index, threshold):
#         ''' function to split the data '''

#         dataset_left = np.array([row for row in dataset if␣
↪row[feature_index]<=threshold])
#         dataset_right = np.array([row for row in dataset if␣
↪row[feature_index]>threshold])
#         return dataset_left, dataset_right

#     def information_gain(self, parent, l_child, r_child, mode="entropy"):
#         ''' function to compute information gain '''

#         weight_l = len(l_child) / len(parent)
#         weight_r = len(r_child) / len(parent)
#         if mode=="gini":
```

```
#             gain = self.gini_index(parent) - (weight_l*self.
↪gini_index(l_child) + weight_r*self.gini_index(r_child))
#         else:
#             gain = self.entropy(parent) - (weight_l*self.entropy(l_child) +␣
↪weight_r*self.entropy(r_child))
#         return gain

#     def entropy(self, y):
#         ''' function to compute entropy '''

#         class_labels = np.unique(y)
#         entropy = 0
#         for cls in class_labels:
#             p_cls = len(y[y == cls]) / len(y)
#             entropy += -p_cls * np.log2(p_cls)
#         return entropy

#     def gini_index(self, y):
#         ''' function to compute gini index '''

#         class_labels = np.unique(y)
#         gini = 0
#         for cls in class_labels:
#             p_cls = len(y[y == cls]) / len(y)
#             gini += p_cls**2
#         return 1 - gini

#     def calculate_leaf_value(self, Y):
#         ''' function to compute leaf node '''

#         Y = list(Y)
#         # return the maximum count element
#         return max(Y, key=Y.count)

#     def print_tree(self, tree=None, indent=" "):
#         ''' function to print the tree '''

#         if not tree:
#             tree = self.root

#         if tree.value is not None:
#             print(tree.value)

#         else:
#             print("X_"+str(tree.feature_index), "<=", tree.threshold, "?",␣
↪tree.info_gain)
#             print("%sleft:" % (indent), end="")
```

```
#             self.print_tree(tree.left, indent + indent)
#             print("%sright:" % (indent), end="")
#             self.print_tree(tree.right, indent + indent)

#     def pretty_print(self,node=None,depth=0,prefix="Root: "):
#         '''Print tree in pretty format using post order traversal'''

#         if node is None:
#             node = self.root

#         indent = "  " * depth * 4

#         # print leaves node
#         if node.value is not None:
#             print(f"{indent}{prefix}Leaf => Value: {node.value} | depth:␣
↪{depth}")
#         # print feature node
#         else:
#             self.pretty_print(node.right, depth + 1, prefix="R--> ")
#             print(f"{indent}{prefix} X_{node.feature_index} <= {node.
↪threshold} | depth: {depth}")
#             self.pretty_print(node.left, depth + 1, prefix="L--> ")

#     def fit(self, X, Y):
#         ''' function to train the tree '''

#         dataset = np.concatenate((X, Y), axis=1)
#         self.root = self.build_tree(dataset)

#     def predict(self, X):
#         ''' function to predict new dataset

#         Returns:
#             List: list contains predictions
#         '''

#         preditions = [self.make_prediction(x, self.root) for x in X]
#         return preditions

#     def make_prediction(self, x, tree):
#         ''' function to predict a single data point '''

#         # if the node is leaf node, return the value
#         if tree.value!=None: return tree.value
#         # otherwise travel to left or right node by the threshold
#         feature_val = x[tree.feature_index]
#         if feature_val<=tree.threshold:
```

```
#             return self.make_prediction(x, tree.left)
#         else:
#             return self.make_prediction(x, tree.right)

#     def accuracy(self, y_true, y_pred):
#         ''' Calculate the accuracy '''

#         count = 0
#         N = len(y_true)

#         for i in range(N):
#             if y_true[i] == y_pred[i]:
#                 count += 1

#         return count / N
# #
 ↪========Classification==========================================================
```

[ ]:
```
from DST import DecisionTreeClassifier
```

[ ]:
```
dt = DecisionTreeClassifier(min_samples_split=5,max_depth=10)
dt.fit(train_X.values,train_y.values.reshape(-1,1))
```

4.2.1 Training set

[ ]:
```
pred_y = dt.predict(train_X.values)
```

[ ]:
```
np.mean(pred_y == train_y)
```

[ ]: 0.8666052604646403

4.2.2 test set

[ ]:
```
pred_y = dt.predict(test_X.values)
np.mean(pred_y == test_y)
```

[ ]: 0.8648272474209923

4.2.3 important features

[ ]:
```
dt.pretty_print()
```

```
                R--> Leaf => Value: p | depth: 2
        R-->  X_68 <= 0.0 | depth: 1
                        R--> Leaf => Value: p | depth: 3
                L-->  X_107 <= 0.0 | depth: 2
```

```
                                R--> Leaf => Value: e | depth: 4
                        L-->  X_72 <= 0.0 | depth: 3
                                        R--> Leaf => Value: p | depth: 5
                                L-->  X_64 <= 0.0 | depth: 4
                                                                R--> Leaf =>
Value: e | depth: 8
                                                        R-->  X_37 <= 0.0 |
depth: 7
R--> Leaf => Value: p | depth: 10
                                                                        R-->
X_90 <= 0.0 | depth: 9
L--> Leaf => Value: e | depth: 10
                                                                L-->  X_0 <=
10.06 | depth: 8
        R--> Leaf => Value: p | depth: 11
R-->  X_33 <= 0.0 | depth: 10
        L--> Leaf => Value: e | depth: 11
                                                                        L-->
X_2 <= 9.26 | depth: 9
L--> Leaf => Value: p | depth: 10
                                                R-->  X_59 <= 0.0 | depth: 6
                                                                R--> Leaf =>
Value: p | depth: 8
                                                        L-->  X_87 <= 0.0 |
depth: 7
                                                                        R-->
Leaf => Value: p | depth: 9
                                                                L-->  X_24 <=
0.0 | depth: 8
        R--> Leaf => Value: p | depth: 11
R-->  X_74 <= 0.0 | depth: 10
        L--> Leaf => Value: e | depth: 11
                                                                        L-->
X_0 <= 3.46 | depth: 9
        R--> Leaf => Value: p | depth: 11
L-->  X_32 <= 0.0 | depth: 10
        L--> Leaf => Value: e | depth: 11
                                        L-->  X_18 <= 0.0 | depth: 5
                                                                R--> Leaf =>
Value: e | depth: 8
                                                        R-->  X_56 <= 0.0 |
depth: 7
                                                                L--> Leaf =>
Value: p | depth: 8
                                                L-->  X_30 <= 0.0 | depth: 6
R--> Leaf => Value: e | depth: 10
                                                                        R-->
X_11 <= 0.0 | depth: 9
```

```
L--> Leaf => Value: p | depth: 10
                                                                R-->  X_108 <=
0.0 | depth: 8
                                                                        L-->
Leaf => Value: e | depth: 9
                                                        L-->  X_46 <= 0.0 |
depth: 7
                                                                        R-->
Leaf => Value: p | depth: 9
                                                                L-->  X_83 <=
0.0 | depth: 8
R--> Leaf => Value: p | depth: 10
                                                                        L-->
X_62 <= 0.0 | depth: 9
        R--> Leaf => Value: e | depth: 11
L-->  X_41 <= 0.0 | depth: 10
        L--> Leaf => Value: e | depth: 11
Root:  X_2 <= 8.22 | depth: 0
                                R--> Leaf => Value: p | depth: 4
                        R-->  X_17 <= 0.0 | depth: 3
                                        R--> Leaf => Value: p | depth: 5
                                L-->  X_11 <= 0.0 | depth: 4
                                                R--> Leaf => Value: e | depth: 6
                                        L-->  X_2 <= 1.79 | depth: 5
                                                L--> Leaf => Value: p | depth: 6
                R-->  X_1 <= 3.69 | depth: 2
                                R--> Leaf => Value: e | depth: 4
                        L-->  X_2 <= 3.01 | depth: 3
                                        R--> Leaf => Value: e | depth: 5
                                L-->  X_3 <= 0.0 | depth: 4
                                                R--> Leaf => Value: e | depth: 6
                                        L-->  X_5 <= 0.0 | depth: 5
                                                        R--> Leaf => Value: e |
depth: 7
                                                L-->  X_21 <= 0.0 | depth: 6
                                                        L--> Leaf => Value: p |
depth: 7
        L-->  X_46 <= 0.0 | depth: 1
                                        R--> Leaf => Value: e | depth: 5
                                R-->  X_17 <= 0.0 | depth: 4
                                                R--> Leaf => Value: e | depth: 6
                                        L-->  X_10 <= 0.0 | depth: 5
                                                L--> Leaf => Value: p | depth: 6
                        R-->  X_117 <= 0.0 | depth: 3
                                                R--> Leaf => Value: p | depth: 6
                                        R-->  X_4 <= 0.0 | depth: 5
                                                        R--> Leaf => Value: p |
depth: 7
```

```
                                                        L-->  X_65 <= 0.0 | depth: 6
R--> Leave => Value: e | depth: 10
                                                                                R-->
X_21 <= 0.0 | depth: 9
        R--> Leaf => Value: e | depth: 11
L-->  X_17 <= 0.0 | depth: 10
        L--> Leaf => Value: p | depth: 11
                                                                        R-->  X_44 <=
0.0 | depth: 8
R--> Leaf => Value: p | depth: 10
                                                                                L-->
X_37 <= 0.0 | depth: 9
L--> Leaf => Value: e | depth: 10
                                                                L-->  X_58 <= 0.0 |
depth: 7
        R--> Leaf => Value: e | depth: 11
R-->  X_0 <= 2.84 | depth: 10
        L--> Leaf => Value: p | depth: 11
                                                                                R-->
X_55 <= 0.0 | depth: 9
        R--> Leaf => Value: p | depth: 11
L-->  X_70 <= 0.0 | depth: 10
        L--> Leaf => Value: e | depth: 11
                                                                        L-->  X_2 <=
0.93 | depth: 8
                                                                                L-->
Leaf => Value: p | depth: 9
                                L-->  X_97 <= 0.0 | depth: 4
                                                R--> Leaf => Value: e | depth: 6
                                        L-->  X_1 <= 7.23 | depth: 5
                                                L--> Leaf => Value: p | depth: 6
                L-->  X_86 <= 0.0 | depth: 2
                                        R--> Leaf => Value: e | depth: 5
                                R-->  X_13 <= 0.0 | depth: 4
                                        L--> Leaf => Value: p | depth: 5
                        L-->  X_4 <= 0.0 | depth: 3
                                                R--> Leaf => Value: e | depth: 6
                                        R-->  X_106 <= 0.0 | depth: 5
                                                                        R--> Leaf =>
Value: e | depth: 8
                                                                R-->  X_11 <= 0.0 |
depth: 7
                                                                                R-->
Leaf => Value: e | depth: 9
                                                                        L-->  X_9 <= 0.0
| depth: 8
                                                                                L-->
Leaf => Value: p | depth: 9
```

```
                                                L-->  X_55 <= 0.0 | depth: 6
R--> Leaf => Value: e | depth: 10
                                                                        R-->
X_43 <= 0.0 | depth: 9
L--> Leaf => Value: p | depth: 10
                                                                R-->  X_58 <=
0.0 | depth: 8
R--> Leaf => Value: e | depth: 10
                                                                        L-->
X_34 <= 0.0 | depth: 9
L--> Leaf => Value: p | depth: 10
                                                        L-->  X_10 <= 0.0 |
depth: 7
        R--> Leaf => Value: p | depth: 11
R-->  X_8 <= 0.0 | depth: 10
        L--> Leaf => Value: e | depth: 11
                                                                        R-->
X_1 <= 4.08 | depth: 9
        R--> Leaf => Value: e | depth: 11
L-->  X_117 <= 0.0 | depth: 10
        L--> Leaf => Value: p | depth: 11
                                                                L-->  X_54 <=
0.0 | depth: 8
        R--> Leaf => Value: p | depth: 11
R-->  X_15 <= 0.0 | depth: 10
        L--> Leaf => Value: e | depth: 11
                                                                        L-->
X_49 <= 0.0 | depth: 9
        R--> Leaf => Value: e | depth: 11
L-->  X_22 <= 0.0 | depth: 10
        L--> Leaf => Value: p | depth: 11
                                L-->  X_2 <= 5.24 | depth: 4
                                                                R--> Leaf =>
Value: e | depth: 8
                                                        R-->  X_9 <= 0.0 |
depth: 7
                                                                L--> Leaf =>
Value: p | depth: 8
                                                R-->  X_73 <= 0.0 | depth: 6
                                                                        R-->
Leaf => Value: e | depth: 9
                                                                R-->  X_43 <=
0.0 | depth: 8
R--> Leaf => Value: p | depth: 10
                                                                        L-->
X_1 <= 2.95 | depth: 9
L--> Leaf => Value: e | depth: 10
                                                        L-->  X_14 <= 0.0 |
```

```
depth: 7
R--> Leaf => Value: e | depth: 10
                                                                        R-->
X_10 <= 0.0 | depth: 9
L--> Leaf => Value: p | depth: 10
                                                                L-->  X_8 <= 0.0
| depth: 8
                                                                        L-->
Leaf => Value: p | depth: 9
                                        L-->  X_34 <= 0.0 | depth: 5
                                                                R--> Leaf =>
Value: e | depth: 8
                                                        R-->  X_11 <= 0.0 |
depth: 7
                                                                L--> Leaf =>
Value: p | depth: 8
                                                L-->  X_0 <= 1.4 | depth: 6
                                                        L--> Leaf => Value: e |
depth: 7
```

The first 3 split is 2,46,68. Since decision tree will find the use best split in each decision node, the most important features will be in the first coupes splits.

```
[ ]: X.iloc[:,[2,26,68]].columns
```

```
[ ]: Index(['stem-width', 'cap-color_l', 'stem-surface_g'], dtype='object')
```

'stem-width', 'cap-color_l', 'stem-surface_g' are the important features.

4.3 KNN

```
[ ]: # import numpy as np
     # from collections import Counter
     # class KNN:

     #     def __init__(self,k=3):
     #         self.k = k

     #     def fit(self,X,y):
     #         self.X_train = X
     #         self.y_train = y

     #     def predict(self,X):
     #         pred_y = [self._predict(x) for x in X]
     #         return np.array(pred_y)


     #     def _predict(self,x):
```

```
#         distances = np.linalg.norm(self.X_train - x, axis=1)

#         # Find the indices of the k nearest neighbors
#         k_index = np.argpartition(distances, self.k)[:self.k]

#         # Retrieve the labels of the k nearest neighbors
#         k_nearest_labels = self.y_train[k_index]

#         return list(Counter(k_nearest_labels).keys())[0]
```

[ ]:
```
from pca import PCA
from KNN import KNN
pca = PCA(n_components=2)
pca.fit(X)
X_transform = pca.transform(X)
X_transform = pd.DataFrame(X_transform,columns=['PC1',"PC2"])
train_X,test_X,train_y,test_y = train_test_split(X_transform,y,test_size=0.
 ↪2,random_state=42)
```

4.3.1 Training set

[ ]:
```
knn = KNN(k=247)
knn.fit(train_X.values,train_y.values)
pred_y = knn.predict(train_X.values)
```

[ ]:
```
print(f'accuracy: {np.mean(train_y == pred_y)}')
```

```
accuracy: 0.6252379490328523
```

4.3.2 Test set

[ ]:
```
pred_y = knn.predict(test_X.values)
print(f'accuracy: {np.mean(test_y == pred_y)}')
```

```
accuracy: 0.6240379891927297
```

KNN perform worse than logistic regression and Decision Tree. I choose coupe k values: 7,11,21,41 they perform similarly as k=247. The best accuracy i got from KNN is 0.71 which is still worse than other models.

4.3.3 important feature

KNN cannot find the most important features

5 Model selection

- Logistic Regression:

  - run time: 1min
  - Train: 0.815
  - Test: 0.811
- Decision Tree:
  - run time: 3hours
  - Train: 0.866
  - Test: 0.864
- KNN:
  - run time: 1min
  - Train: 0.625
  - Test: 0.624

The model I will choose is Decision Tree, It has the best performance compare with other two models, but it takes long time to train the model. In addition, Decision Tree can find the important features easily. I think I can optimize the run time using some data structure and using vectorization by numpy.