CSM148_Project3_Yaman_Yucel-Final

February 22, 2023

You are exploring the wilderness of *Mushroomia*, a land populated by a plethora of diverse fauna and flora. In particular, *Mushroomia* is known for its unparalleled variety in mushrooms. However, not all the mushrooms in *Mushroomia* are edible. As you make your way through *Mushroomia*, you would like to know which mushrooms are edible, in order to forage for supplies for your daily mushroom soup.

You have access to: * *Shroomster Pro Max TM* - a state of the art data collection device, developed by *Mushroomia*, that allows you to collect various data points about any mushroom you encounter in the wild * *The National Archives on Mushrooms* - a dataset collected over the years by the government of *Mushroomia*

To address this problem, you decide to use the skills you learnt in CSM148 and train machine learning models on the *The National Archives on Mushrooms* in order to use your *Shroomster Pro Max TM* to determine whether the mushrooms you encounter on your adventure can be added to your daily mushroom soup.

This project will be more unstructured than the previous two projects in order to allow you to experience how data science problems are solved in practice. There are two parts to this project: a Jupyter Notebook with your code (where you explore, visualize, process your data and train machine learning models) and a report (where you explain the various choices you make in your implementation and analyze the final performance of your models).

1 1. Loading and Viewing Data

[1]:
```python
import pandas as pd
import warnings
warnings.filterwarnings('ignore')

from sklearn.metrics import *
import numpy as np # linear algebra
import matplotlib.pyplot as plt # this is used for the plot the graph
import os
import seaborn as sns # used for plot interactive graph.
from sklearn.model_selection import train_test_split,␣
↪cross_val_score,GridSearchCV
from sklearn import metrics
from sklearn.svm import SVC
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
```

```
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import confusion_matrix
import sklearn.metrics.cluster as smc
from sklearn.model_selection import KFold
from pandas.plotting import scatter_matrix

train_df = pd.read_csv("mushroom_train.csv", delimiter = ";")
test_df = pd.read_csv("mushroom_test.csv", delimiter = ";")
train_df = train_df.sample(frac = 1,random_state = 42)
test_df = test_df.sample(frac = 1,random_state = 42)
 #note delimitter for this file is semi-colon (;) not comma
```

[2]:
```
def␣
↪report_classifier_performance(clf,train_data_tf,test_data_tf,train_label,test_label):
↪
    print(clf)
    clf.fit(train_data_tf,train_label)
    prediction = clf.predict(test_data_tf)
    accuracy_tf = metrics.accuracy_score(test_label,prediction)
    precision_tf = metrics.precision_score(test_label,prediction)
    recall_tf = metrics.recall_score(test_label,prediction)
    f1_tf = metrics.f1_score(test_label,prediction)
    confusion_matrix_tf = metrics.confusion_matrix(test_label, prediction)
    print("Accuracy with transformed data: ",accuracy_tf)
    print("Precision with transformed data: ",precision_tf)
    print("Recall with transformed data: ",recall_tf)
    print("F1 score with transformed data: ",f1_tf)
    cm_display = metrics.ConfusionMatrixDisplay(confusion_matrix␣
↪=confusion_matrix_tf,display_labels = ["poisonous","edible"] )
    cm_display.plot()
    metrics.plot_roc_curve(clf,test_data_tf ,test_label)
    plt.plot([0, 1], [0, 1], color='navy', linestyle='--')
    plt.xlim([0.0, 1.0])
    plt.ylim([0.0, 1.0])
    plt.show()
```

[3]:
```
train_df
```

[3]:
```
      class  cap-diameter cap-shape cap-surface cap-color  \
21982     e          3.91         x         NaN         y
12387     e          1.58         x           s         y
16701     e          7.56         f           t         o
28593     p          6.53         s           d         e
44850     p          3.83         b           y         n
…       …             …       …         …       …
11284     p          2.37         x           g         n
44732     p          8.00         b           y         w
```

```
38158     p          7.68          x           e          n
860       p         12.28          f         NaN          n
15795     p          6.78          x           s          n

      does-bruise-or-bleed gill-attachment gill-spacing gill-color  \
21982                    f               a            c          y
12387                    f               d          NaN          w
16701                    f               s          NaN          y
28593                    t               d            c          y
44850                    f             NaN            c          g
…                      …             …          …        …
11284                    f               a          NaN          p
44732                    f             NaN          NaN          p
38158                    f               a          NaN          n
860                      f               e          NaN          w
15795                    t               s            d          r

       stem-height  …  stem-root stem-surface stem-color veil-type  \
21982         4.84  …        NaN          NaN          w       NaN
12387         6.05  …        NaN            t          y       NaN
16701         8.21  …        NaN            i          o       NaN
28593         5.33  …        NaN          NaN          n       NaN
44850         5.60  …          s            s          w       NaN
…              …  …        …          …        …       …
11284         7.45  …        NaN          NaN          w       NaN
44732        12.99  …        NaN          NaN          w       NaN
38158        11.95  …          s          NaN          n       NaN
860          10.79  …        NaN          NaN          w         u
15795         6.43  …          r            y          w       NaN

      veil-color has-ring ring-type spore-print-color habitat season
21982        NaN        f         f               NaN       d      u
12387        NaN        f         f               NaN       h      a
16701        NaN        f         f               NaN       d      a
28593        NaN        f         f               NaN       d      u
44850        NaN        f         f               NaN       d      a
…            …      …       …               …     …    …
11284        NaN        f         f               NaN       d      u
44732        NaN        f         f               NaN       d      a
38158          n        f         f               NaN       h      a
860            w        t         g               NaN       d      u
15795        NaN        f         f               NaN       d      u

[50213 rows x 21 columns]
```

[4]:
```
test_df
```

```
[4]:      class  cap-diameter cap-shape cap-surface cap-color does-bruise-or-bleed  \
     33       p          2.88         b         NaN         g                    f
     7233     e          3.22         s         NaN         y                    f
     4582     e          6.46         x         NaN         g                    t
     5981     p          9.35         s           t         n                    t
     3272     p          9.54         x         NaN         n                    f
     …     …           …       …        …        …                …
     5734     p         10.67         x           t         r                    t
     5191     e          9.43         x           h         n                    t
     5390     e          8.98         x           h         n                    f
     860      e         17.05         x           t         n                    f
     7270     e          3.15         s         NaN         n                    f

          gill-attachment gill-spacing gill-color  stem-height  …  stem-root  \
     33                 a          NaN          n         9.26  …        NaN
     7233               f            f          f         6.36  …        NaN
     4582               p          NaN          g        12.58  …        NaN
     5981               d            c          n         5.63  …        NaN
     3272               p          NaN          p        11.09  …          c
     …               …           …        …          …  …        …
     5734               d            c          n         6.01  …        NaN
     5191               p          NaN          y         8.09  …        NaN
     5390               p            d          y         7.42  …        NaN
     860                p          NaN          w        19.89  …        NaN
     7270               f            f          f         5.67  …        NaN

          stem-surface stem-color veil-type  veil-color has-ring ring-type  \
     33            NaN          n       NaN           w        f         f
     7233          NaN          o       NaN         NaN        f         f
     4582            y          w       NaN         NaN        f         f
     5981          NaN          n       NaN         NaN        f         f
     3272          NaN          n       NaN         NaN        f         f
     …           …        …       …         …       …       …
     5734          NaN          n       NaN         NaN        f         f
     5191          NaN          n       NaN           w        t         p
     5390            s          n       NaN         NaN        f         f
     860           NaN          n       NaN         NaN        f         f
     7270          NaN          o       NaN         NaN        f         f

          spore-print-color habitat season
     33                   k       g      a
     7233               NaN       d      a
     4582               NaN       d      a
     5981               NaN       h      a
     3272                 p       d      a
     …                 …     …    …
     5734               NaN       h      a
```

```
5191                 NaN        d       a
5390                 NaN        d       u
860                  NaN        d       a
7270                 NaN        d       a

[10856 rows x 21 columns]
```

2 2. Splitting Data into Features and Labels

[5]:
```python
# Only keep features that shroomster can detect!
train_features = train_df.drop("class",axis = 1)
train_labels = train_df["class"]
test_features = test_df.drop("class",axis = 1)
test_labels = test_df["class"]
```

3 3. Data Exploration and Visualization

[6]:
```python
# Hint: We have done this in both project 1 & 2

%matplotlib inline
import matplotlib.pyplot as plt #plotting package
train_df.head()
```

[6]:
```
      class  cap-diameter cap-shape cap-surface cap-color  \
21982     e          3.91         x         NaN         y
12387     e          1.58         x           s         y
16701     e          7.56         f           t         o
28593     p          6.53         s           d         e
44850     p          3.83         b           y         n

      does-bruise-or-bleed gill-attachment gill-spacing gill-color  \
21982                    f               a            c          y
12387                    f               d          NaN          w
16701                    f               s          NaN          y
28593                    t               d            c          y
44850                    f             NaN            c          g

       stem-height  …  stem-root stem-surface stem-color veil-type  \
21982         4.84  …        NaN          NaN          w       NaN
12387         6.05  …        NaN            t          y       NaN
16701         8.21  …        NaN            i          o       NaN
28593         5.33  …        NaN          NaN          n       NaN
44850         5.60  …          s            s          w       NaN

      veil-color has-ring ring-type spore-print-color habitat season
```

```
21982         NaN        f          f               NaN        d       u
12387         NaN        f          f               NaN        h       a
16701         NaN        f          f               NaN        d       a
28593         NaN        f          f               NaN        d       u
44850         NaN        f          f               NaN        d       a

[5 rows x 21 columns]
```

[7]:
```python
train_df.iloc[1]
```

[7]:
```
class                       e
cap-diameter             1.58
cap-shape                   x
cap-surface                 s
cap-color                   y
does-bruise-or-bleed        f
gill-attachment             d
gill-spacing              NaN
gill-color                  w
stem-height              6.05
stem-width               2.25
stem-root                 NaN
stem-surface                t
stem-color                  y
veil-type                 NaN
veil-color                NaN
has-ring                    f
ring-type                   f
spore-print-color         NaN
habitat                     h
season                      a
Name: 12387, dtype: object
```

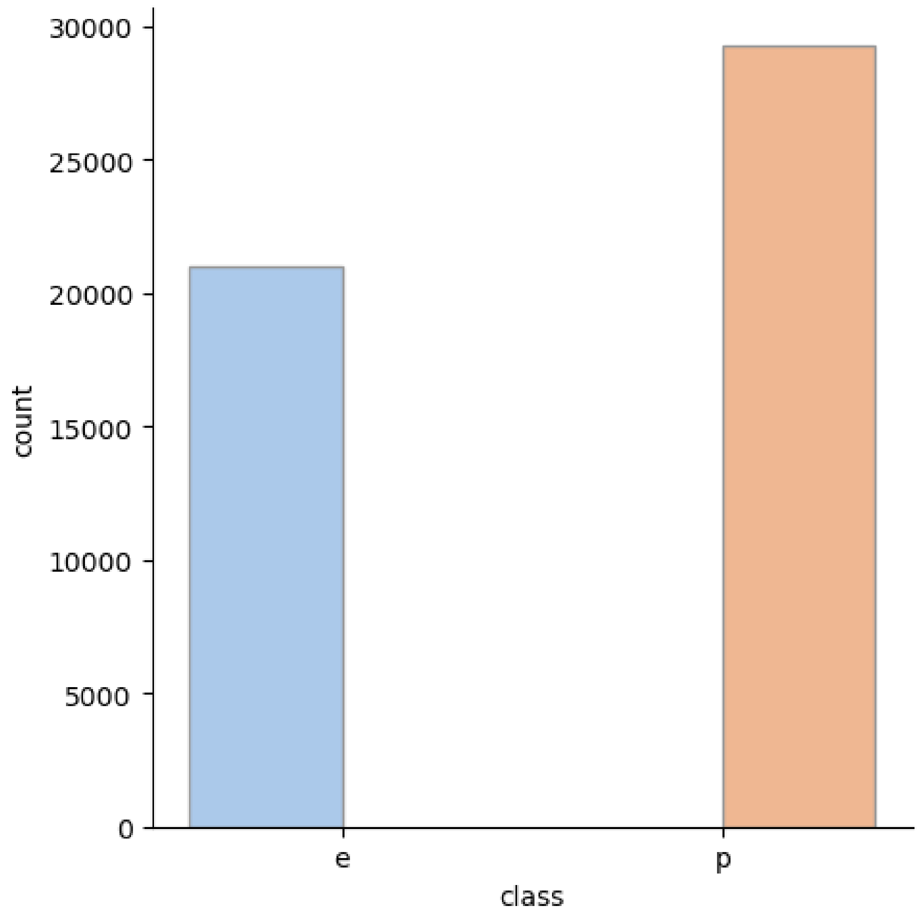
[8]:
```python
train_df.describe()
```

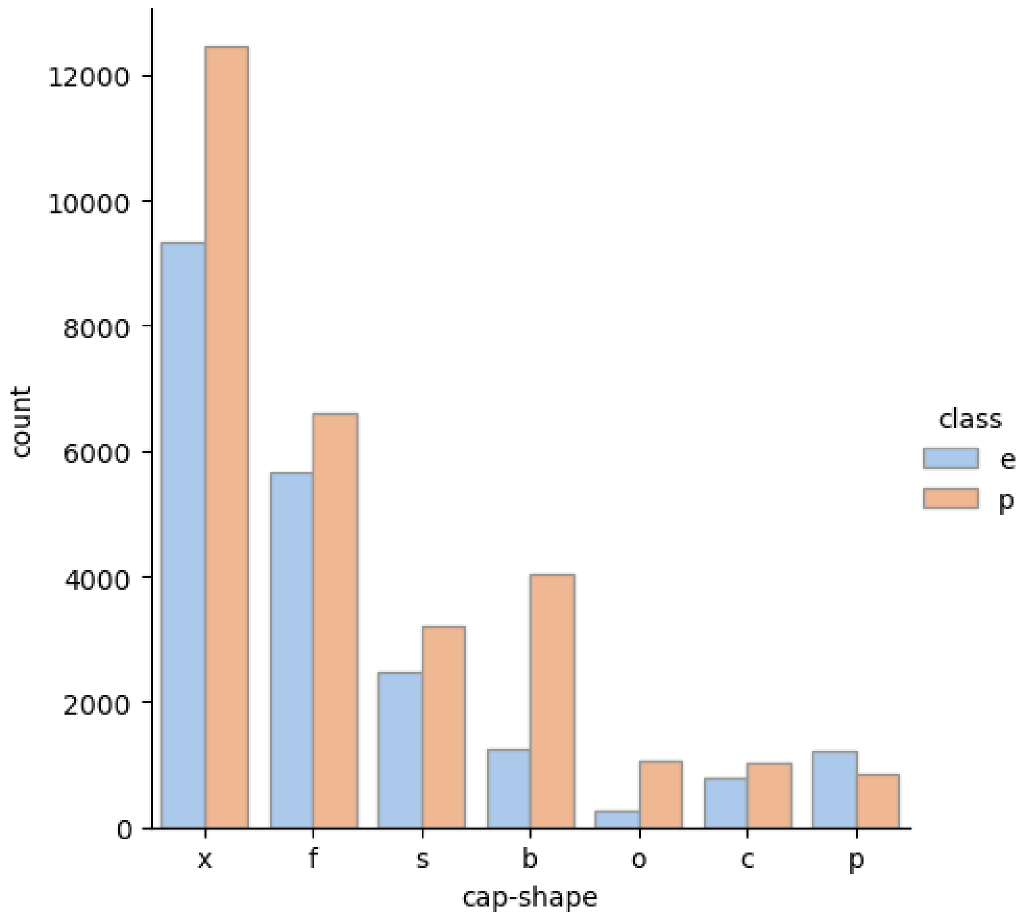
[8]:

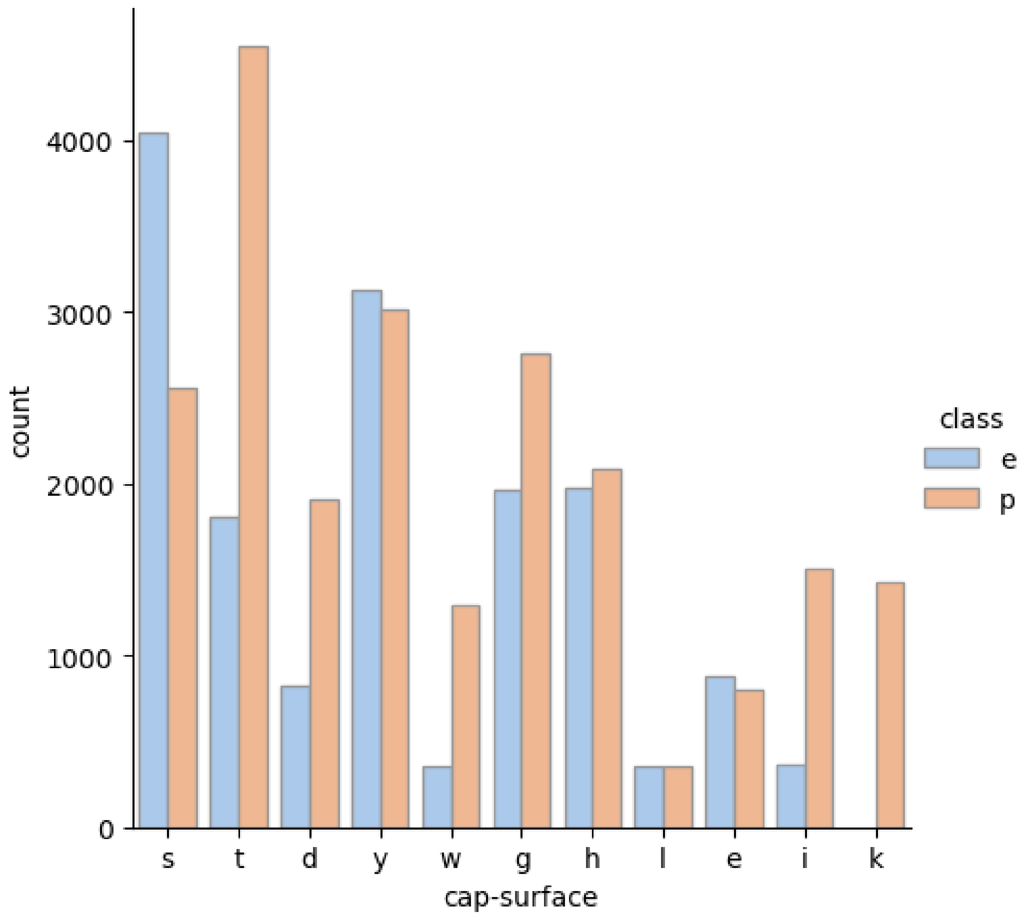
	cap-diameter	stem-height	stem-width
count	50213.000000	50213.000000	50213.000000
mean	6.245186	6.600561	10.763191
std	4.542552	3.221714	7.744992
min	0.380000	1.200000	0.520000
25%	3.290000	4.680000	4.720000
50%	5.540000	5.900000	9.130000
75%	8.100000	7.600000	15.210000
max	58.890000	33.920000	58.950000

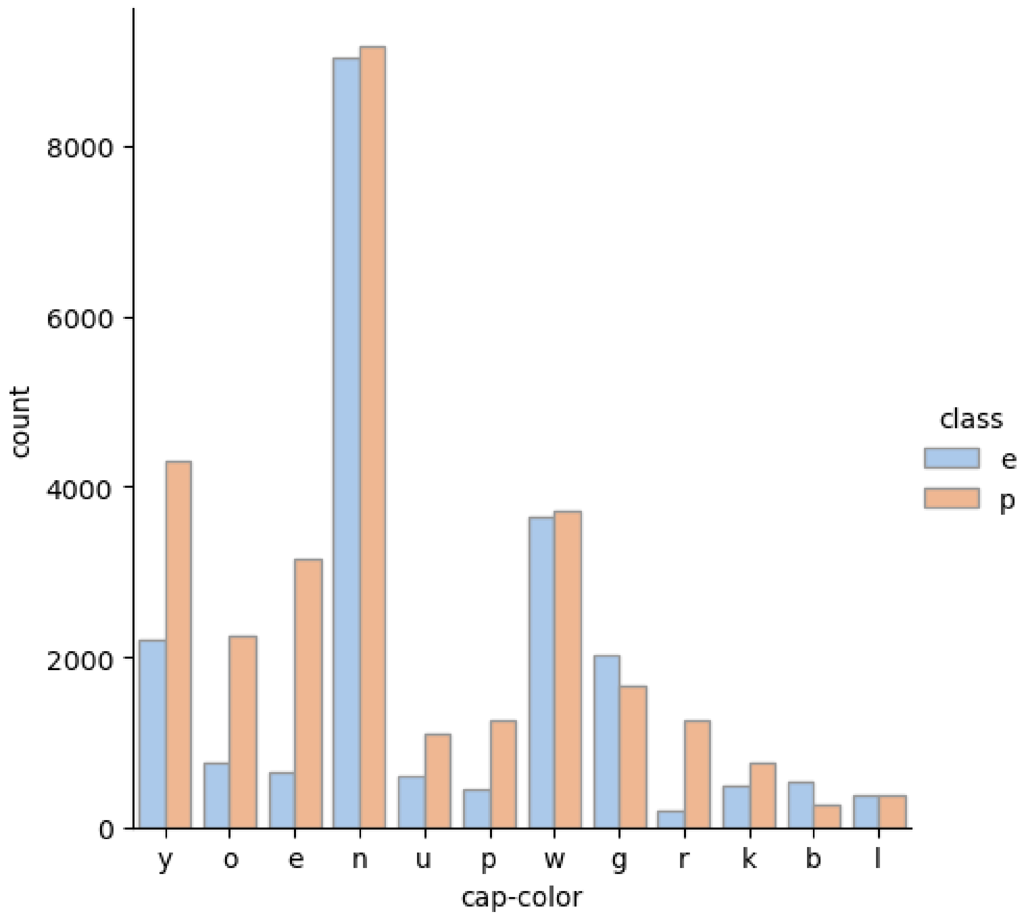
[9]:
```python
import seaborn as sns
```

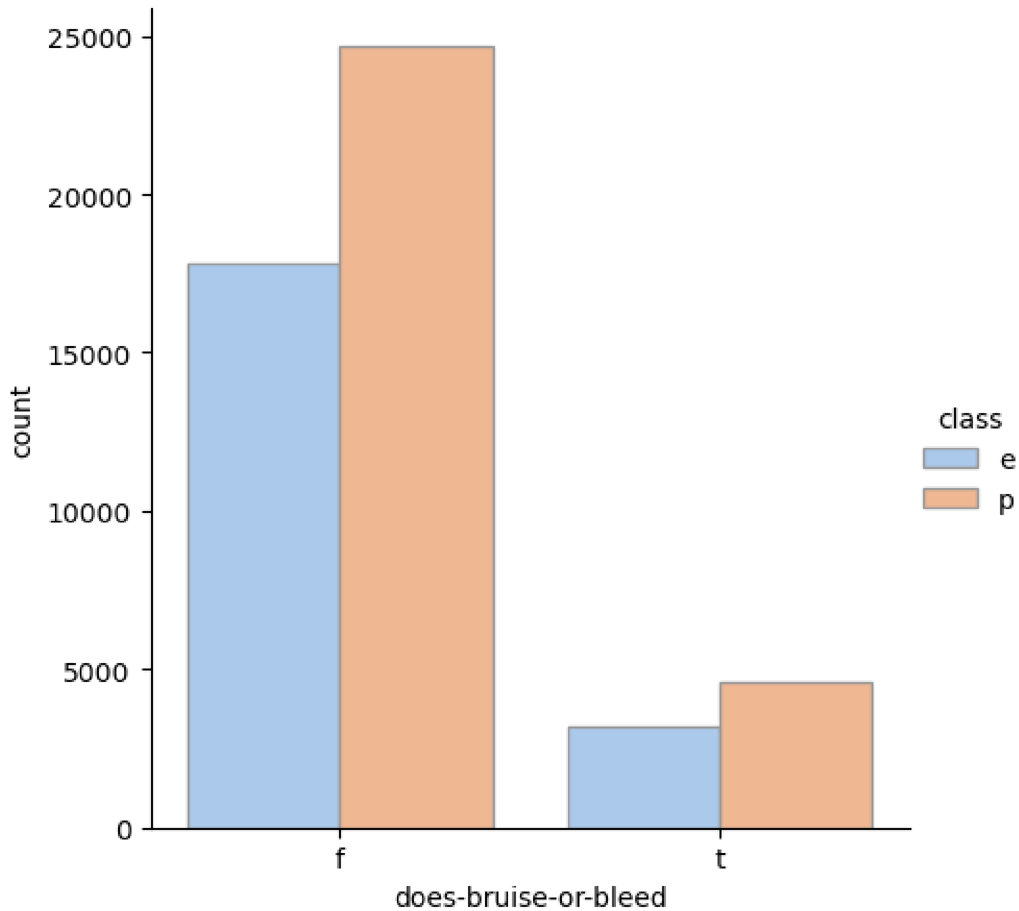
```python
for name in train_df.columns:
    if train_df[name].dtype == 'O':
        sns.catplot(
            data=train_df, x=name, hue="class", kind="count",
            palette="pastel", edgecolor=".6"
        )
        plt.show()
```

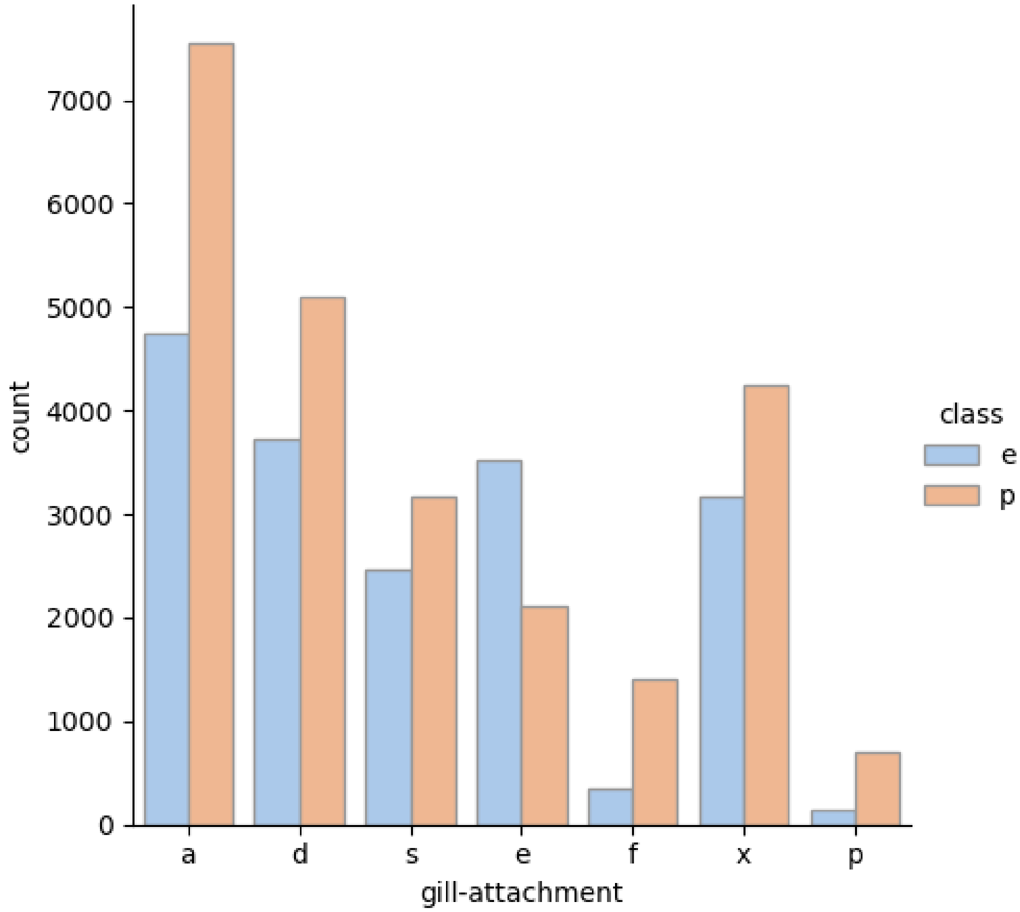



12000
10000
8000
6000
4000
2000
0
count
x
f
s
b
o
c
p
cap-shape
class
e
p

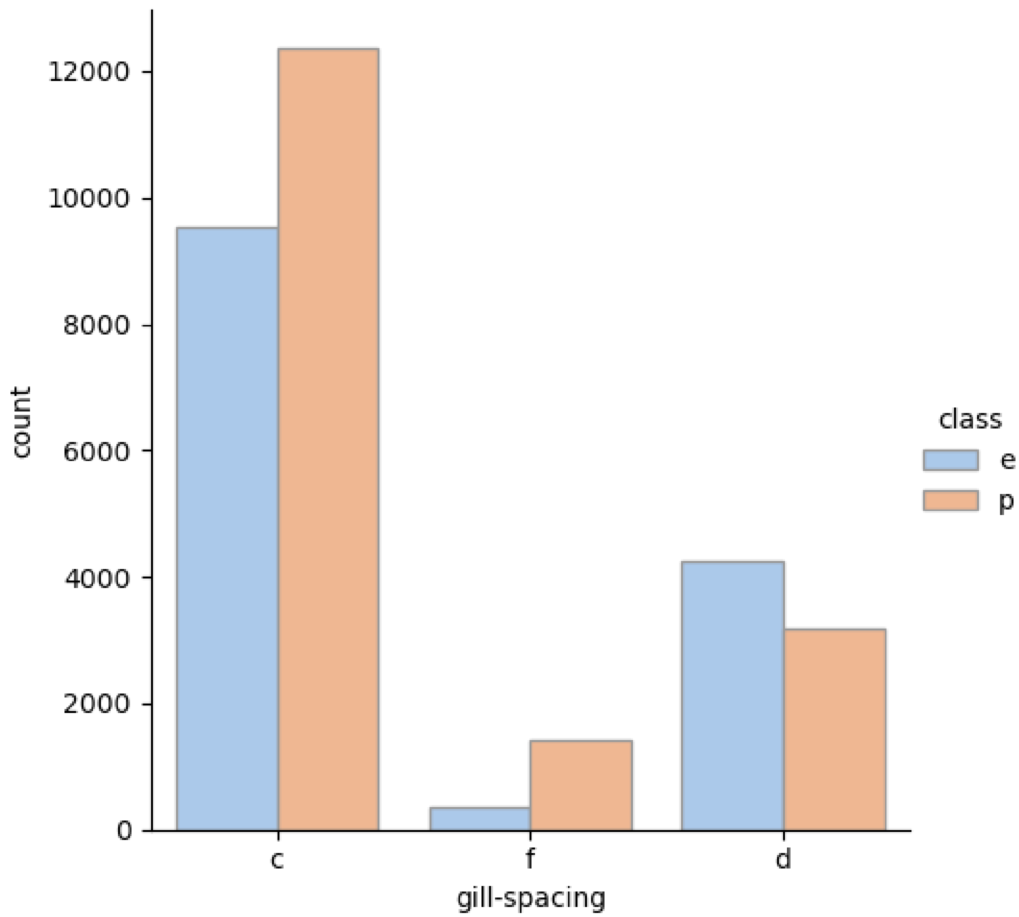

4000
3000
2000
1000
0
count
s
t
d
y
w
g
h
l
e
i
k
cap-surface
class
e
p

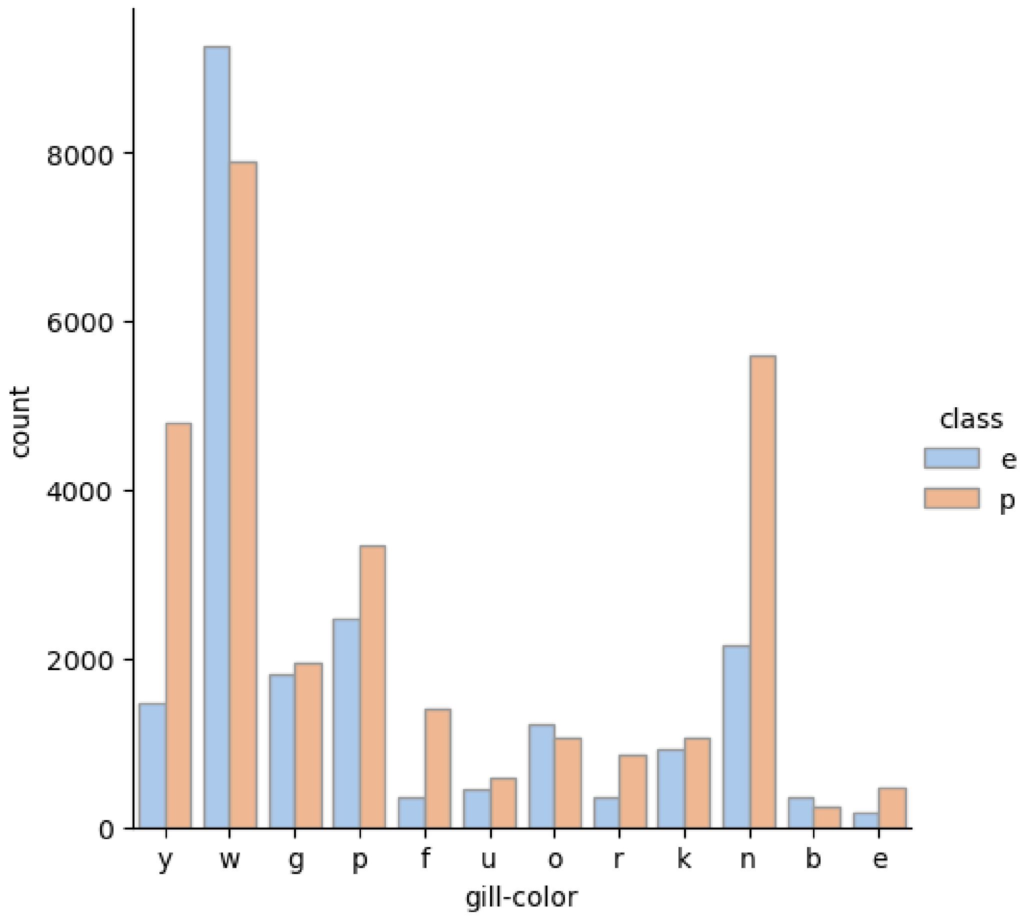

8000
6000
4000
2000
0
count
y
o
e
n
u
p
w
g
r
k
b
l
cap-color
class
e
p


25000
20000
15000
10000
5000
0
count
f
t
does-bruise-or-bleed
class
e
p

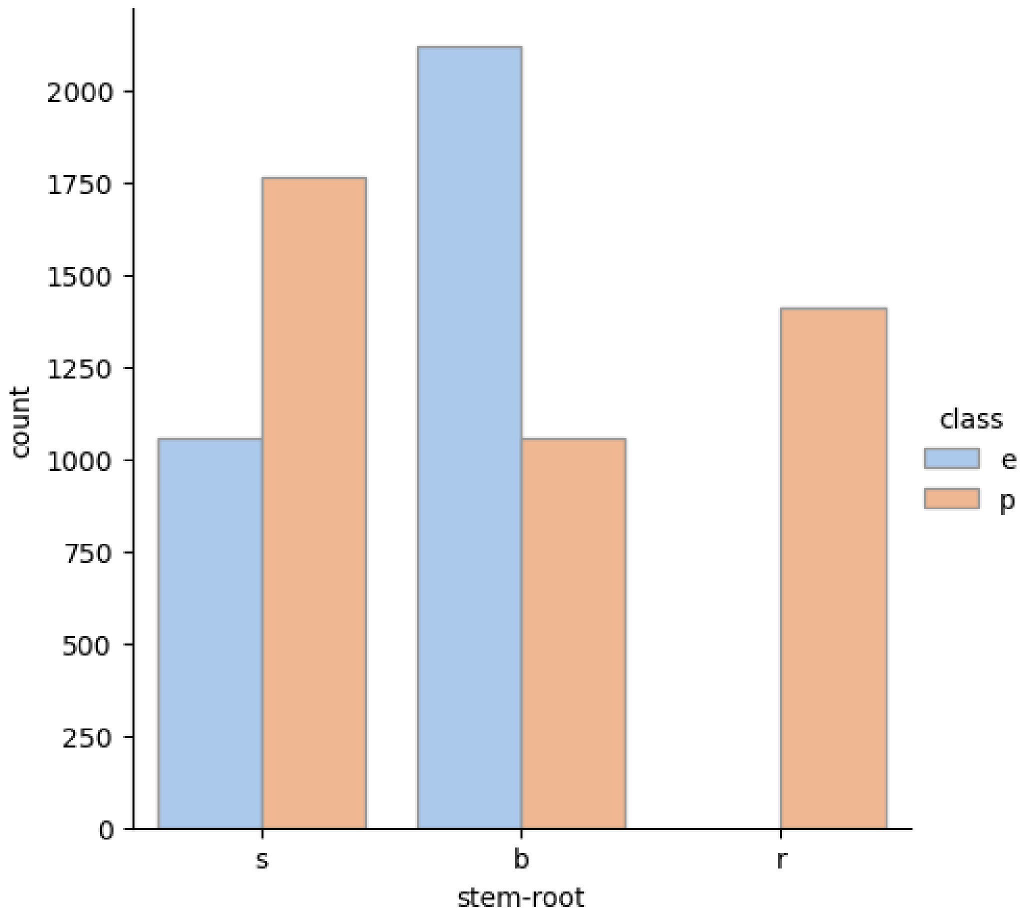


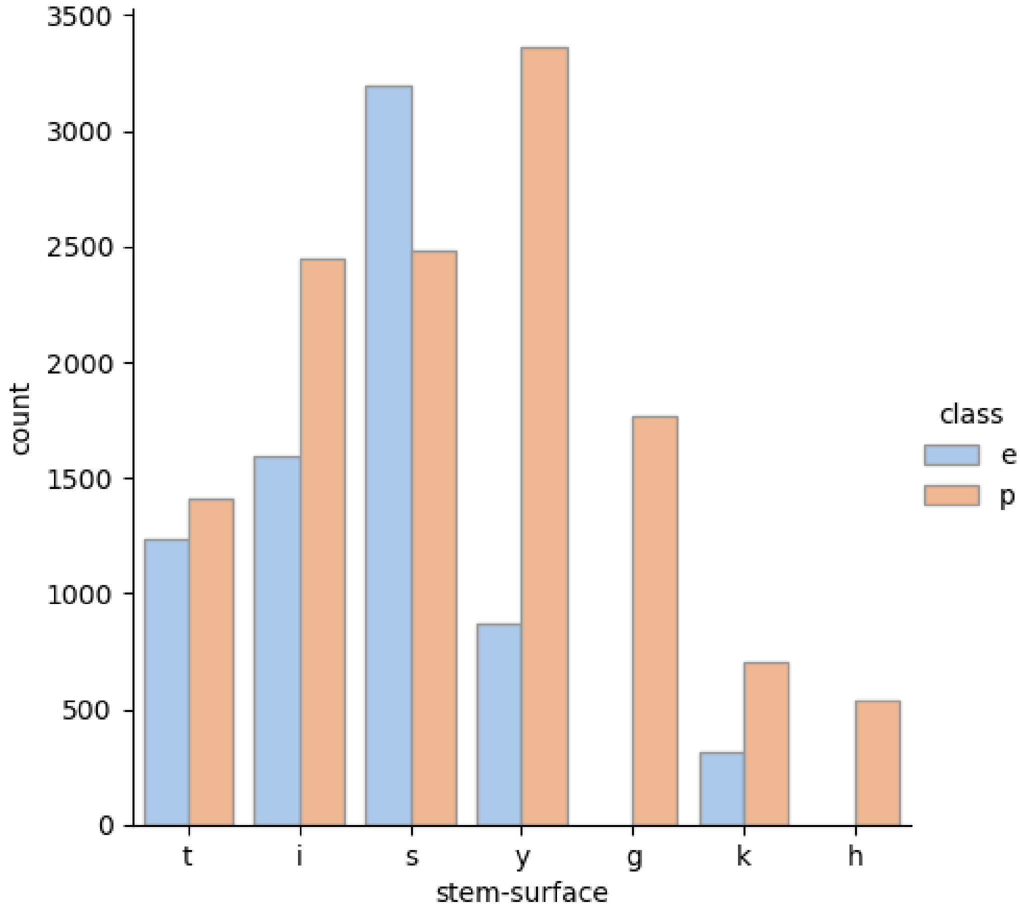
count
7000
6000
5000
4000
3000
2000
1000
0
a
d
s
e
f
x
p
gill-attachment
class
e
p

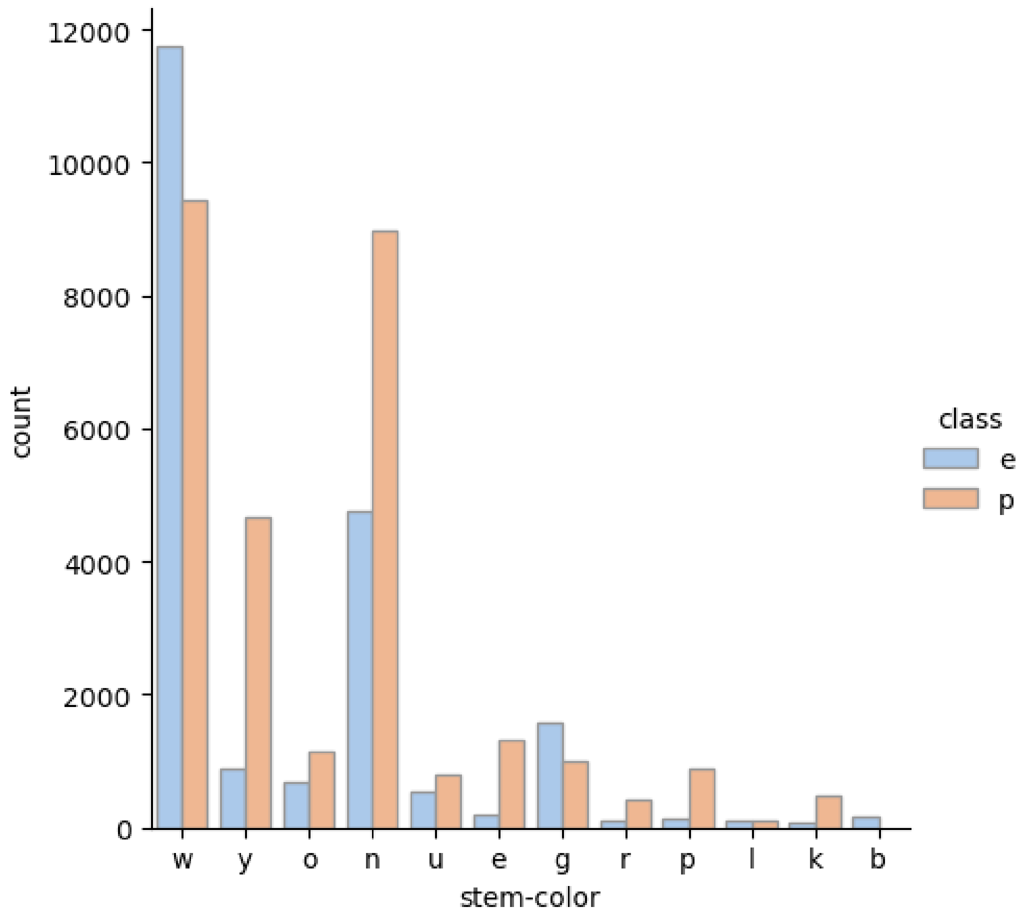

count
12000
10000
8000
6000
4000
2000
0
c
f
d
gill-spacing
class
e
p



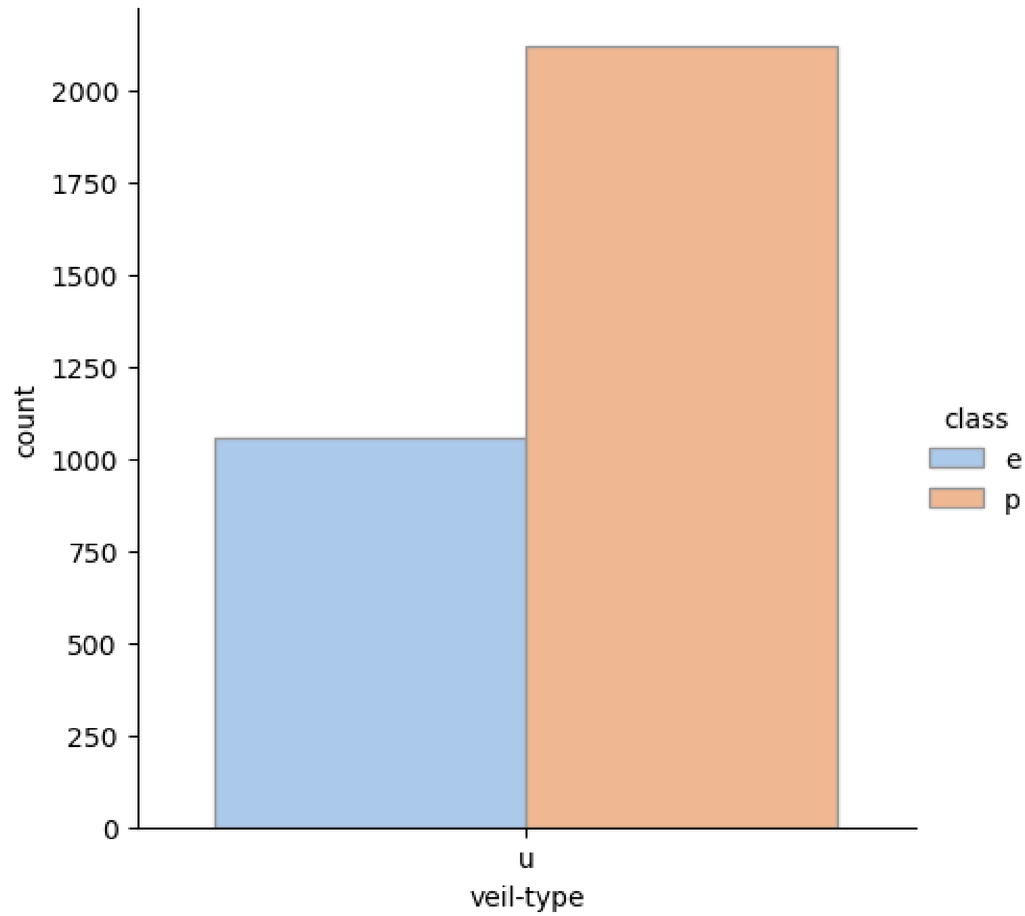
count
8000
6000
4000
2000
0
y
w
g
p
f
u
o
r
k
n
b
e
gill-color
class
e
p


2000
1750
1500
1250
1000
750
500
250
0
count
s
b
r
stem-root
class
e
p

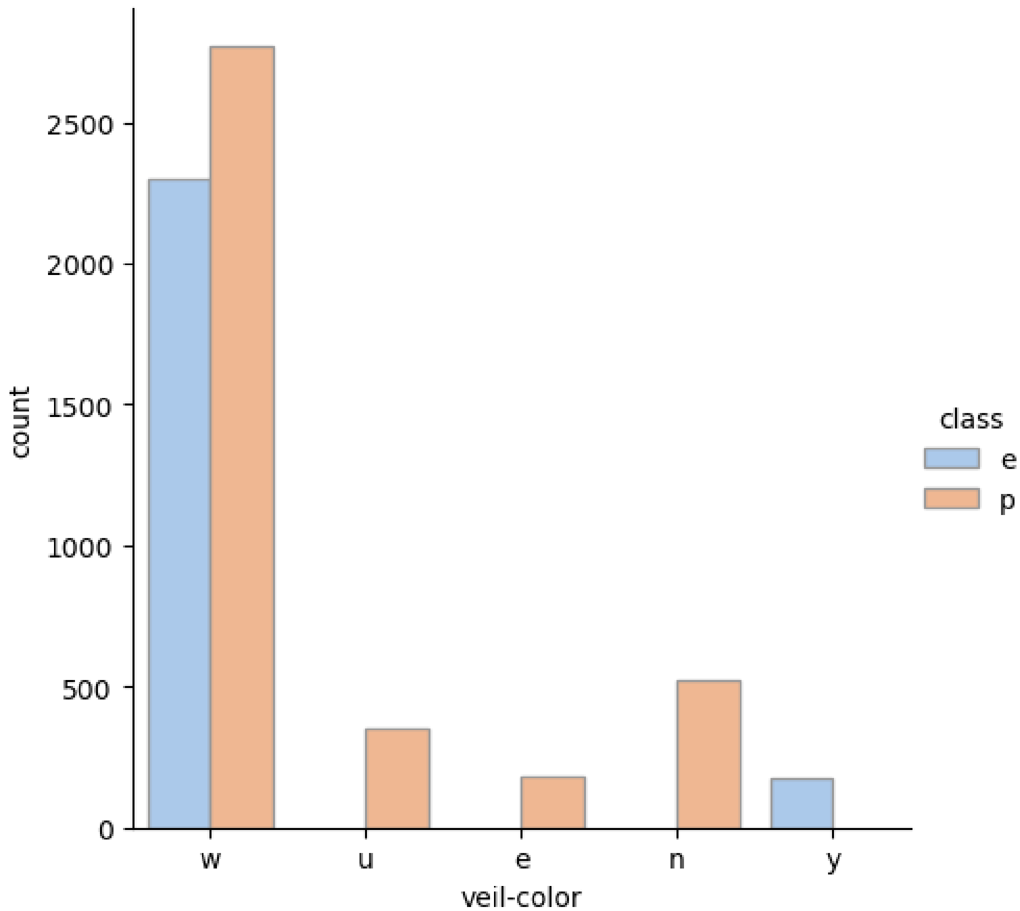

count
3500
3000
2500
2000
1500
1000
500
0
t
i
s
y
g
k
h
stem-surface
class
e
p

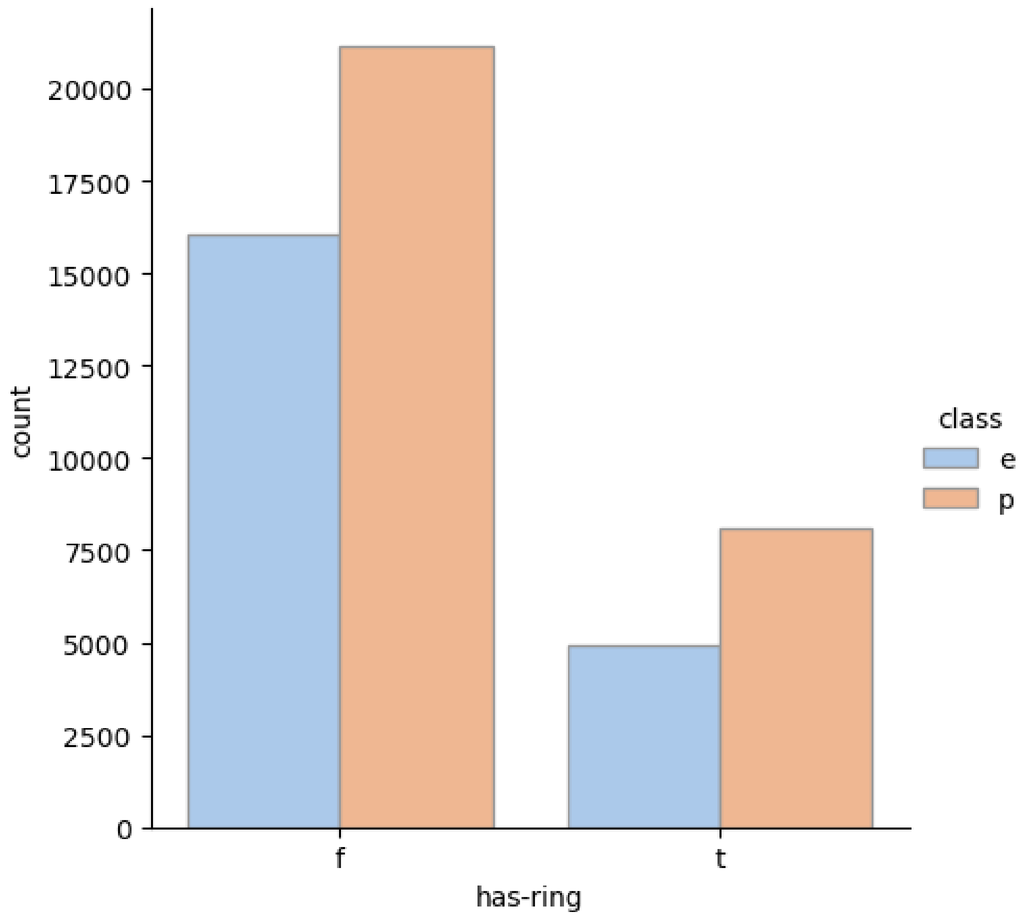


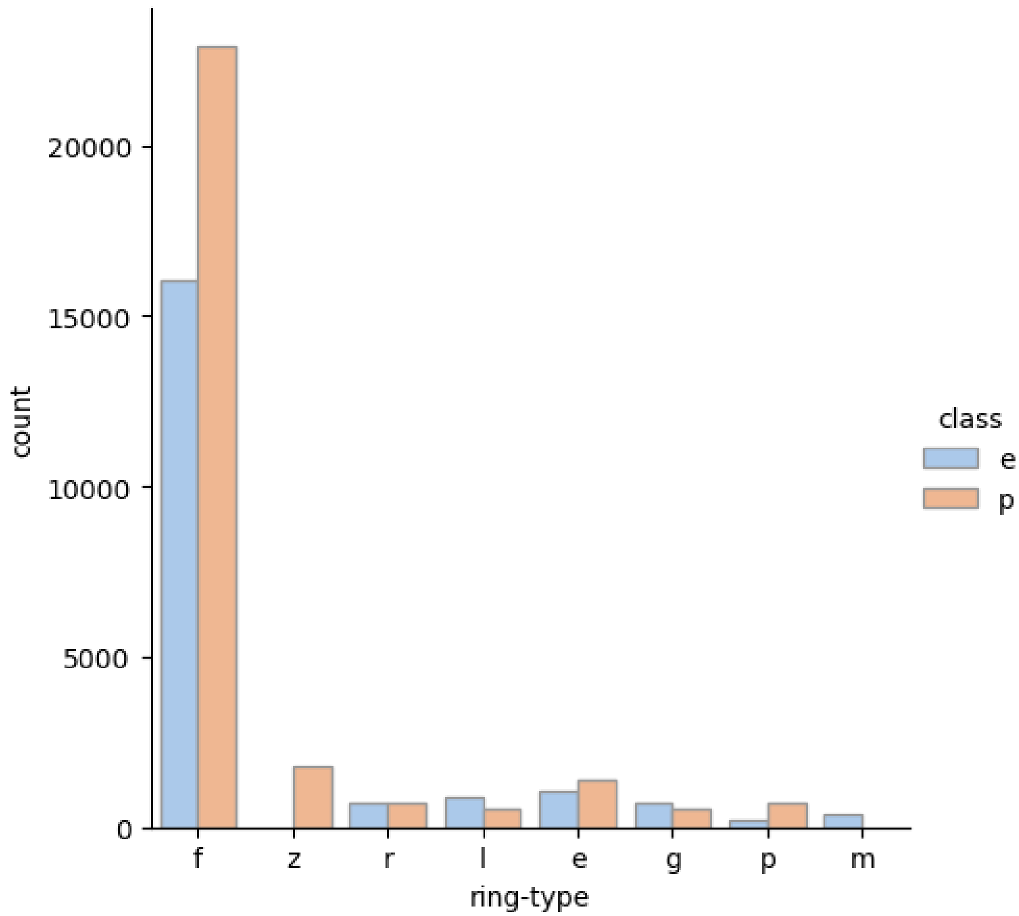
12000
10000
8000
6000
4000
2000
0
count
w
y
o
n
u
e
g
r
p
l
k
b
stem-color
class
e
p

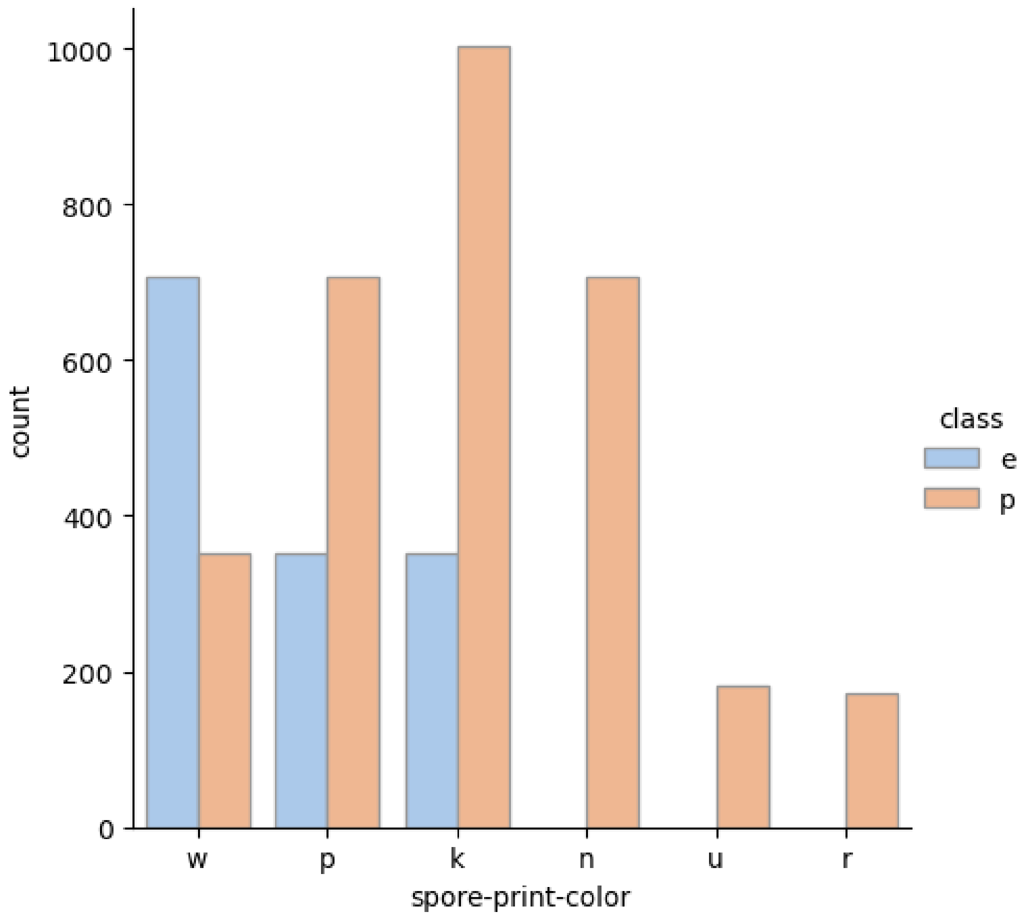


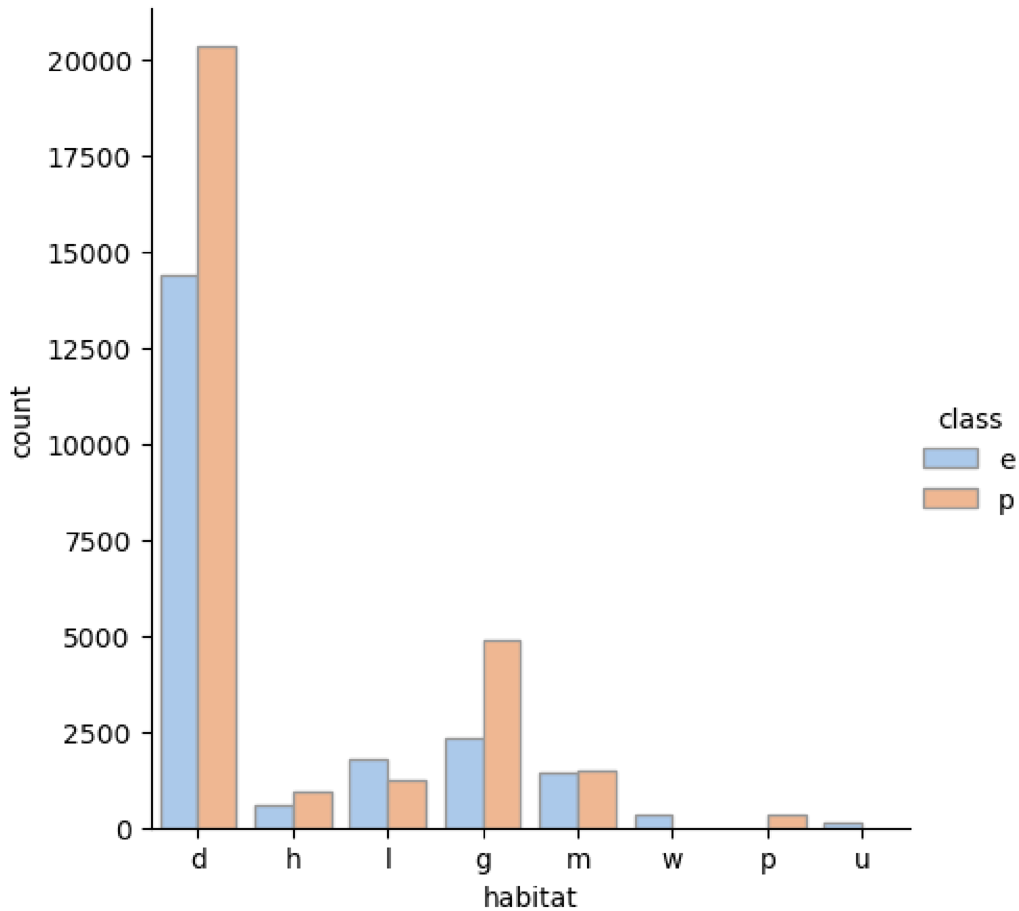
2000
1750
1500
1250
1000
750
500
250
0
count
u
veil-type
class
e
p

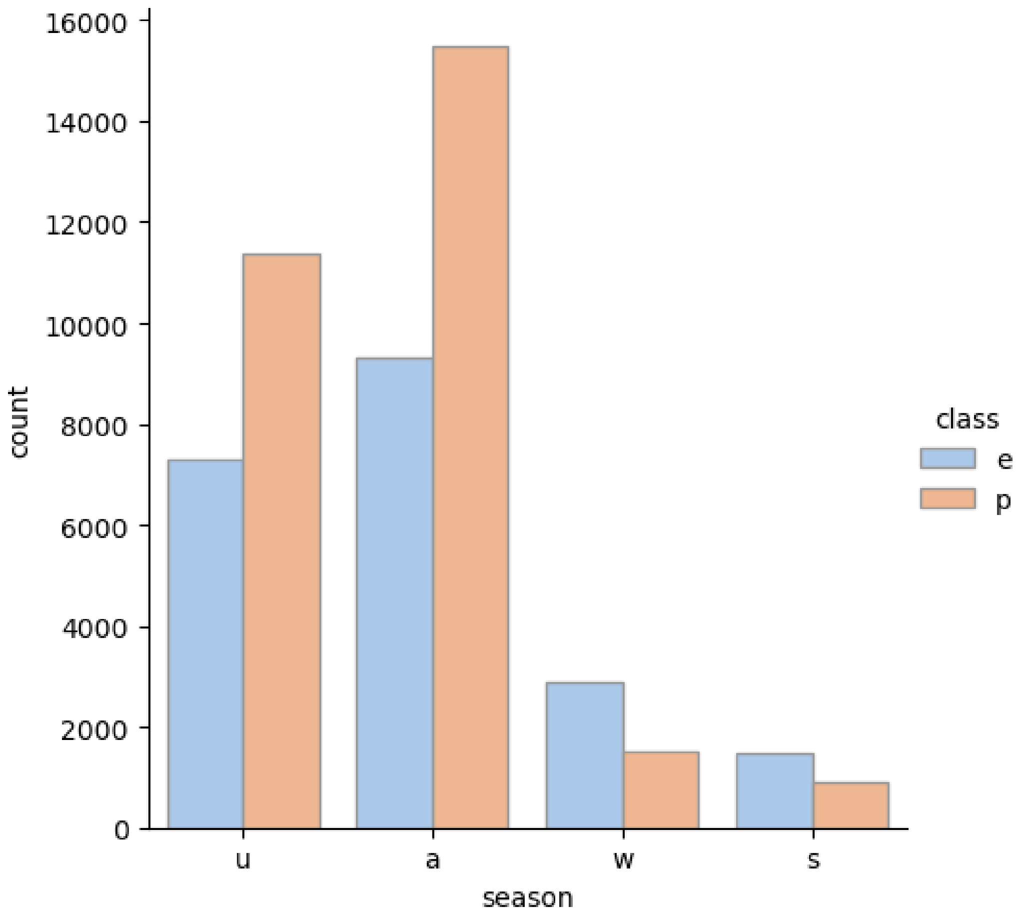

count
2500
2000
1500
1000
500
0
w
u
e
n
y
veil-color
class
e
p


count
has-ring
class
e
p
f
t
0
2500
5000
7500
10000
12500
15000
17500
20000

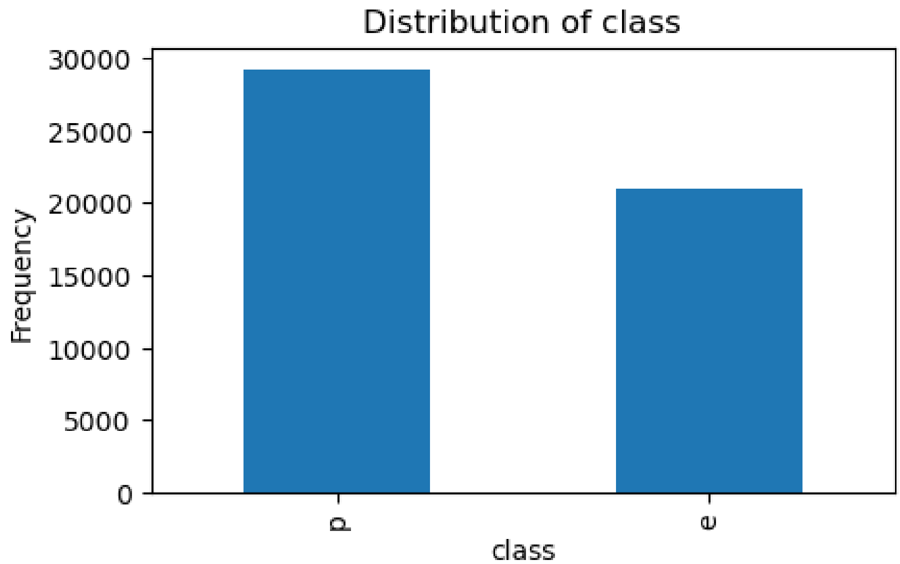

20000
15000
10000
5000
0
count
f
z
r
l
e
g
p
m
ring-type
class
e
p

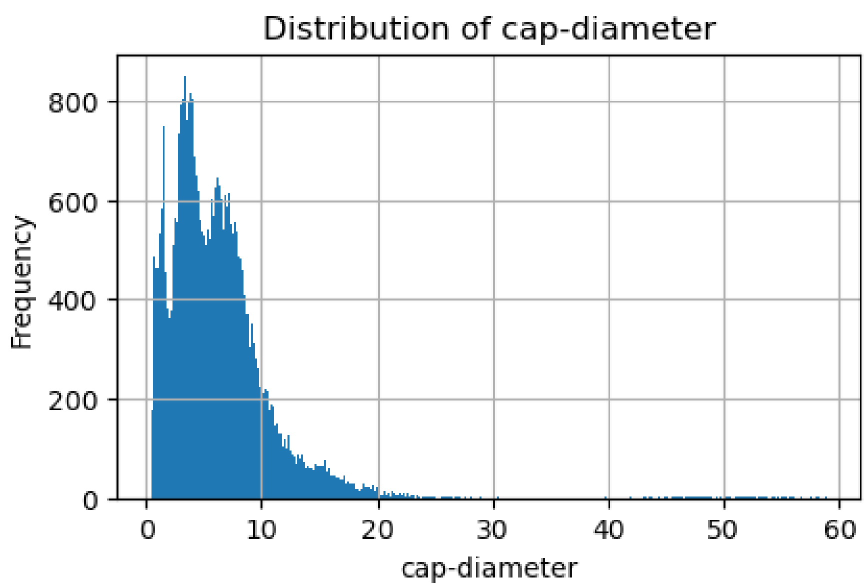

1000
800
600
400
200
0
count
w
p
k
n
u
r
spore-print-color
class
e
p

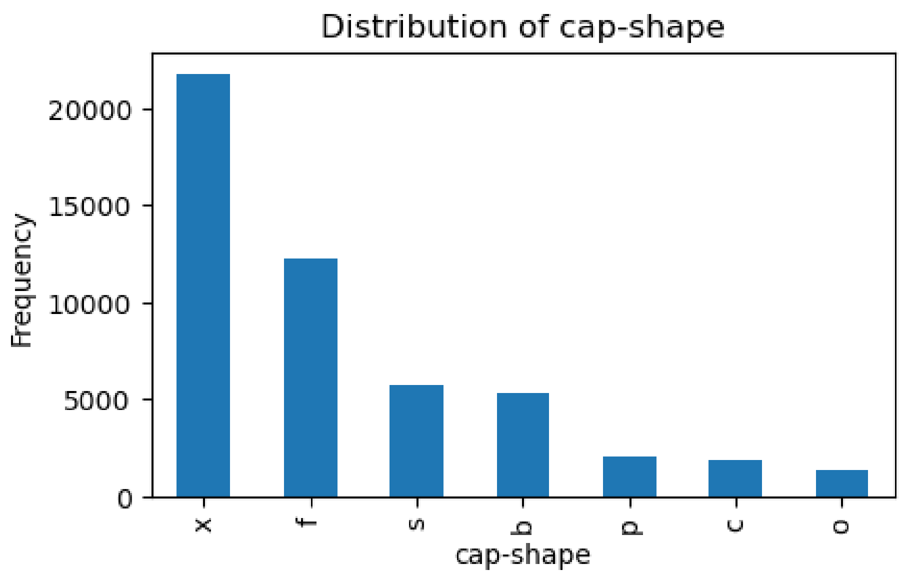

20000
17500
15000
12500
10000
7500
5000
2500
0
count
d
h
l
g
m
w
p
u
habitat
class
e
p

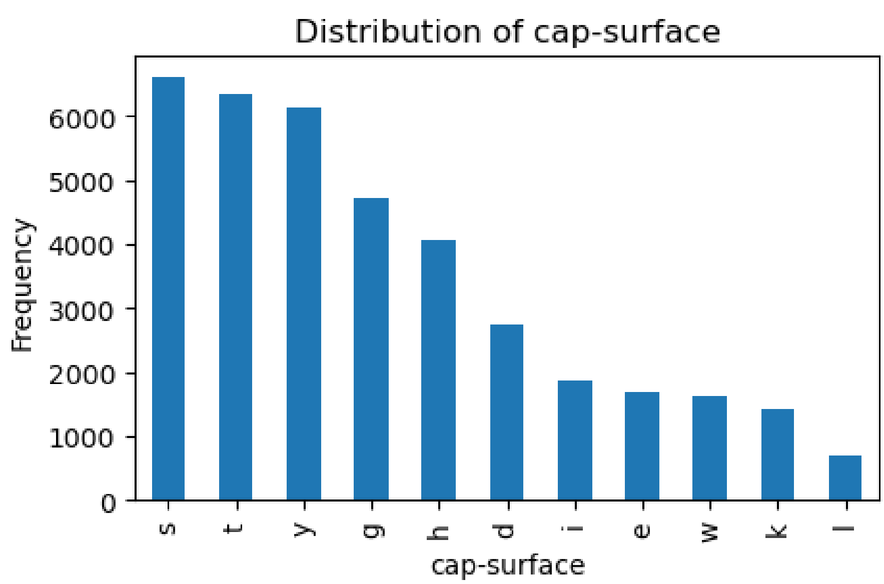


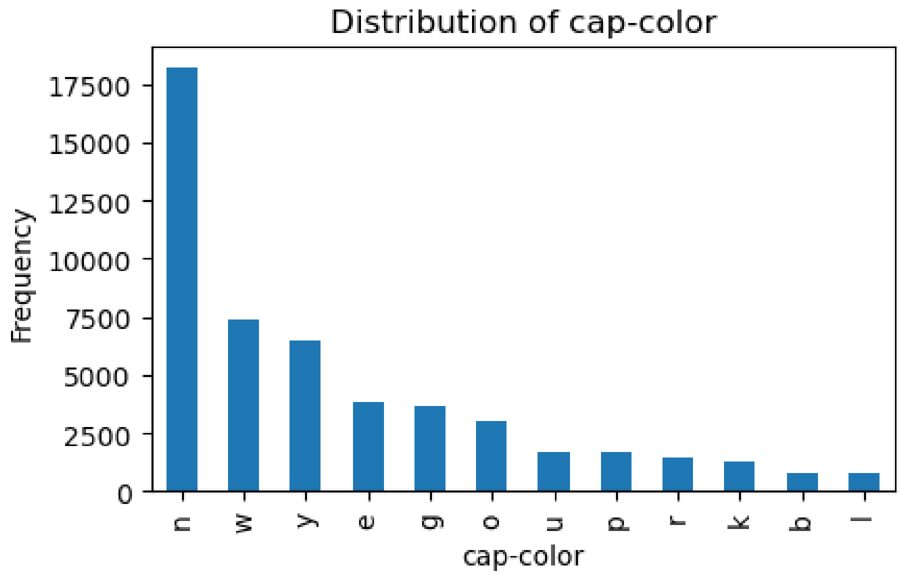
[10]:
```
for name in train_df.columns:
    if train_df[name].dtype == 'O':
        train_df[name].value_counts().plot(kind = 'bar',figsize = (5,3))
        plt.xlabel(name)
        plt.ylabel("Frequency")
        plt.title("Distribution of " + name)
        plt.show()
    else:
        train_df[name].hist(bins = 500, figsize = (5,3))
        plt.xlabel(name)
        plt.ylabel("Frequency")
        plt.title("Distribution of " + name)
        plt.show()
```


Distribution of class
Frequency
30000
25000
20000
15000
10000
5000
0
p
e
class

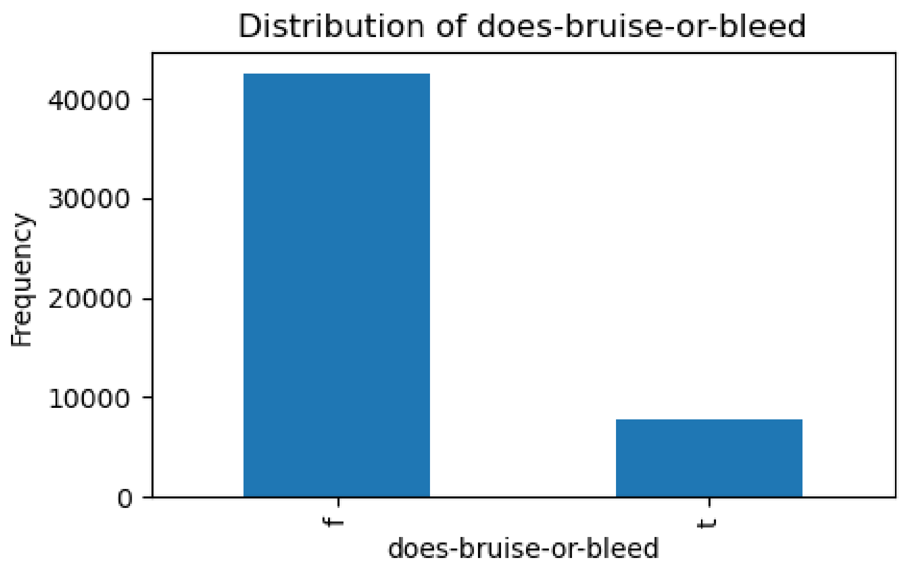

Distribution of cap-diameter
Frequency
800
600
400
200
0
0
10
20
30
40
50
60
cap-diameter


Distribution of cap-shape
Frequency
20000
15000
10000
5000
0
x
f
s
b
p
c
o
cap-shape

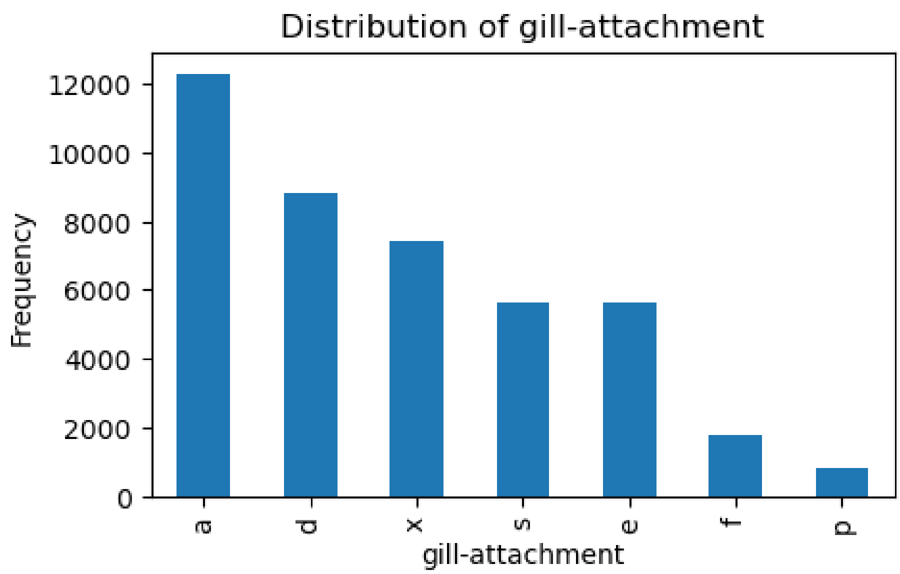

Distribution of cap-surface
Frequency
6000
5000
4000
3000
2000
1000
0
s
t
y
g
h
d
i
e
w
k
l
cap-surface

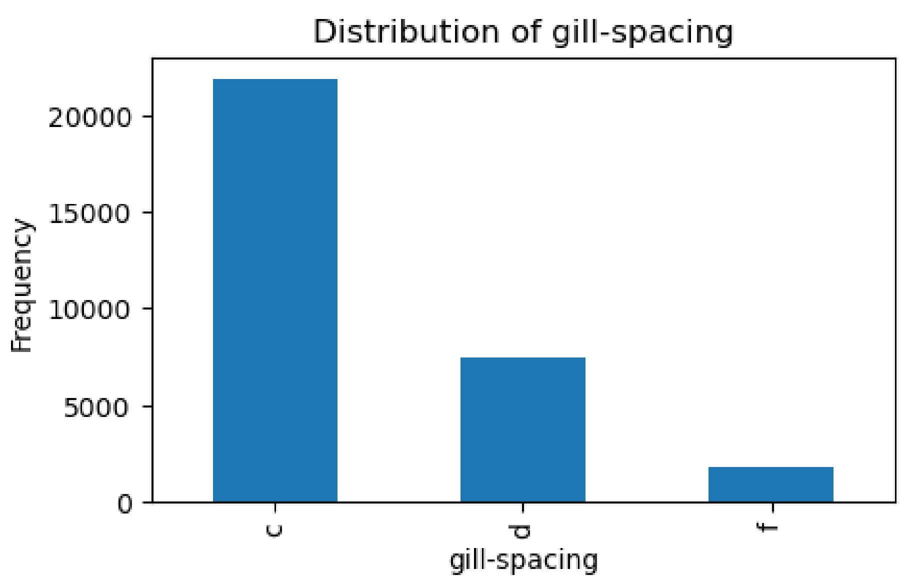


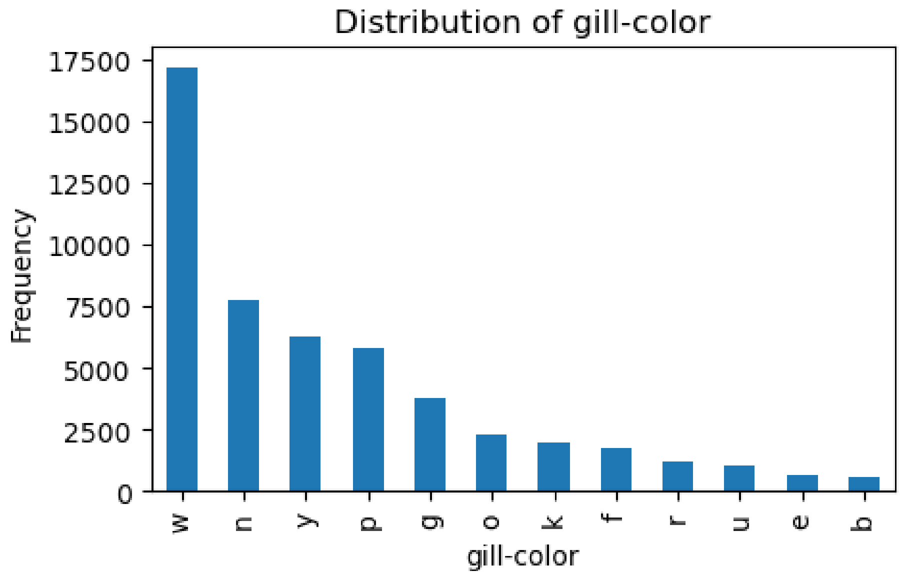
Distribution of cap-color
Frequency
17500
15000
12500
10000
7500
5000
2500
0
n
w
y
e
g
o
u
p
r
k
b
l
cap-color

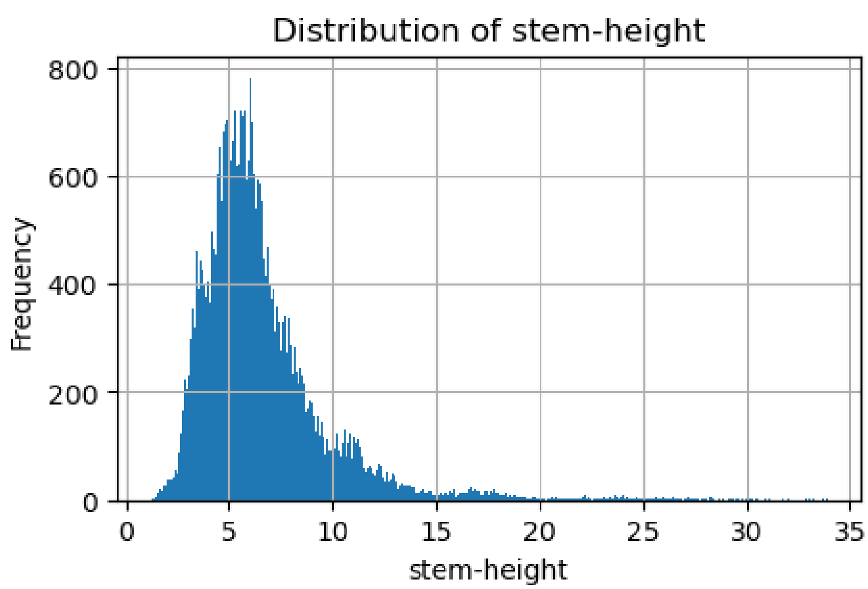


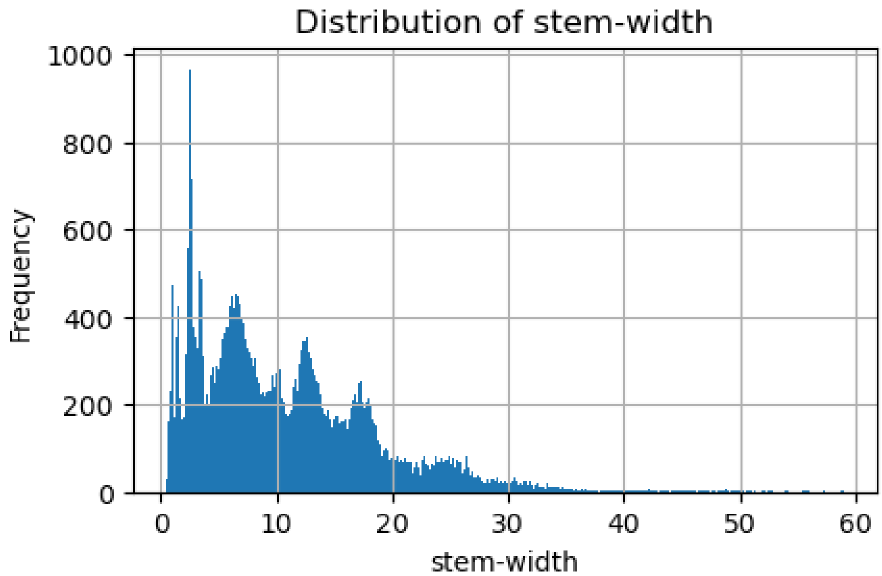
Distribution of does-bruise-or-bleed
Frequency
40000
30000
20000
10000
0
f
t
does-bruise-or-bleed


Distribution of gill-attachment
Frequency
0
2000
4000
6000
8000
10000
12000
a
d
x
s
e
f
p
gill-attachment

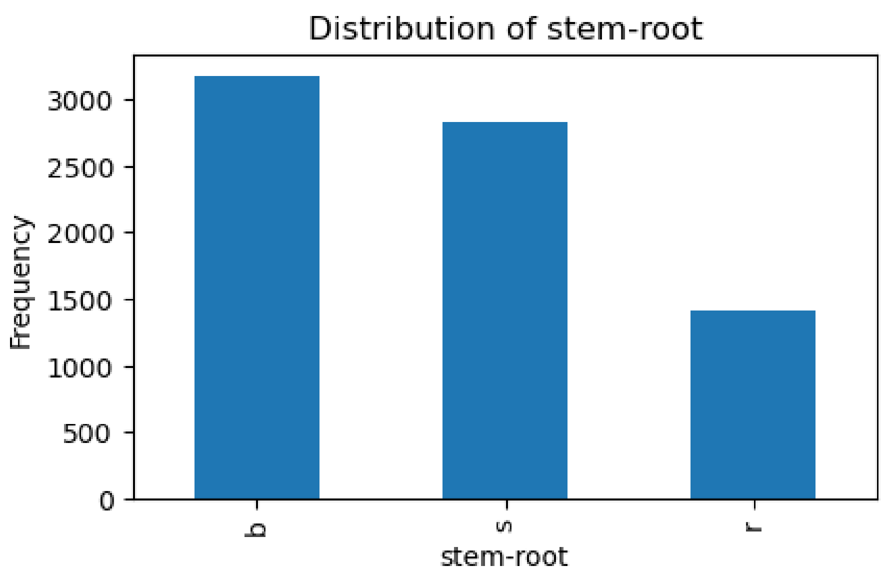

Distribution of gill-spacing
Frequency
0
5000
10000
15000
20000
c
d
f
gill-spacing


Distribution of gill-color
Frequency
0
2500
5000
7500
10000
12500
15000
17500
w
n
y
p
g
o
k
f
r
u
e
b
gill-color

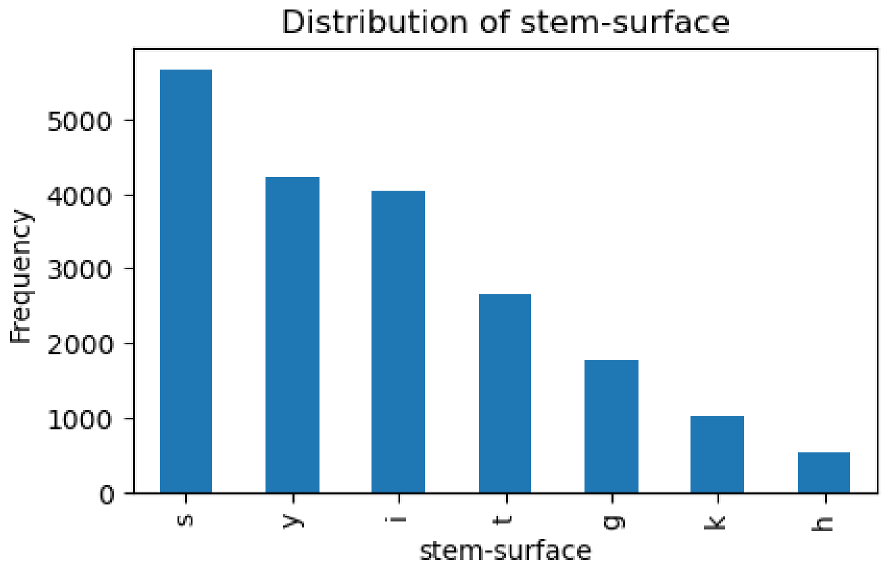

Distribution of stem-height
Frequency
0
200
400
600
800
0
5
10
15
20
25
30
35
stem-height

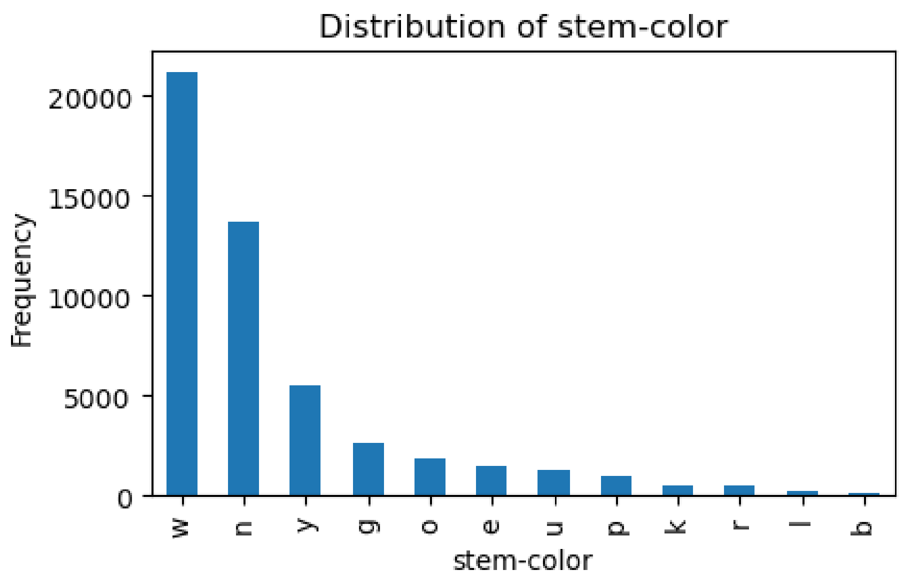


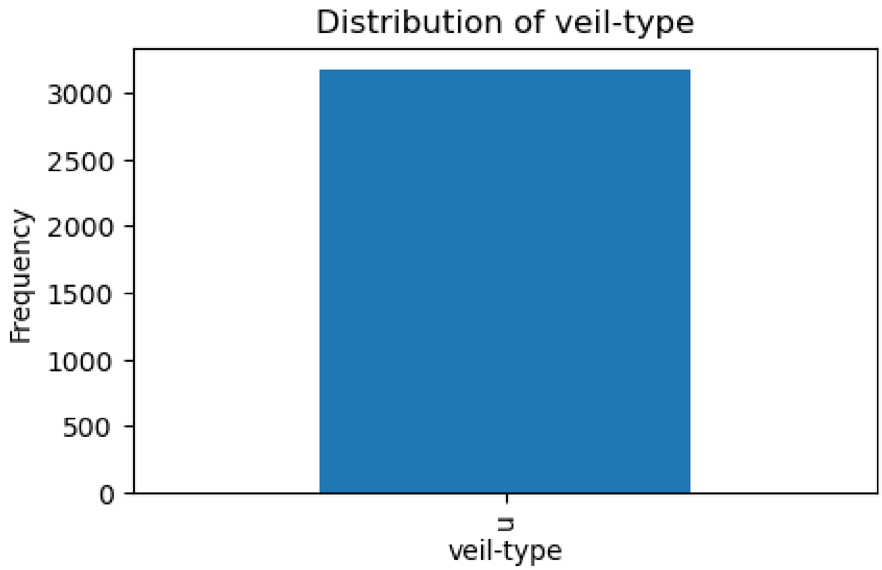
Distribution of stem-width
Frequency
1000
800
600
400
200
0
0
10
20
30
40
50
60
stem-width

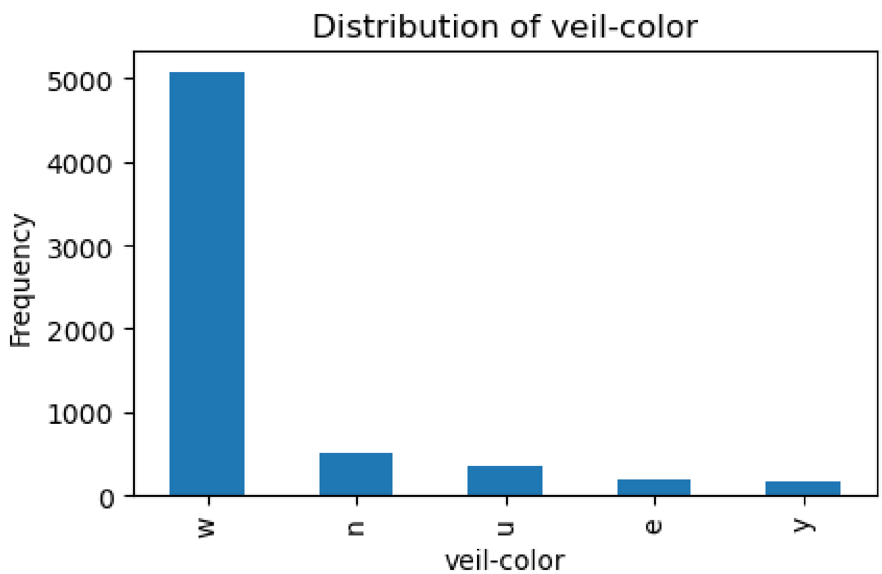


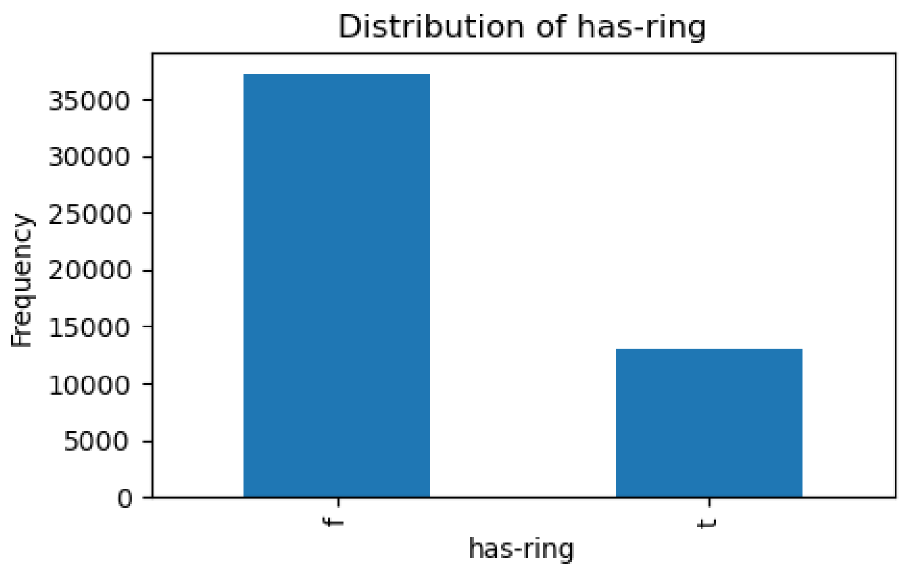
Distribution of stem-root
Frequency
3000
2500
2000
1500
1000
500
0
b
s
r
stem-root

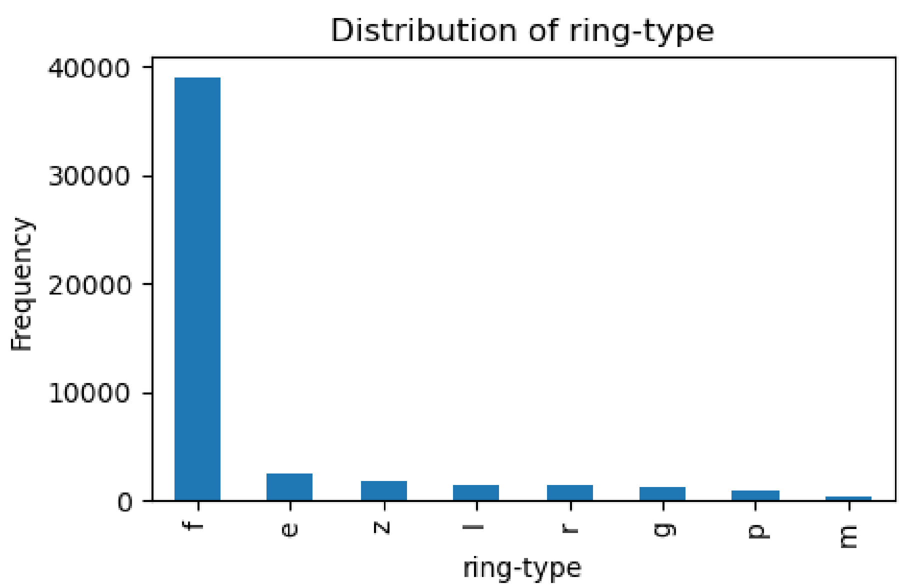

Distribution of stem-surface
Frequency
0
1000
2000
3000
4000
5000
s
y
i
t
g
k
h
stem-surface

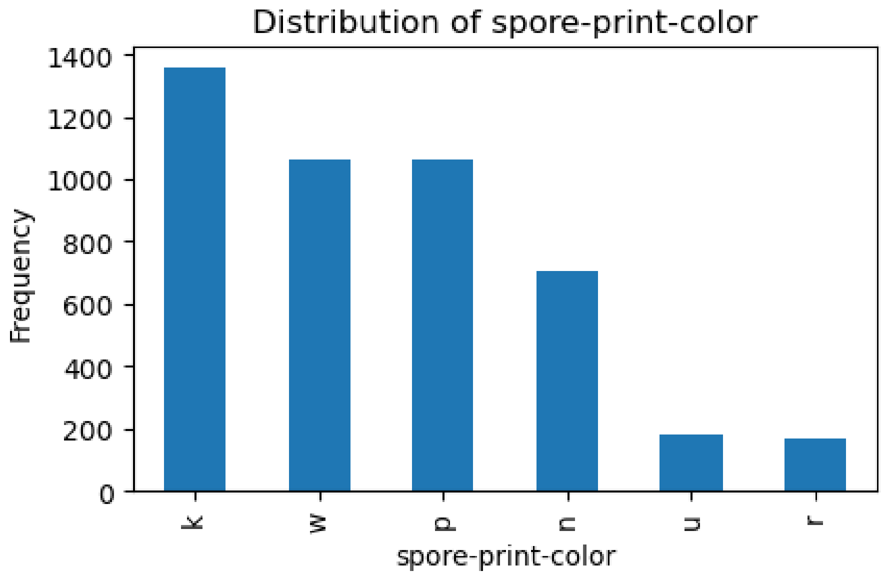

Distribution of stem-color
Frequency
0
5000
10000
15000
20000
w
n
y
g
o
e
u
p
k
r
l
b
stem-color

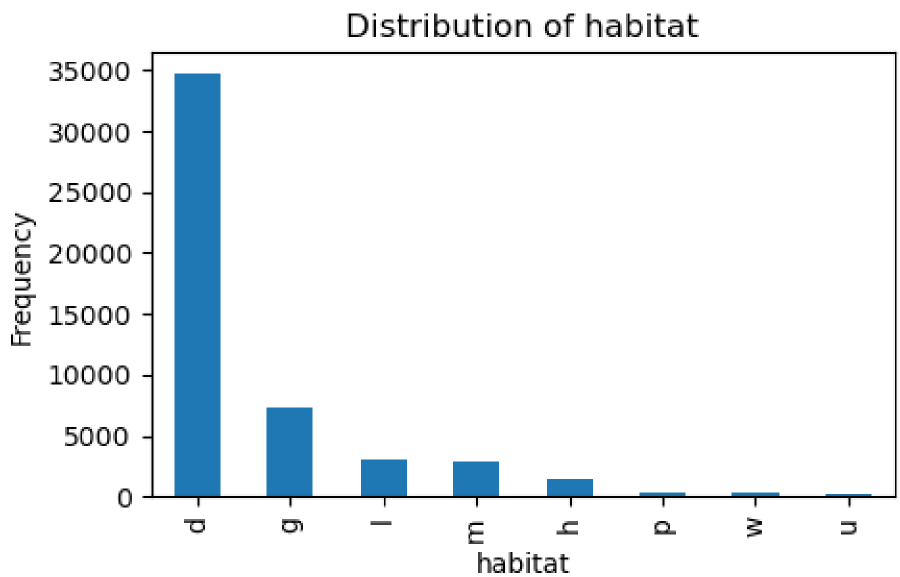

Distribution of veil-type
Frequency
0
500
1000
1500
2000
2500
3000
u
veil-type

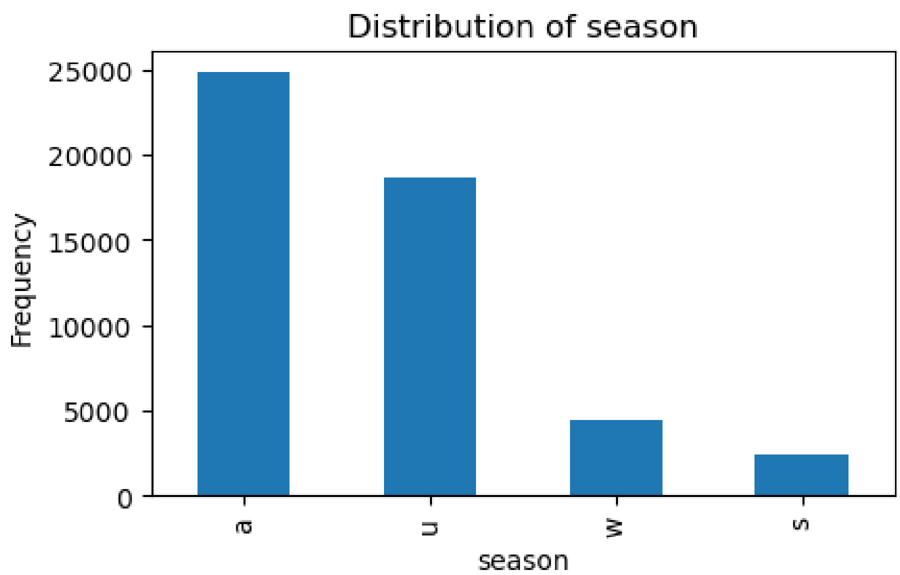

Distribution of veil-color
Frequency
0
1000
2000
3000
4000
5000
w
n
u
e
y
veil-color


Distribution of has-ring
Frequency
35000
30000
25000
20000
15000
10000
5000
0
f
t
has-ring


Distribution of ring-type
Frequency
40000
30000
20000
10000
0
f
e
z
l
r
g
p
m
ring-type


Distribution of spore-print-color
Frequency
1400
1200
1000
800
600
400
200
0
k
w
p
n
u
r
spore-print-color


Distribution of habitat
Frequency
35000
30000
25000
20000
15000
10000
5000
0
d
g
l
m
h
p
w
u
habitat



[11]:
```
train_df.isnull().sum()
```

[11]:
```
class                       0
cap-diameter                0
cap-shape                   0
cap-surface             12298
cap-color                   0
does-bruise-or-bleed        0
gill-attachment          7766
gill-spacing            19149
gill-color                  0
stem-height                 0
stem-width                  0
stem-root               42800
stem-surface            30301
stem-color                  0
veil-type               47036
veil-color              43916
has-ring                    0
ring-type                1765
spore-print-color       45681
habitat                     0
season                      0
dtype: int64
```

[12]:
```
null_features = []
sum_dict = train_df.isnull().sum()
```

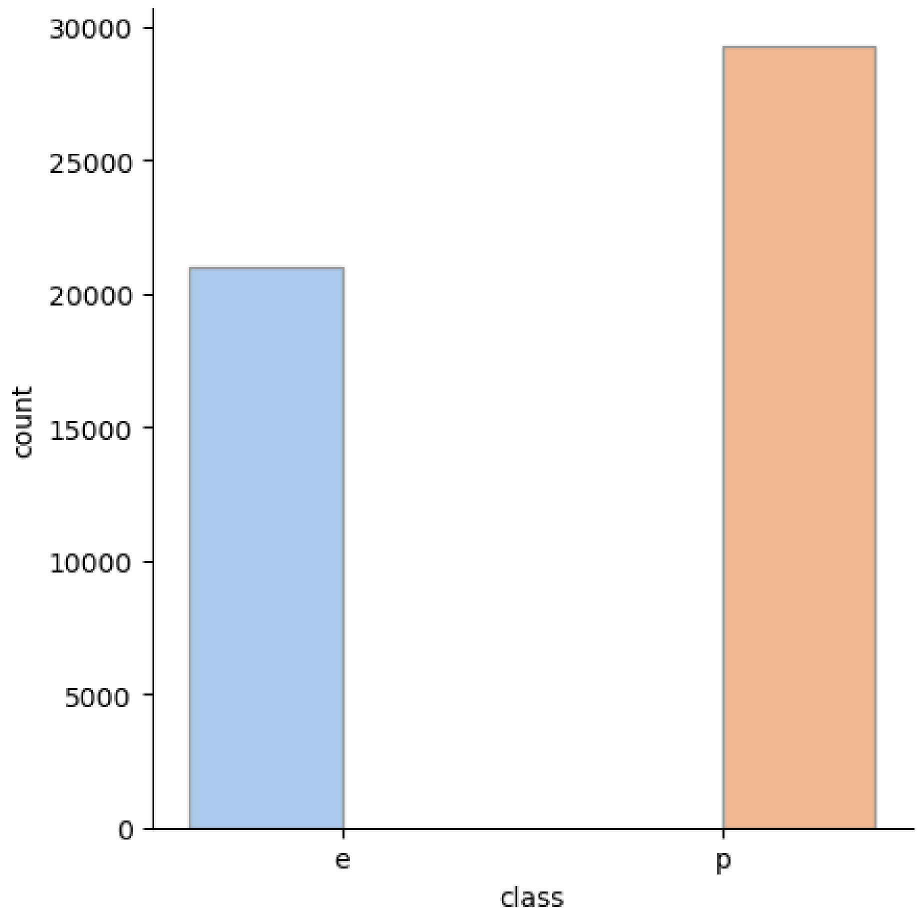
```
for key in sum_dict.keys():
    if(sum_dict[key] != 0):
        null_features.append(key)
```

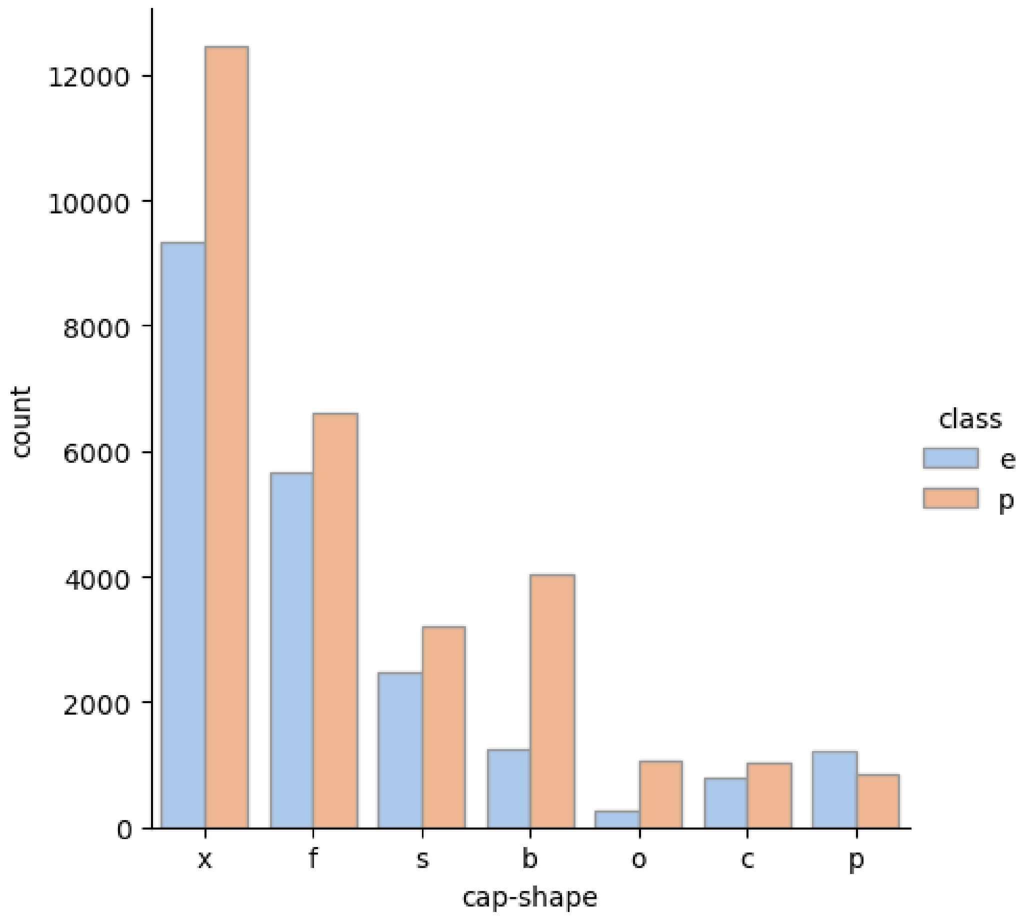
[13]:
```
null_features
```

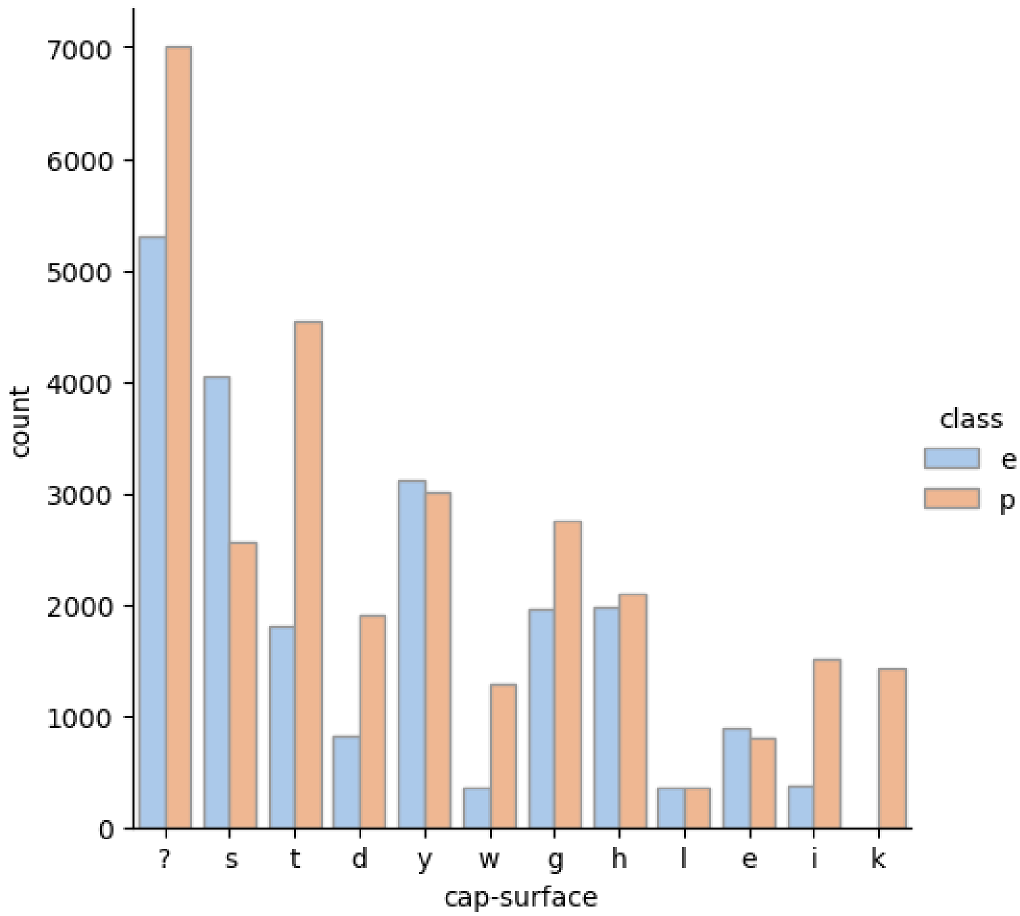
[13]:
```
['cap-surface',
 'gill-attachment',
 'gill-spacing',
 'stem-root',
 'stem-surface',
 'veil-type',
 'veil-color',
 'ring-type',
 'spore-print-color']
```

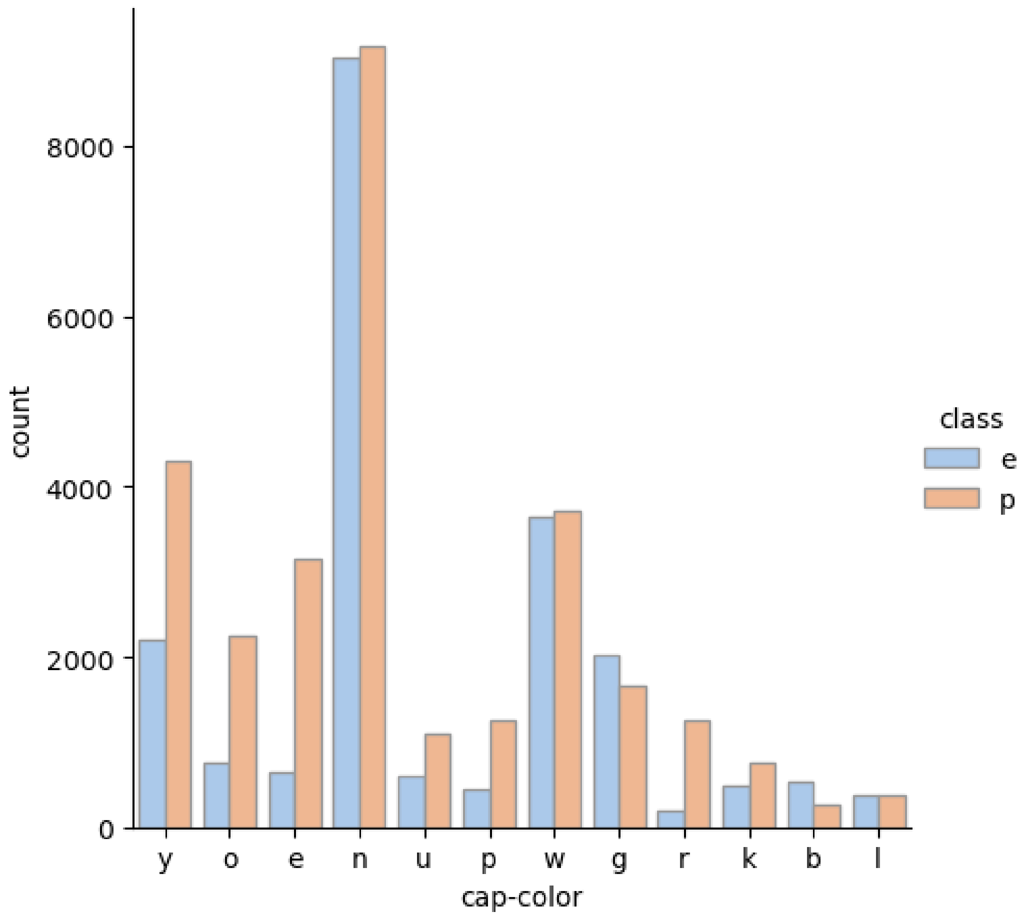
[14]:
```
train_df_rep = train_df.fillna('?')
test_df_rep = test_df.fillna('?')
train_features_rep = train_df_rep.drop("class",axis = 1)
test_features_rep = test_df_rep.drop("class",axis = 1)
```

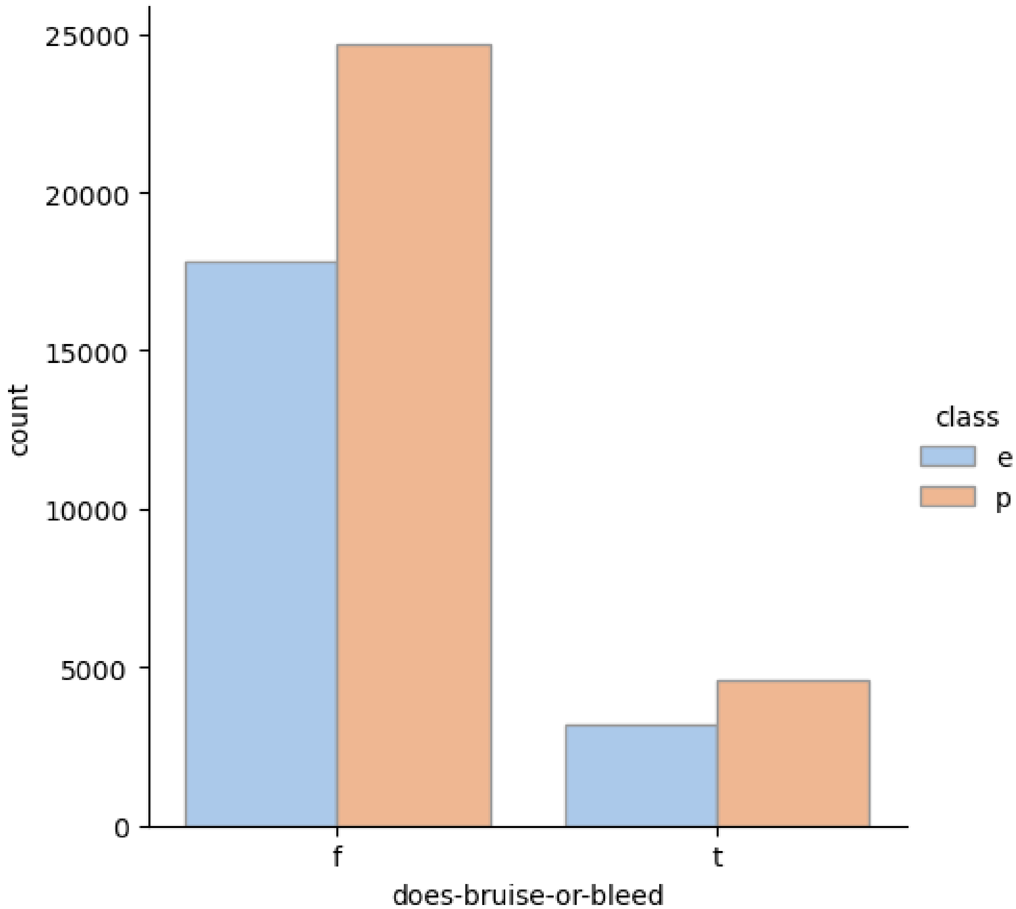
[15]:
```
for name in train_df_rep.columns:
    if train_df_rep[name].dtype == 'O':
        sns.catplot(
            data=train_df_rep, x=name, hue="class", kind="count",
            palette="pastel", edgecolor=".6"
        )
        plt.show()
```

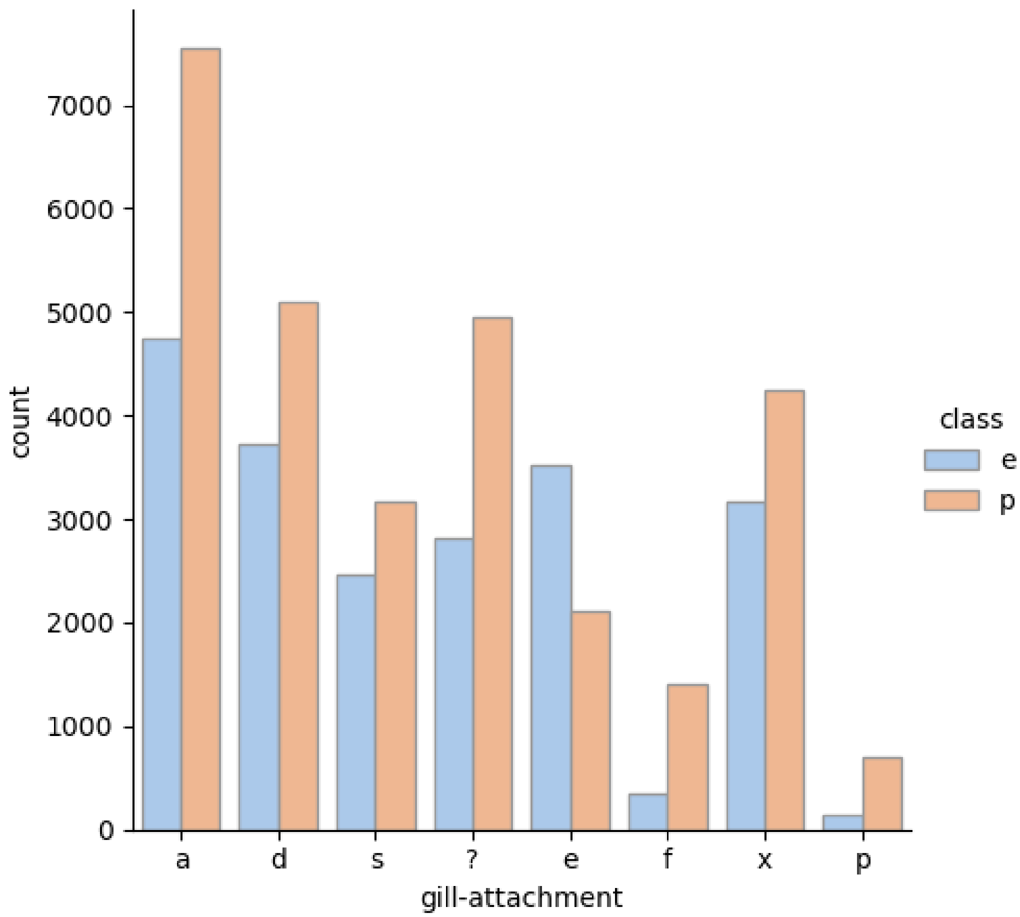

30000
25000
20000
15000
10000
5000
0
count
e
p
class

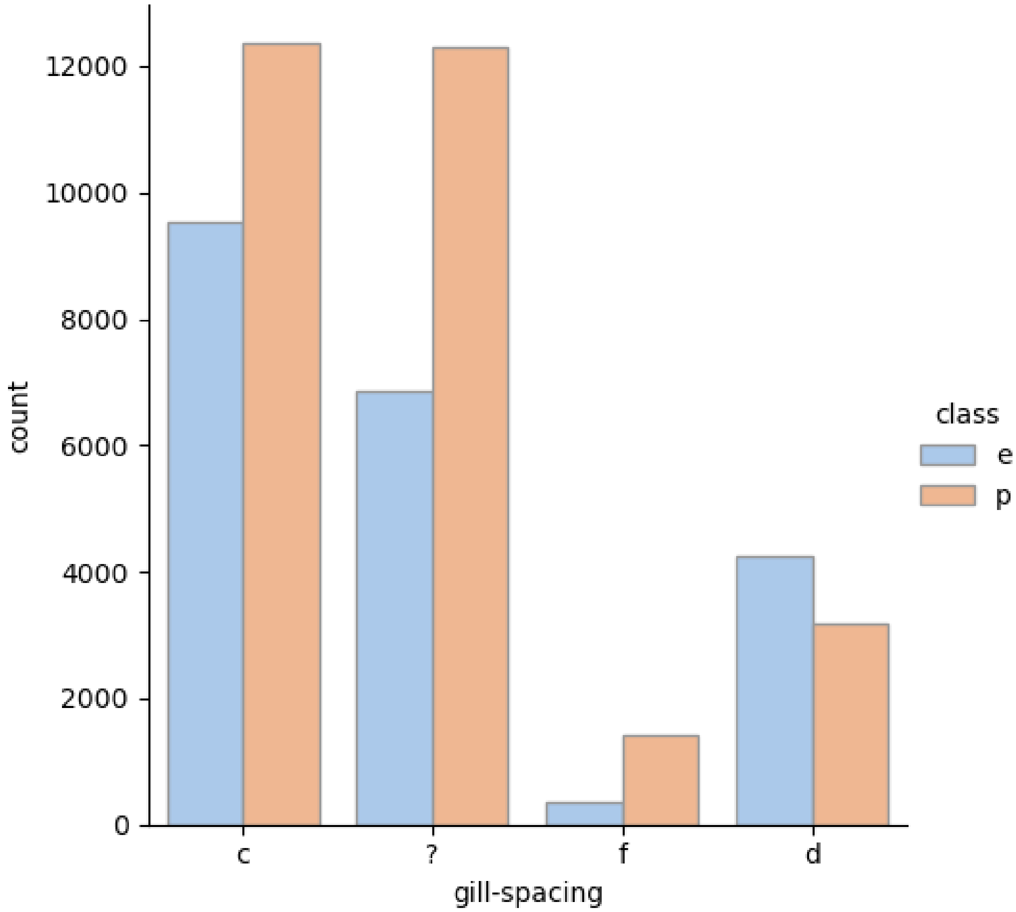

12000
10000
8000
6000
4000
2000
0
count
x
f
s
b
o
c
p
cap-shape
class
e
p

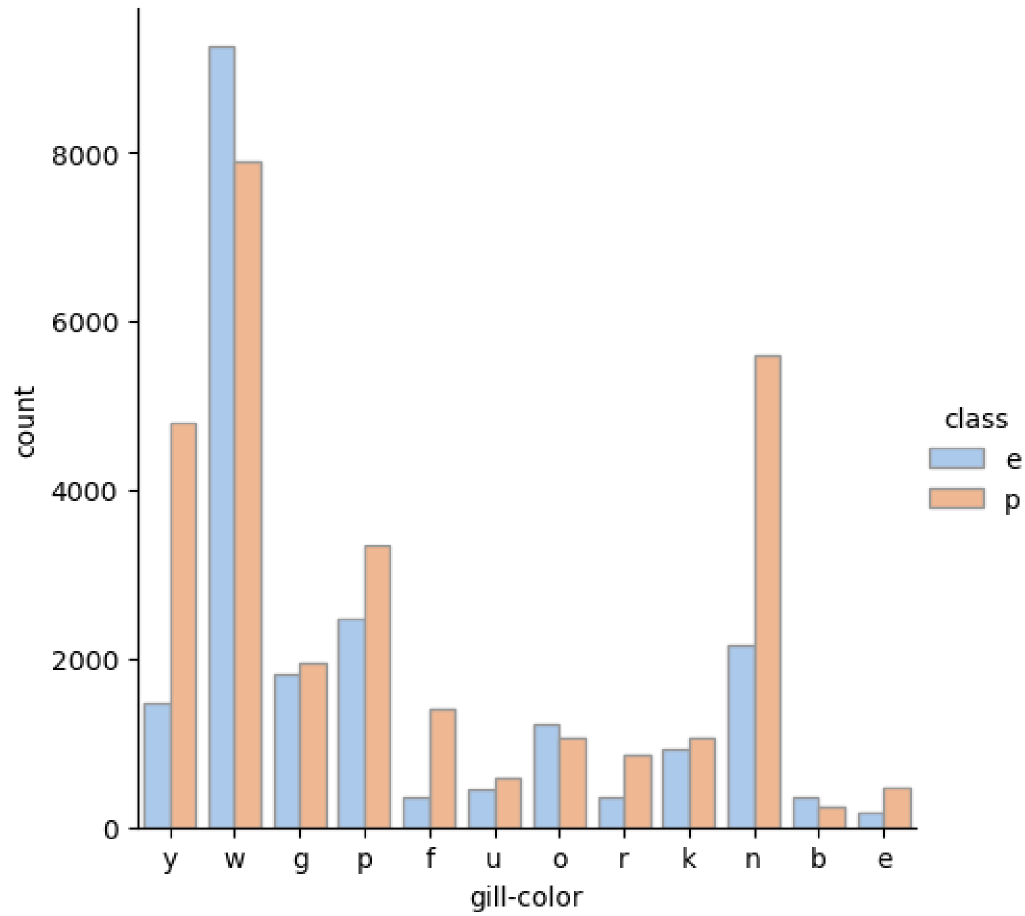

7000
6000
5000
4000
3000
2000
1000
0
count
? s t d y w g h l e i k
cap-surface
class
e
p


8000
6000
4000
2000
0
count
class
e
p
y
o
e
n
u
p
w
g
r
k
b
l
cap-color

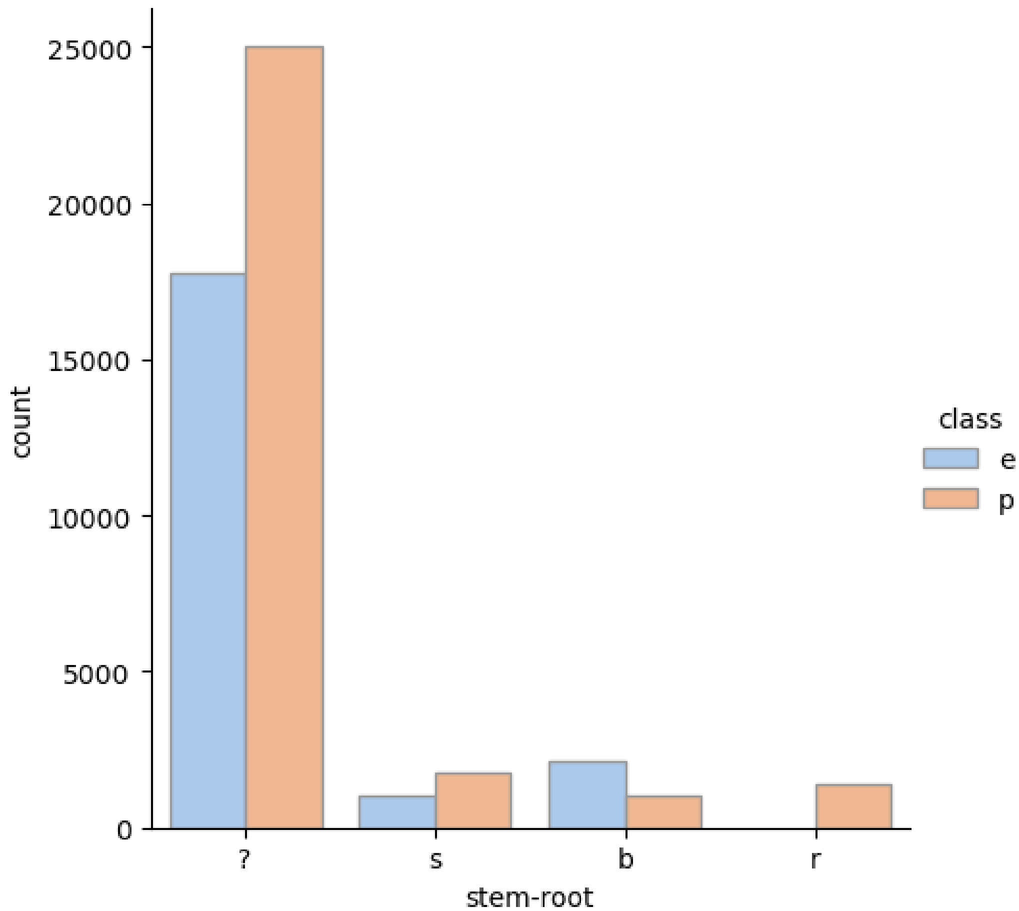

25000
20000
15000
10000
5000
0
count
f
t
does-bruise-or-bleed
class
e
p

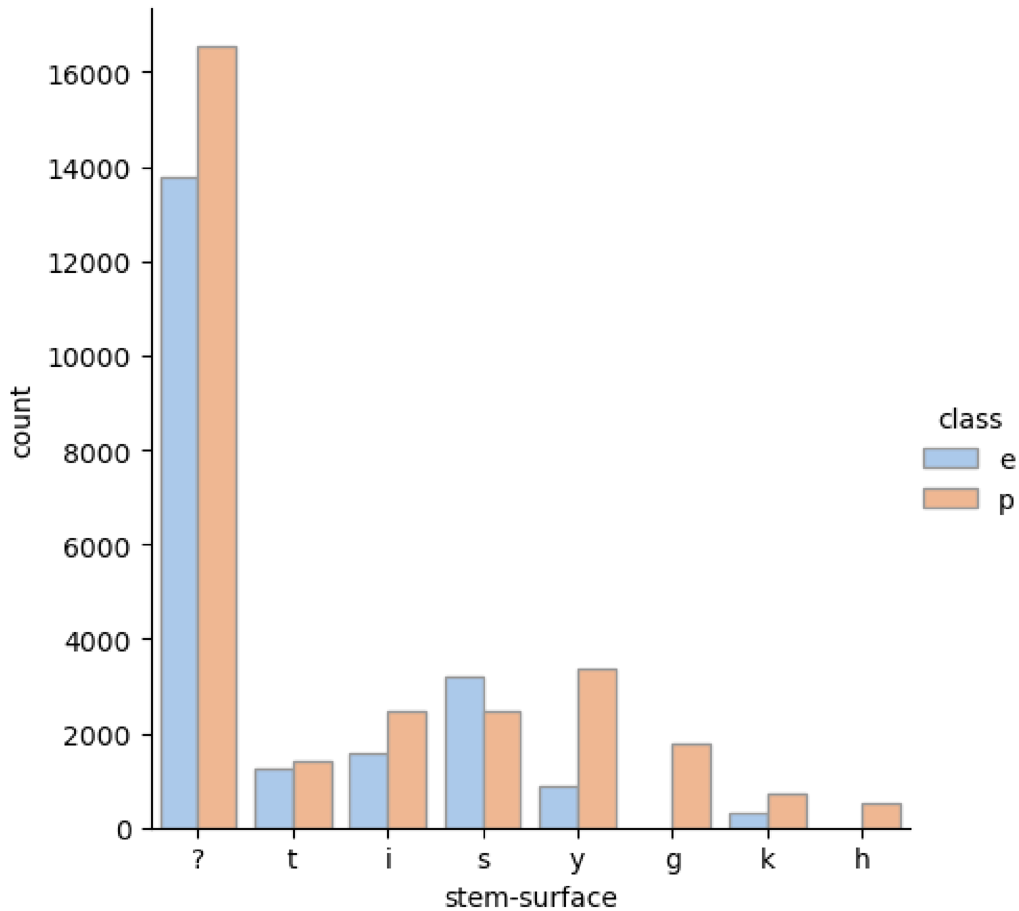

7000
6000
5000
4000
3000
2000
1000
0
count
a
d
s
?
e
f
x
p
gill-attachment
class
e
p

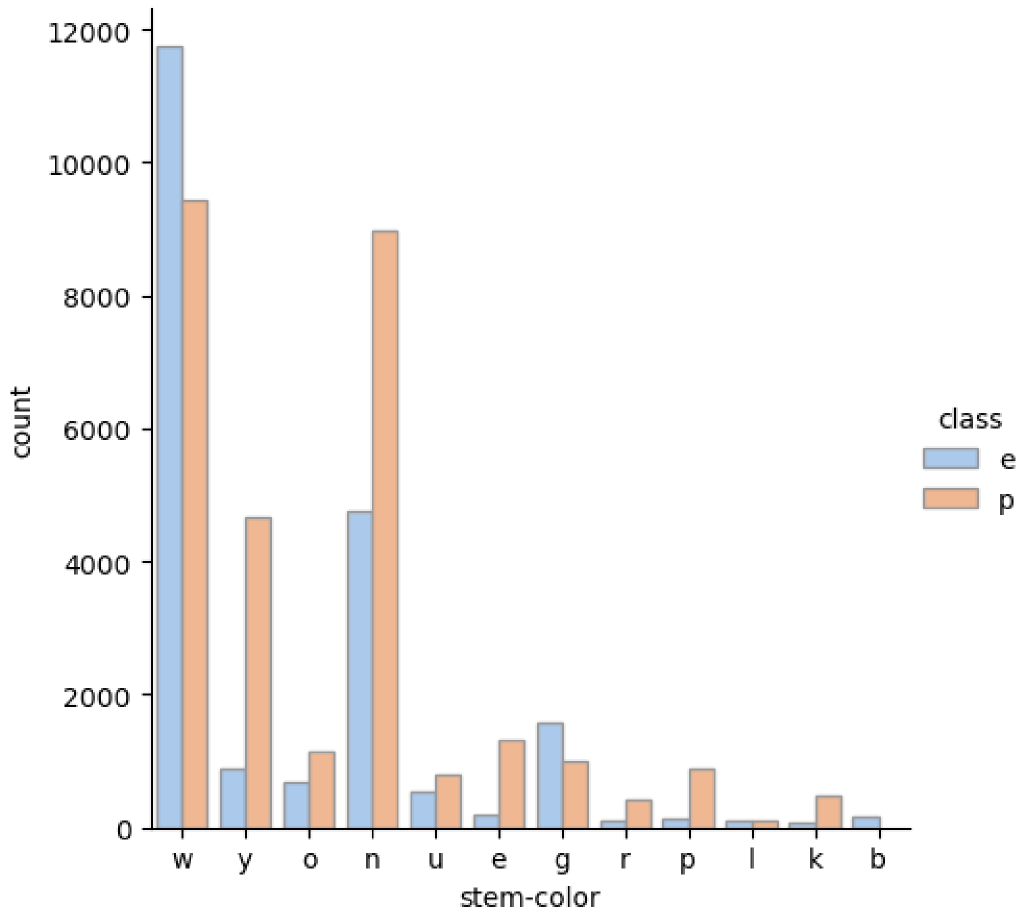

12000
10000
8000
6000
4000
2000
0
count
c
?
f
d
gill-spacing
class
e
p



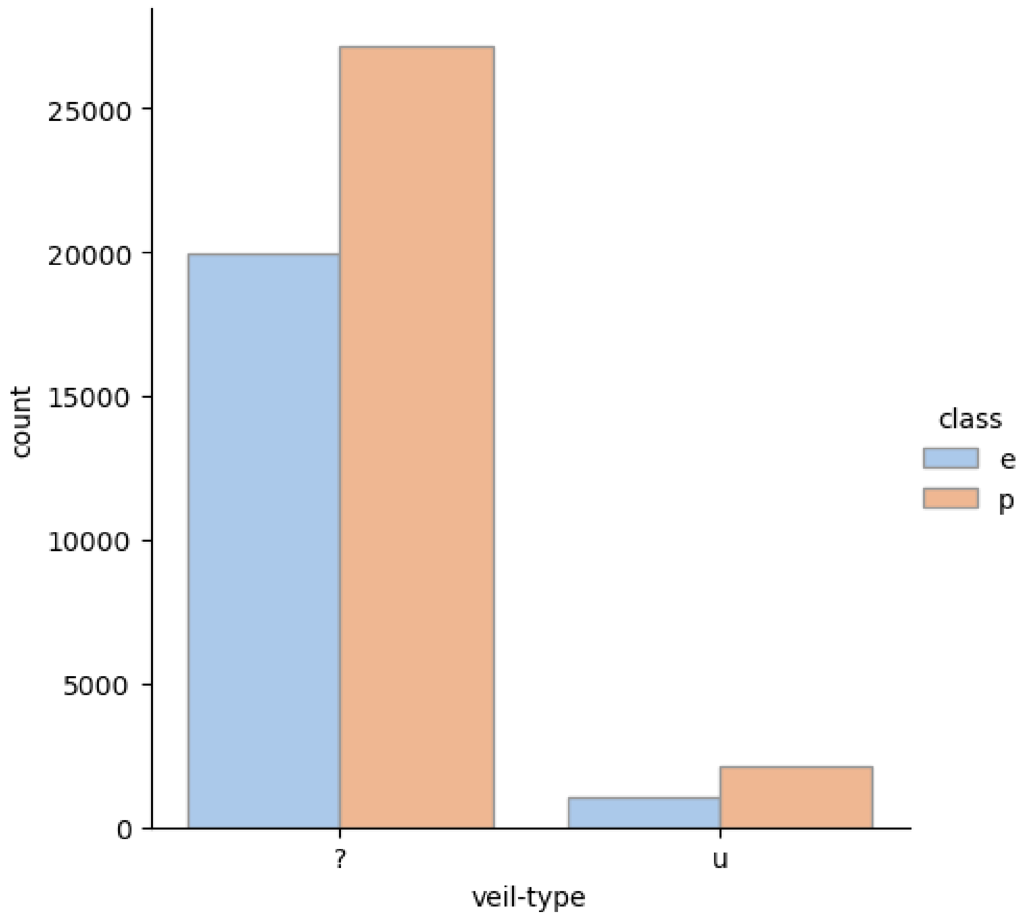
8000
6000
4000
2000
0
count
y
w
g
p
f
u
o
r
k
n
b
e
gill-color
class
e
p

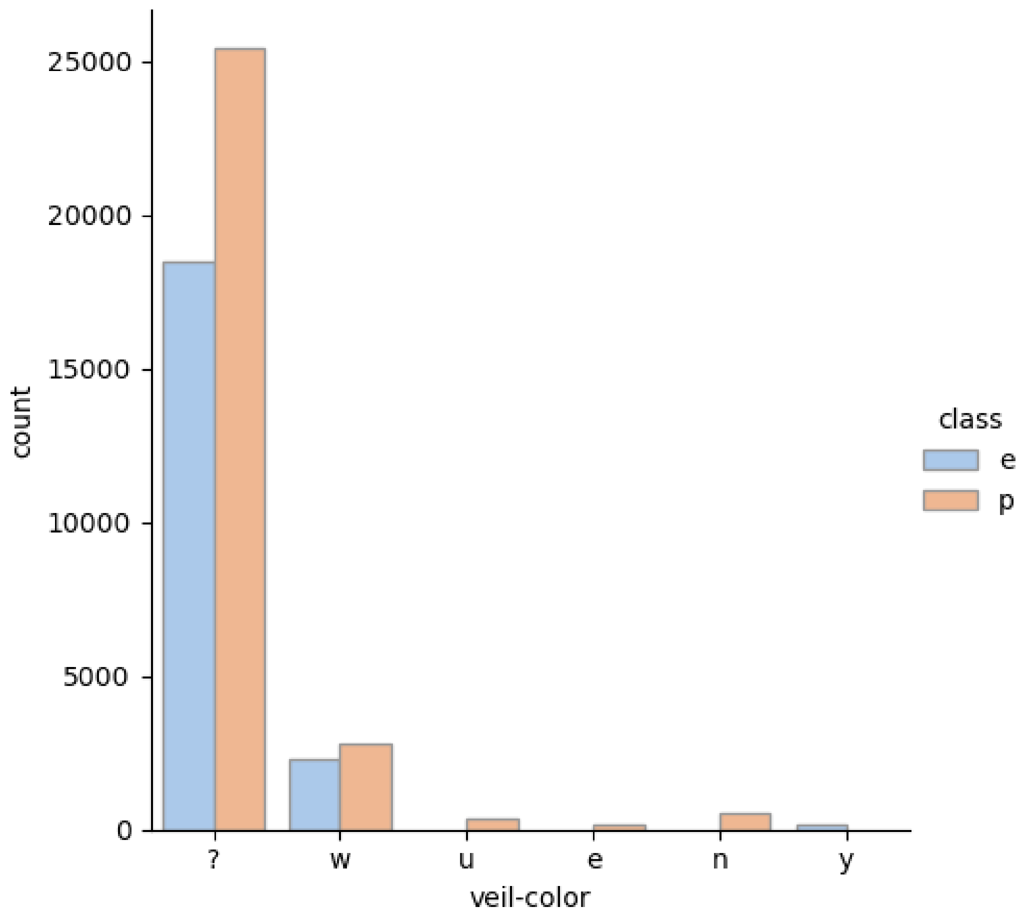

25000
20000
15000
10000
5000
0
count
?
s
b
r
stem-root
class
e
p

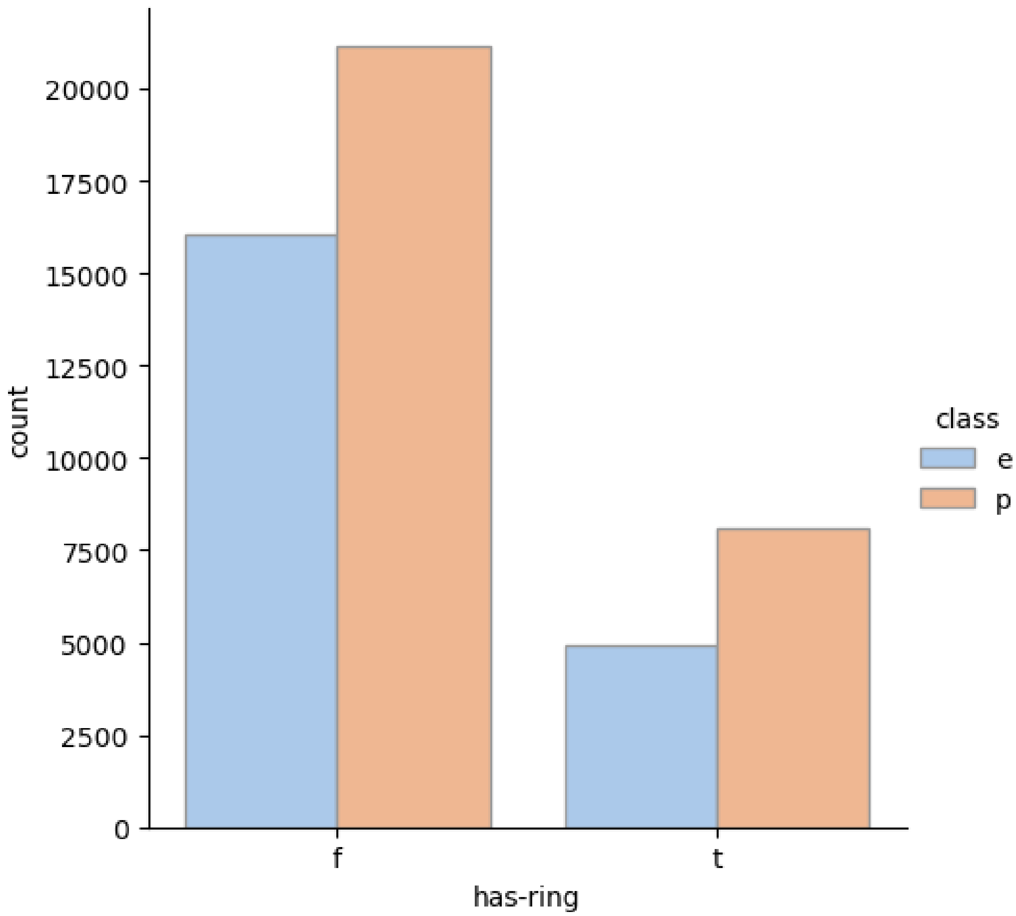

16000
14000
12000
10000
8000
6000
4000
2000
0
count
?
t
i
s
y
g
k
h
stem-surface
class
e
p

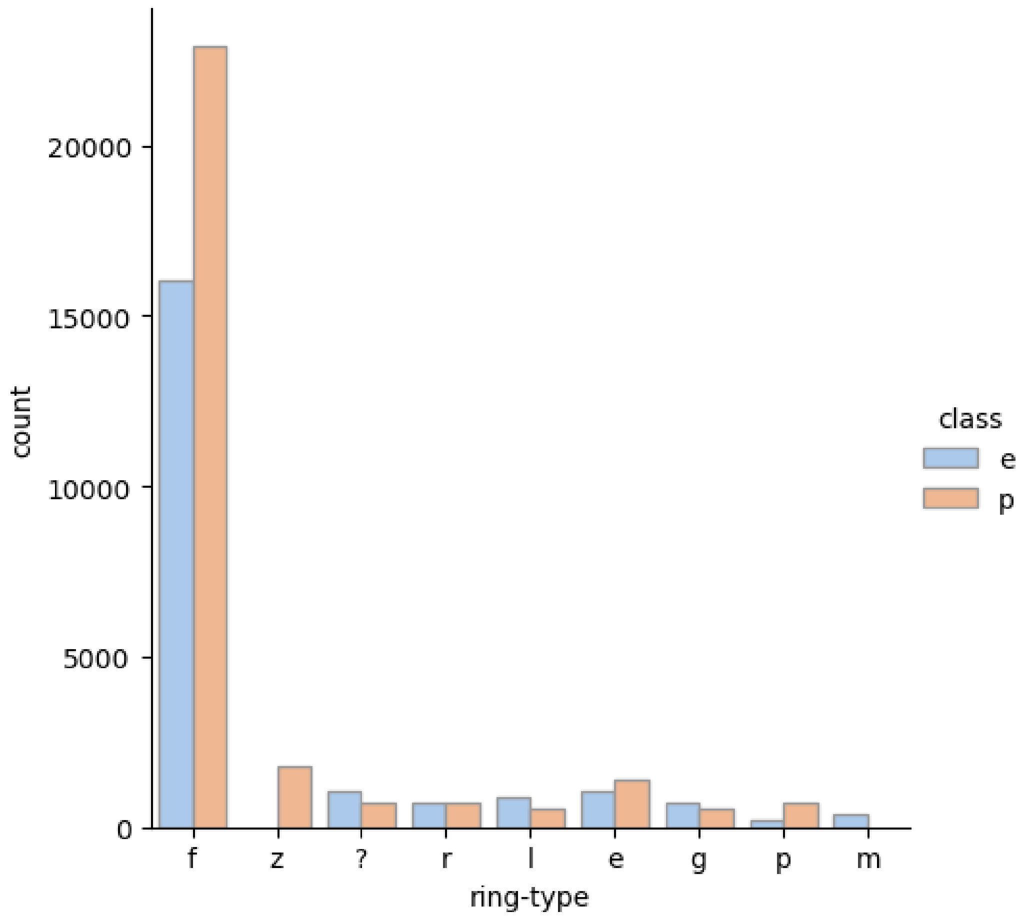


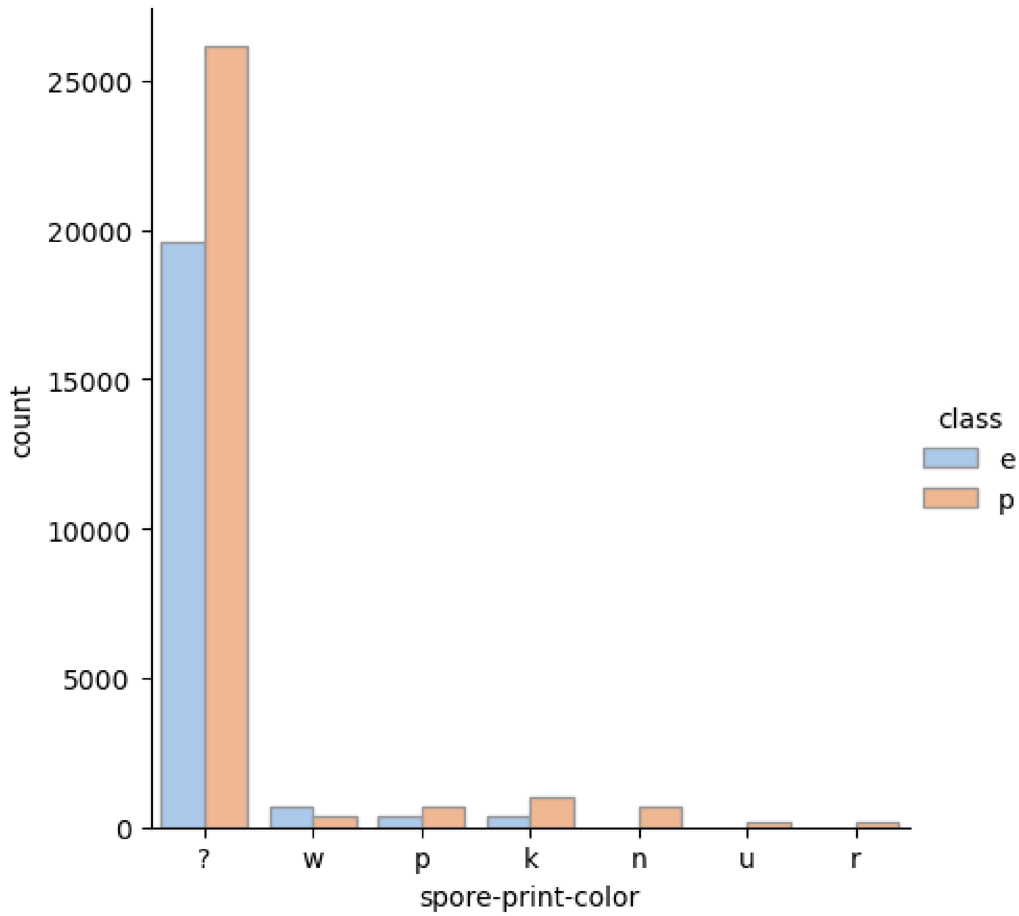
12000
10000
8000
6000
4000
2000
0
count
w
y
o
n
u
e
g
r
p
l
k
b
stem-color
class
e
p

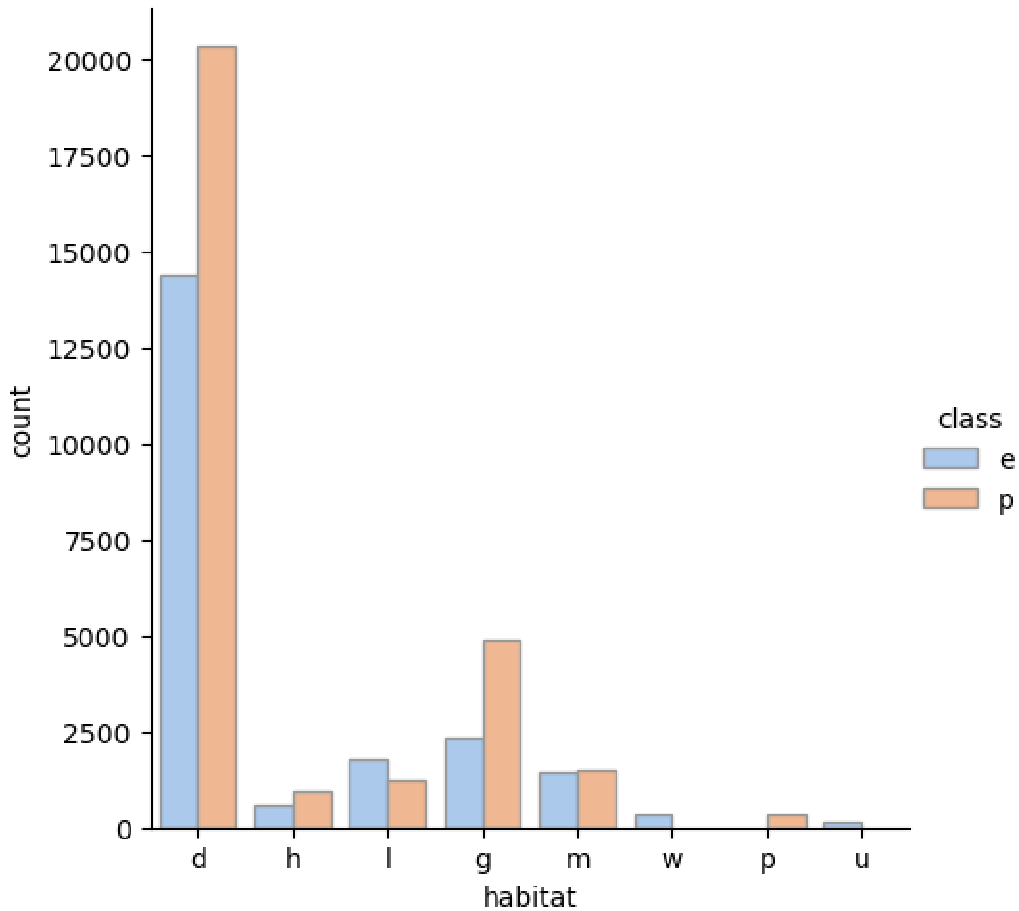

25000
20000
15000
10000
5000
0
count
?
u
veil-type
class
e
p

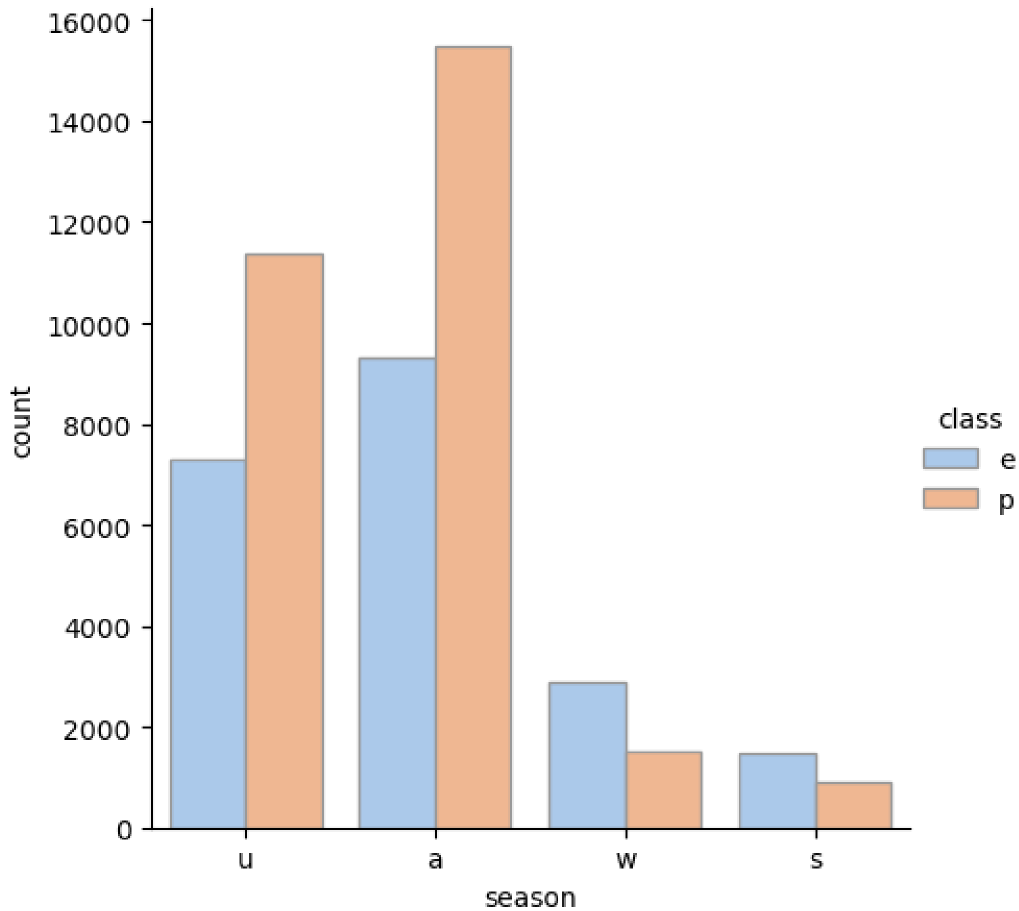

25000
20000
15000
10000
5000
0
count
?
w
u
e
n
y
veil-color
class
e
p


20000
17500
15000
12500
10000
7500
5000
2500
0
count
f
t
has-ring
class
e
p


count
ring-type
class
e
p
0
5000
10000
15000
20000
f
z
?
r
l
e
g
p
m


25000
20000
15000
10000
5000
0
count
?
w
p
k
n
u
r
spore-print-color
class
e
p


20000
17500
15000
12500
10000
7500
5000
2500
0
count
d
h
l
g
m
w
p
u
habitat
class
e
p



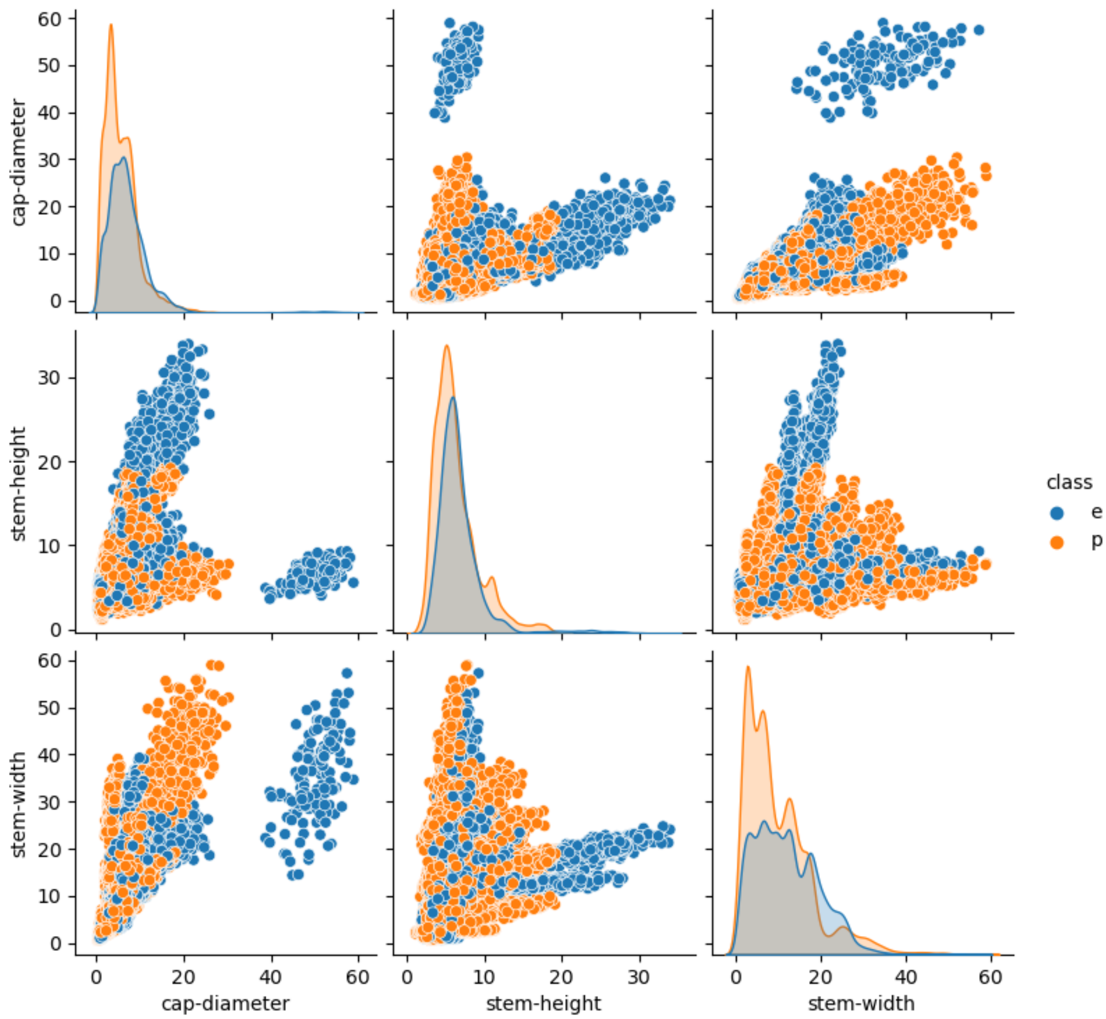
[16]:
```
test_df.isnull().sum()
```

[16]:
```
class                      0
cap-diameter               0
cap-shape                  0
cap-surface             1822
cap-color                  0
does-bruise-or-bleed       0
gill-attachment         2118
gill-spacing            5914
gill-color                 0
stem-height                0
stem-width                 0
stem-root               8738
stem-surface            7823
stem-color                 0
veil-type              10856
veil-color              9740
```

```
has-ring                    0
ring-type                 706
spore-print-color        9034
habitat                     0
season                      0
dtype: int64
```

cap-surface, gill-attachment, gill-spacing, stem-root, stem-surface, veil-type, veil-color, ring-type, spore-print-color contains null values. Columns that contain null values should be dropped.

[17]:
```
attributes = []
for name in train_df.columns:
    if train_df[name].dtype != 'O':
        attributes.append(name)

attributes.append("class")

sns.pairplot(train_df[attributes], hue="class")
plt.show()
```



[18]:
```
print("Number of edible mushroom is",sum(train_df["class"] == 'e'), "in training set")
print("Number of posionous mushroom is",sum(train_df["class"] == 'p'), "in training set")
print("Number of edible mushroom is",sum(test_df["class"] == 'e')," in test set")
print("Number of posionous mushroom is",sum(test_df["class"] == 'p')," in test set") # no class imbalance
```

```
Number of edible mushroom is 20971 in training set
Number of posionous mushroom is 29242 in training set
Number of edible mushroom is 6210  in test set
Number of posionous mushroom is 4646  in test set
```

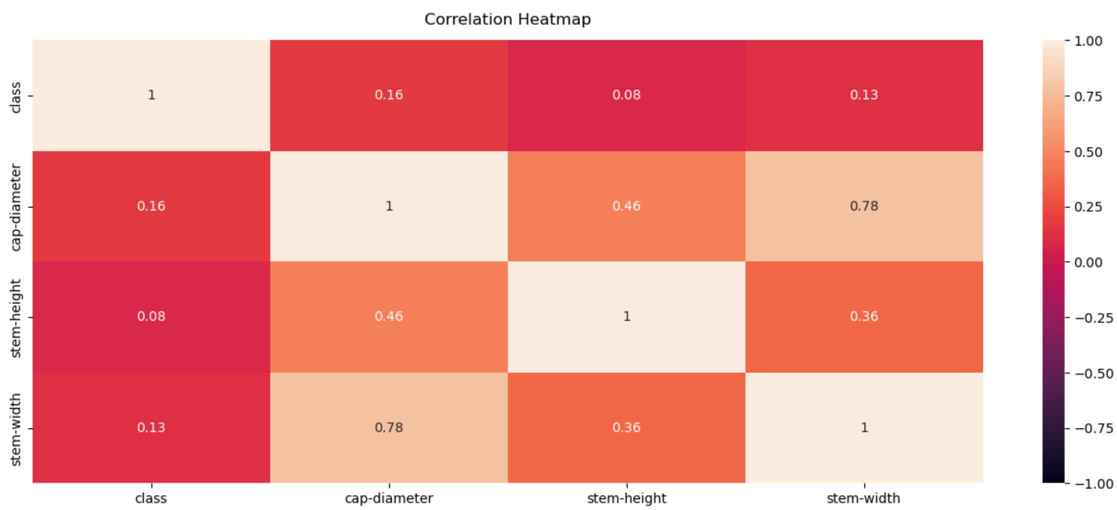
[19]:
```
train_df.corr()
```

[19]:

	cap-diameter	stem-height	stem-width
cap-diameter	1.000000	0.464897	0.778005
stem-height	0.464897	1.000000	0.360779
stem-width	0.778005	0.360779	1.000000

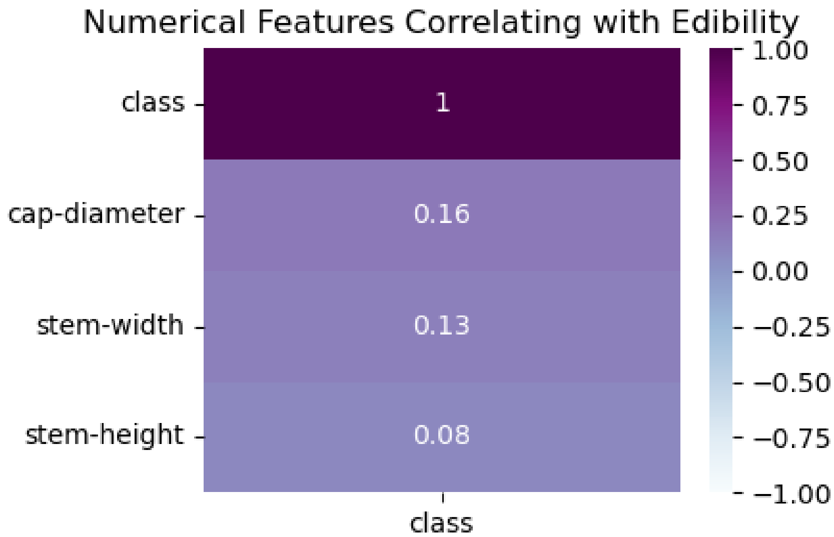
[20]:

```
train_df_v2 = train_df.copy()
train_df_v2["class"] = (train_df_v2["class"] == "e")

plt.figure(figsize = (16,6))
h_map = sns.heatmap(train_df_v2.corr(),vmin=-1, vmax=1, annot=True)
h_map.set_title('Correlation Heatmap', fontdict={'fontsize':12}, pad=12);
```



[21]:

```
plt.figure(figsize = (4,3))
h_map = sns.heatmap(train_df_v2.corr()[["class"]].sort_values(by =
↪"class",ascending=False),vmin=-1, vmax=1, annot=True,cmap ='BuPu')
h_map.set_title("Numerical Features Correlating with Edibility")
plt.show()
```



4 4. Data Processing

[22]:
```
# Hints:
# 1. Convert the "class" column into labels: 'p' (poisonous) -> 0,  'e'␣
↪(edible) -> 1
# 2. You can drop columns if you see fit
# 3. See any imcomplete data? We learned how to deal with them in project 1.

#train_features
#train_labels
#test_features
#test_labels

from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer, make_column_transformer
```

[23]:
```
def pipeline_data(train_features,test_features):
    num_attributes = []
    cat_attributes = []
    for name in train_features.columns:
        if train_features[name].dtype == 'O':
            cat_attributes.append(name)
        else:
            num_attributes.append(name)
```

```
    num_pipeline = Pipeline([
    ('std_scaler',StandardScaler()),
    ])

    full_pipeline = ColumnTransformer([
    ("num", num_pipeline, num_attributes),
    ("cat", OneHotEncoder(categories = 'auto', handle_unknown =␣
 ↪'ignore'),cat_attributes)])

    tf_train_features = full_pipeline.fit_transform(train_features)
    tf_test_features = full_pipeline.transform(test_features)

    if(full_pipeline.sparse_output_):
        tf_train_features = tf_train_features.toarray()
        tf_test_features = tf_test_features.toarray()

    return tf_train_features,tf_test_features,full_pipeline
```

[24]:
```
train_labels = (train_labels == 'e').astype("int")
test_labels = (test_labels == 'e').astype("int")
```

[25]:
```
drop_set = []
for name in train_features.keys():
    if train_df[name].isnull().sum() != 0:
        drop_set.append(name)
print("Features that contain null values : ",drop_set)
```

```
Features that contain null values :  ['cap-surface', 'gill-attachment', 'gill-
spacing', 'stem-root', 'stem-surface', 'veil-type', 'veil-color', 'ring-type',
'spore-print-color']
```

[26]:
```
dropped_train_features = train_features.drop(columns = drop_set)
dropped_test_features = test_features.drop(columns = drop_set)
```

[27]:
```
dropped_train_features.isnull().sum()
```

[27]:
```
cap-diameter            0
cap-shape               0
cap-color               0
does-bruise-or-bleed    0
gill-color              0
stem-height             0
stem-width              0
stem-color              0
has-ring                0
habitat                 0
season                  0
dtype: int64
```

[28]:
```
dropped_test_features.isnull().sum()
```

[28]:
```
cap-diameter            0
cap-shape               0
cap-color               0
does-bruise-or-bleed    0
gill-color              0
stem-height             0
stem-width              0
stem-color              0
has-ring                0
habitat                 0
season                  0
dtype: int64
```

[29]:
```
tf_train_features_rep, tf_test_features_rep, full_pipeline_rep =␣
 ↪pipeline_data(train_features_rep,test_features_rep)
tf_train_features, tf_test_features, full_pipeline =␣
 ↪pipeline_data(dropped_train_features,dropped_test_features)
```

[30]:
```
index_list = []
index = 0
for name in full_pipeline_rep.get_feature_names_out():
    if not("?" in name):
        index_list.append(index)
    index += 1
tf_train_features_no_null = tf_train_features_rep[:,index_list]
tf_test_features_no_null = tf_test_features_rep[:,index_list]
```

[31]:
```
print("Processed training data size: ",tf_train_features.shape)
print("Processed test data size: ",tf_test_features.shape)

print("Processed filled training data size: ",tf_train_features_rep.shape)
print("Processed filled test data size: ",tf_test_features_rep.shape)

print("Processed no ? training data size: ",tf_train_features_no_null.shape)
print("Processed no ? test data size: ",tf_test_features_no_null.shape)
```

```
Processed training data size:  (50213, 62)
Processed test data size:  (10856, 62)
Processed filled training data size:  (50213, 122)
Processed filled test data size:  (10856, 122)
Processed no ? training data size:  (50213, 113)
Processed no ? test data size:  (10856, 113)
```

[32]:
```
from sklearn.model_selection import cross_validate

clf = LogisticRegression(solver = 'liblinear')
```

```
scores = cross_validate(clf, tf_train_features, train_labels, cv= 10,␣
↪scoring=('accuracy','precision', 'recall','f1'))
scores_rep = cross_validate(clf, tf_train_features_rep, train_labels, cv= 10,␣
↪scoring=('accuracy','precision', 'recall','f1'))
scores_no_null = cross_validate(clf, tf_train_features_no_null, train_labels,␣
↪cv= 10, scoring=('accuracy','precision', 'recall','f1'))
```

[33]:
```
print("Dropped Columns:")
print("Average accuracy, " , scores['test_accuracy'].mean())
print("Average precision, " , scores['test_precision'].mean())
print("Average recall, " , scores['test_recall'].mean())
print("Average f1, " , scores['test_f1'].mean())
print("All features")
print("Average accuracy, " , scores_rep['test_accuracy'].mean())
print("Average precision, " , scores_rep['test_precision'].mean())
print("Average recall, " , scores_rep['test_recall'].mean())
print("Average f1, " , scores_rep['test_f1'].mean())
print("Dropped ?:")
print("Average accuracy, " , scores_no_null['test_accuracy'].mean())
print("Average precision, " , scores_no_null['test_precision'].mean())
print("Average recall, " , scores_no_null['test_recall'].mean())
print("Average f1, " , scores_no_null['test_f1'].mean())
```

```
Dropped Columns:
Average accuracy,  0.7419989330356114
Average precision,  0.7023029763572095
Average recall,  0.6635828204348397
Average f1,  0.6823727629718468
All features
Average accuracy,  0.8772031660573976
Average precision,  0.8610036737026052
Average recall,  0.8419722805242225
Average f1,  0.8513587832718971
Dropped ?:
Average accuracy,  0.8765260299414699
Average precision,  0.8600631956689881
Average recall,  0.8413047283035869
Average f1,  0.8505609132666235
```

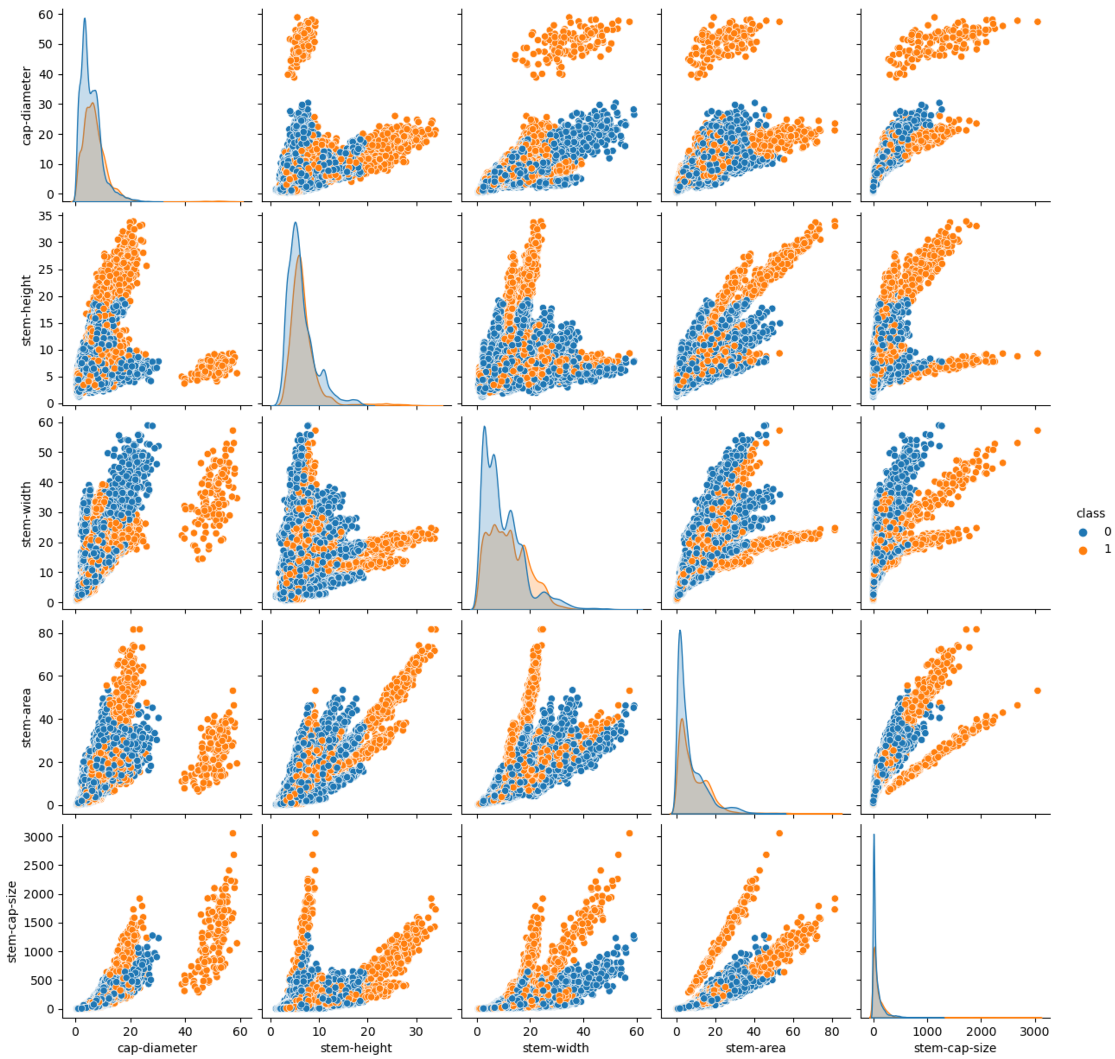
5 5. Data Augmentation (Creating at least 2 New Features)

[34]:
```
# Similar to Project 1 and 2.
# NEW FEATURE STEM-AREA
aug_train_features_rep = train_features_rep.copy()
aug_test_features_rep = test_features_rep.copy()
aug_train_features_rep["stem-area"] = aug_train_features_rep["stem-width"] *0.
↪1* aug_train_features_rep["stem-height"]
```

```
aug_test_features_rep["stem-area"] = aug_test_features_rep["stem-width"] * 0.1␣
↪* aug_test_features_rep["stem-height"]

# new feature stem-area and cap-diameter
aug_train_features_rep["stem-cap-size"] = aug_train_features_rep["stem-area"] *␣
↪aug_train_features_rep["cap-diameter"]
aug_test_features_rep["stem-cap-size"] = aug_test_features_rep["stem-area"] *␣
↪aug_test_features_rep["cap-diameter"]
```

[35]:

```
attributes = []
for name in aug_train_features_rep.columns:
    if aug_train_features_rep[name].dtype != 'O':
        attributes.append(name)

to_pairplot = aug_train_features_rep[attributes]
to_pairplot["class"] = train_labels
sns.pairplot(to_pairplot, hue="class")
plt.show()
```

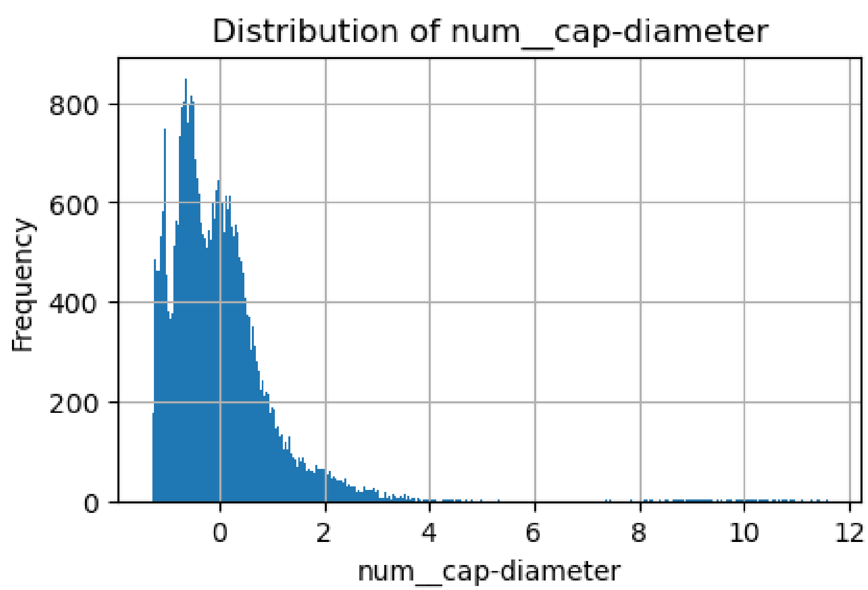


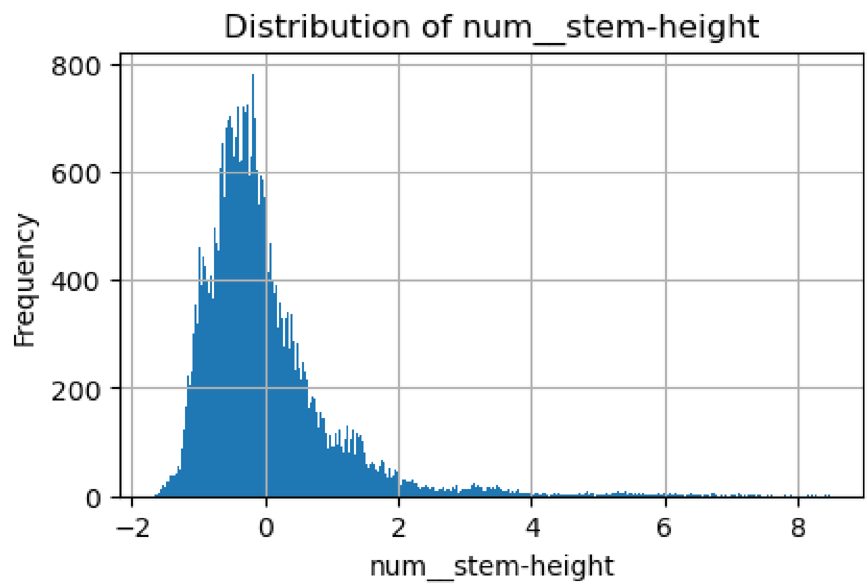
[36]:
```python
aug_tf_train_features_rep,aug_tf_test_features_rep, aug_full_pipeline_rep =␣
    ↪pipeline_data(aug_train_features_rep,aug_test_features_rep)
index_list = []
index = 0
for name in aug_full_pipeline_rep.get_feature_names_out():
    if not("?" in name):
        index_list.append(index)
    index += 1

aug_tf_train_features_no_null = aug_tf_train_features_rep[:,index_list]
aug_tf_test_features_no_null = aug_tf_test_features_rep[:,index_list]
aug_feature_list = aug_full_pipeline_rep.get_feature_names_out()[index_list]
```

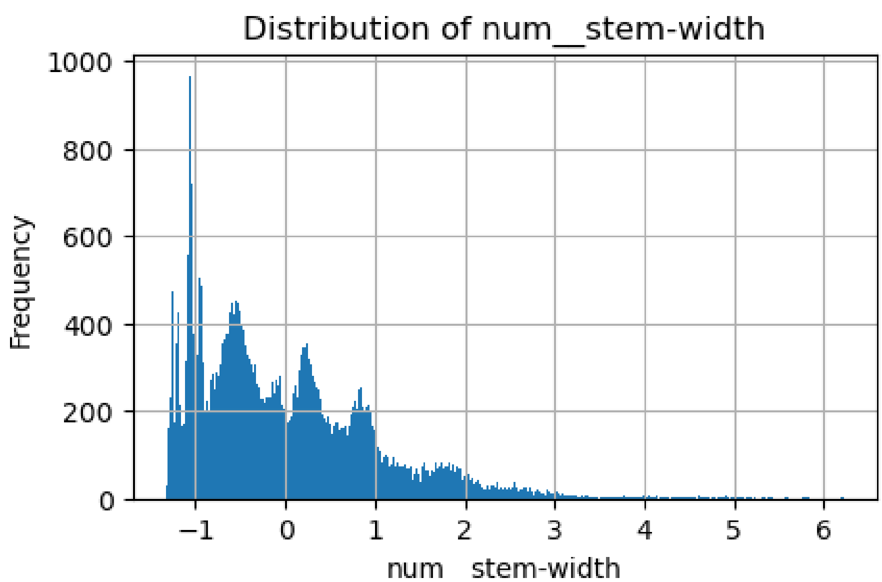
[37]:
```
print("Processed augmented training data size: ",aug_tf_train_features_no_null.
 ↪shape)
print("Processed augmented test data size: ",aug_tf_test_features_no_null.shape)
```

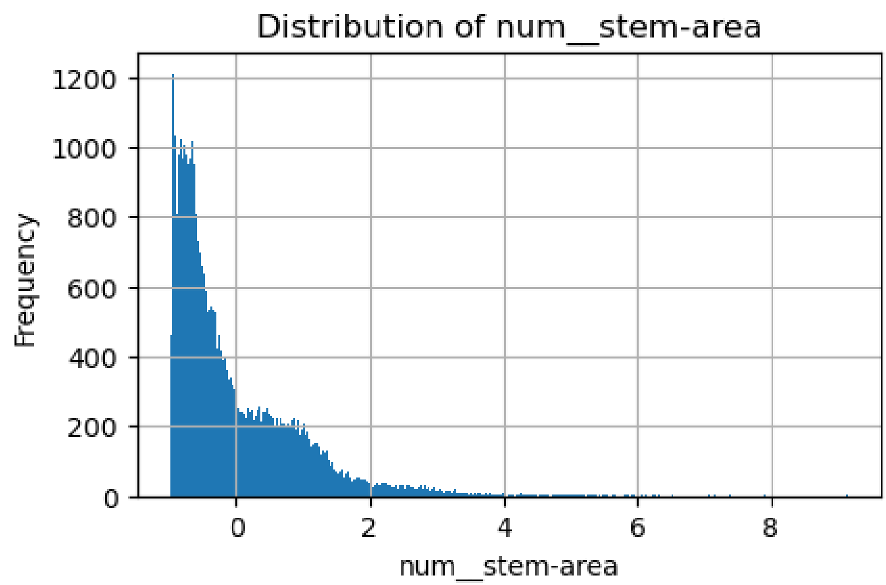
```
Processed augmented training data size:  (50213, 115)
Processed augmented test data size:  (10856, 115)
```

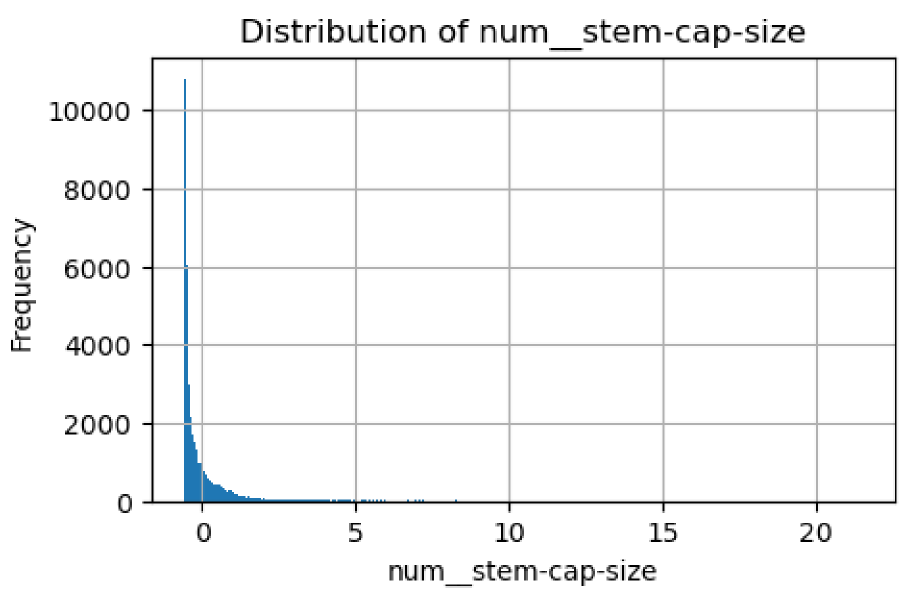
[38]:
```
df_aug_train = pd.
 ↪DataFrame(aug_tf_train_features_no_null,columns=aug_feature_list)
df_aug_test = pd.
 ↪DataFrame(aug_tf_test_features_no_null,columns=aug_feature_list)
for name in df_aug_train.columns:
    if "num__" in name:
        df_aug_train[name].hist(bins = 500, figsize = (5,3))
        plt.xlabel(name)
        plt.ylabel("Frequency")
        plt.title("Distribution of " + name)
        plt.show()
```




Distribution of num__stem-height
Frequency
800
600
400
200
0
−2
0
2
4
6
8
num__stem-height


Distribution of num__stem-width
Frequency
1000
800
600
400
200
0
−1
0
1
2
3
4
5
6
num__stem-width





[39]:

```
index = 0
for name in df_aug_train.columns:
    print(index," ",name)
    index += 1
```

```
0   num__cap-diameter
1   num__stem-height
2   num__stem-width
```

```
3   num__stem-area
4   num__stem-cap-size
5   cat__cap-shape_b
6   cat__cap-shape_c
7   cat__cap-shape_f
8   cat__cap-shape_o
9   cat__cap-shape_p
10   cat__cap-shape_s
11   cat__cap-shape_x
12   cat__cap-surface_d
13   cat__cap-surface_e
14   cat__cap-surface_g
15   cat__cap-surface_h
16   cat__cap-surface_i
17   cat__cap-surface_k
18   cat__cap-surface_l
19   cat__cap-surface_s
20   cat__cap-surface_t
21   cat__cap-surface_w
22   cat__cap-surface_y
23   cat__cap-color_b
24   cat__cap-color_e
25   cat__cap-color_g
26   cat__cap-color_k
27   cat__cap-color_l
28   cat__cap-color_n
29   cat__cap-color_o
30   cat__cap-color_p
31   cat__cap-color_r
32   cat__cap-color_u
33   cat__cap-color_w
34   cat__cap-color_y
35   cat__does-bruise-or-bleed_f
36   cat__does-bruise-or-bleed_t
37   cat__gill-attachment_a
38   cat__gill-attachment_d
39   cat__gill-attachment_e
40   cat__gill-attachment_f
41   cat__gill-attachment_p
42   cat__gill-attachment_s
43   cat__gill-attachment_x
44   cat__gill-spacing_c
45   cat__gill-spacing_d
46   cat__gill-spacing_f
47   cat__gill-color_b
48   cat__gill-color_e
49   cat__gill-color_f
50   cat__gill-color_g
```

51 cat__gill-color_k
52 cat__gill-color_n
53 cat__gill-color_o
54 cat__gill-color_p
55 cat__gill-color_r
56 cat__gill-color_u
57 cat__gill-color_w
58 cat__gill-color_y
59 cat__stem-root_b
60 cat__stem-root_r
61 cat__stem-root_s
62 cat__stem-surface_g
63 cat__stem-surface_h
64 cat__stem-surface_i
65 cat__stem-surface_k
66 cat__stem-surface_s
67 cat__stem-surface_t
68 cat__stem-surface_y
69 cat__stem-color_b
70 cat__stem-color_e
71 cat__stem-color_g
72 cat__stem-color_k
73 cat__stem-color_l
74 cat__stem-color_n
75 cat__stem-color_o
76 cat__stem-color_p
77 cat__stem-color_r
78 cat__stem-color_u
79 cat__stem-color_w
80 cat__stem-color_y
81 cat__veil-type_u
82 cat__veil-color_e
83 cat__veil-color_n
84 cat__veil-color_u
85 cat__veil-color_w
86 cat__veil-color_y
87 cat__has-ring_f
88 cat__has-ring_t
89 cat__ring-type_e
90 cat__ring-type_f
91 cat__ring-type_g
92 cat__ring-type_l
93 cat__ring-type_m
94 cat__ring-type_p
95 cat__ring-type_r
96 cat__ring-type_z
97 cat__spore-print-color_k
98 cat__spore-print-color_n

```
99   cat__spore-print-color_p
100   cat__spore-print-color_r
101   cat__spore-print-color_u
102   cat__spore-print-color_w
103   cat__habitat_d
104   cat__habitat_g
105   cat__habitat_h
106   cat__habitat_l
107   cat__habitat_m
108   cat__habitat_p
109   cat__habitat_u
110   cat__habitat_w
111   cat__season_a
112   cat__season_s
113   cat__season_u
114   cat__season_w
```

[40]:
```
#discard_list = [35,36,81,87,88,111,112,113,114]
discard_list = []
train_data = np.array(df_aug_train.drop(columns = df_aug_train.
 ↪columns[discard_list]))
test_data = np.array(df_aug_test.drop(columns = df_aug_test.
 ↪columns[discard_list]))
```

[41]:
```
print(train_data.shape)
print(test_data.shape)
```

```
(50213, 115)
(10856, 115)
```

6 6. Logistic Regression and Hypothesis Testing

[42]:
```
from sklearn.feature_selection import RFECV
from sklearn.model_selection import StratifiedKFold
from sklearn.linear_model import LogisticRegression
select = False
if select:
    min_features_to_select = 1  # Minimum number of features to consider
    clf = LogisticRegression(penalty = 'l1', C = 0.01, solver = "liblinear" )
    cv = StratifiedKFold(5)

    rfecv = RFECV(
        estimator=clf,
        step=1,
        cv=cv,
        scoring="f1",
        min_features_to_select=min_features_to_select,
```

```
        n_jobs=-1,
        verbose = 100
    )
    rfecv.fit(train_data, train_labels)
```

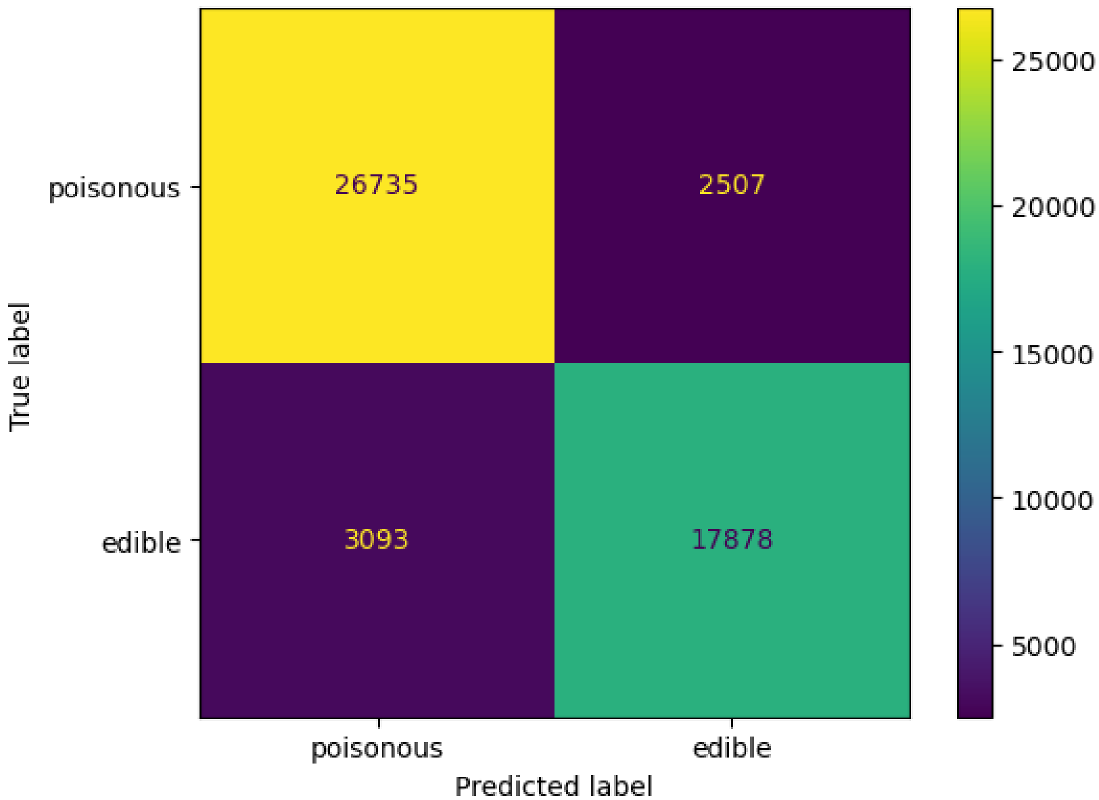
[43]:
```
if select:
    print(f"Optimal number of features: {rfecv.n_features_}")
    print("Feature ranking: ", rfecv.ranking_)
```

[44]:
```
select = False
if select:
    selected_train_data = train_data[:,rfecv.support_]
    selected_test_data = test_data[:,rfecv.support_]
else:
    selected_train_data = train_data.copy()
    selected_test_data = test_data.copy()
with open('selected.npy', 'wb') as f:
    np.save(f, selected_train_data)
    np.save(f, selected_test_data)
```

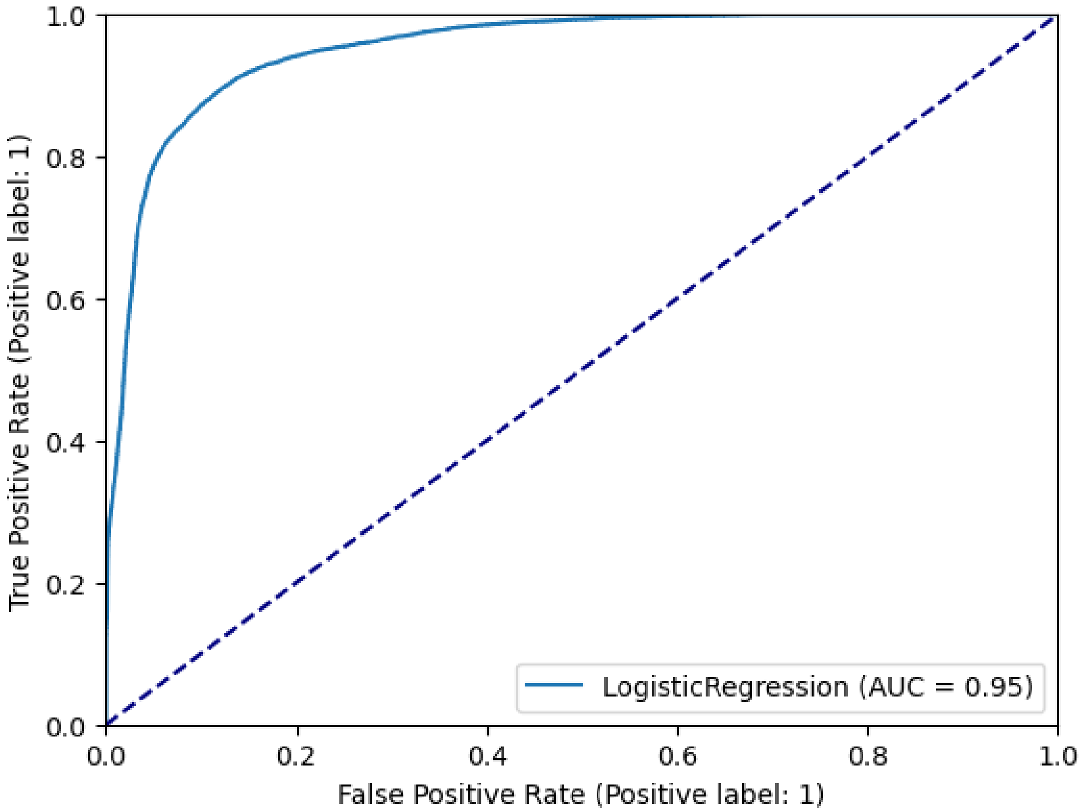
[45]:
```
with open('selected.npy', 'rb') as f:
    selected_train_data = np.load(f)
    selected_test_data = np.load(f)
```

[46]:
```
report_classifier_performance(clf,selected_train_data,selected_train_data,train_labels,train_l
```

```
LogisticRegression(solver='liblinear')
Accuracy with transformed data:  0.8884750960906538
Precision with transformed data:  0.8770174147657591
Recall with transformed data:  0.8525106098898478
F1 score with transformed data:  0.8645903859174001
```



poisonous
edible
True label
26735
2507
3093
17878
poisonous
edible
Predicted label
25000
20000
15000
10000
5000



[47]:
```
import statsmodels.api as sm

from statsmodels.genmod.generalized_linear_model import GLM
from statsmodels.genmod import families

y_train = train_labels.copy()
x_train = selected_train_data.copy()[:,:15]

x_train_c = sm.add_constant(x_train)
res = GLM(
    y_train,
    x_train_c,
    family=families.Binomial(),
    ).fit(attach_wls=True,maxiter  = 1000)
```

[48]:
```
print(res.summary())
```

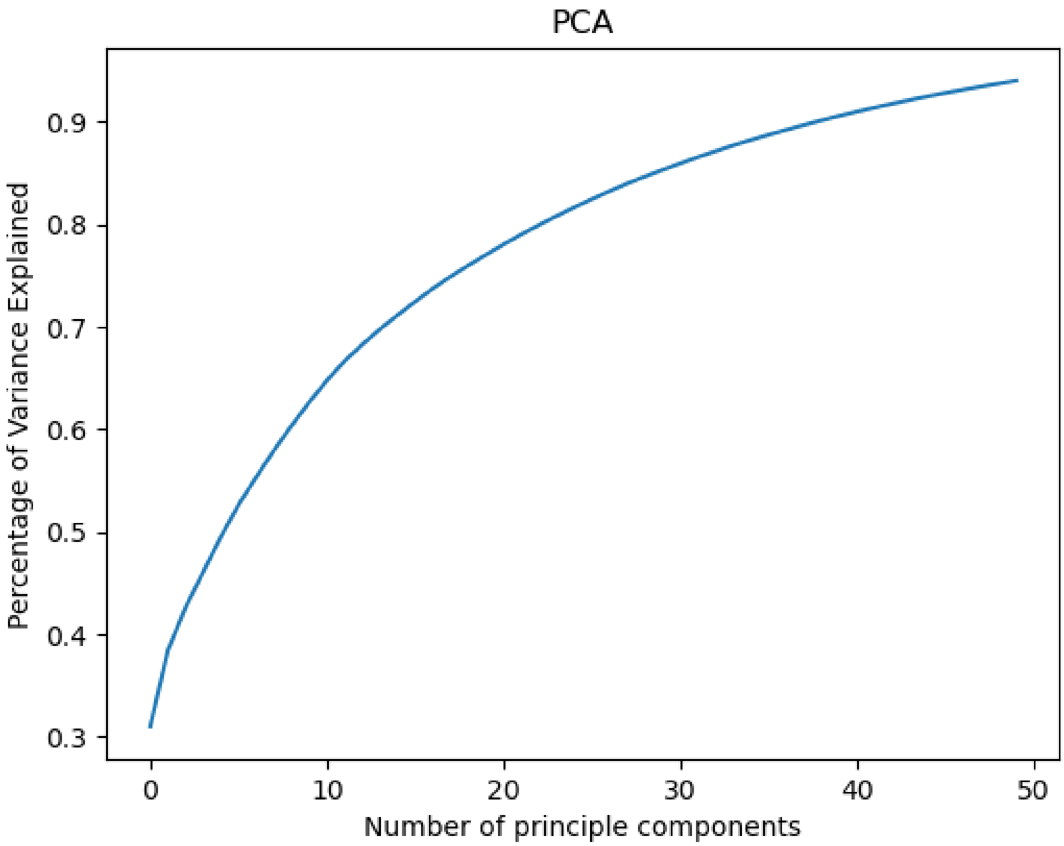
```
                 Generalized Linear Model Regression Results
==============================================================================
Dep. Variable:                  class   No. Observations:                50213
Model:                            GLM   Df Residuals:                    50198
```

```
Model Family:                Binomial   Df Model:                       14
Link Function:                  Logit   Scale:                      1.0000
Method:                          IRLS   Log-Likelihood:            -32589.
Date:                Tue, 21 Feb 2023   Deviance:                   65178.
Time:                        22:44:26   Pearson chi2:             5.01e+04
No. Iterations:                  1000   Pseudo R-squ. (CS):        0.05918
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          z      P>|z|      [0.025      0.975]
------------------------------------------------------------------------------
const         -0.4696      0.015    -30.413      0.000      -0.500      -0.439
x1             0.4668      0.029     16.312      0.000       0.411       0.523
x2             0.0448      0.031      1.451      0.147      -0.016       0.105
x3             0.1468      0.040      3.700      0.000       0.069       0.225
x4            -0.1316      0.062     -2.126      0.033      -0.253      -0.010
x5            -0.1593      0.034     -4.718      0.000      -0.226      -0.093
x6            -0.5120      0.033    -15.456      0.000      -0.577      -0.447
x7             0.2866      0.045      6.388      0.000       0.199       0.374
x8             0.3167      0.022     14.352      0.000       0.273       0.360
x9            -1.6063      0.079    -20.392      0.000      -1.761      -1.452
x10            0.7785      0.044     17.809      0.000       0.693       0.864
x11            0.1128      0.029      3.853      0.000       0.055       0.170
x12            0.1541      0.019      7.912      0.000       0.116       0.192
x13           -0.5539      0.044    -12.474      0.000      -0.641      -0.467
x14            0.0725      0.052      1.398      0.162      -0.029       0.174
x15            0.3716      0.035     10.569      0.000       0.303       0.441
==============================================================================
```

7 7. Dimensionality Reduction using PCA

[49]:
```python
# PCA: https://scikit-learn.org/stable/modules/generated/sklearn.decomposition.
 ↪PCA.html
from sklearn.decomposition import PCA
dim_red_pca = PCA(n_components = 50, random_state = 42)
pca_train_features = dim_red_pca.fit_transform(selected_train_data)
pca_test_features = dim_red_pca.transform(selected_test_data)
```

[50]:
```python
percentage_of_variance = np.cumsum(np.sort(dim_red_pca.
 ↪explained_variance_ratio_)[::-1])
plt.plot(percentage_of_variance)
plt.ylabel("Percentage of Variance Explained")
plt.xlabel("Number of principle components")
plt.title("PCA")
plt.show()
```



8 8. Experiment with any 2 other models (Non-Ensemble)

[51]:
```
svm = SVC(kernel = "rbf")
scores = cross_validate(svm, selected_train_data, train_labels, cv= 10,␣
↪scoring=('accuracy','precision', 'recall','f1'),n_jobs = -1,verbose = 1)
print(svm)
print("Average accuracy, " , scores['test_accuracy'].mean())
print("Average precision, " , scores['test_precision'].mean())
print("Average recall, " , scores['test_recall'].mean())
print("Average f1, " , scores['test_f1'].mean())
```

```
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 20 concurrent workers.
[Parallel(n_jobs=-1)]: Done   4 out of  10 | elapsed:   48.8s remaining:  1.2min
[Parallel(n_jobs=-1)]: Done  10 out of  10 | elapsed:   49.5s finished
```

```
SVC()
Average accuracy,  1.0
Average precision,  1.0
Average recall,  1.0
Average f1,  1.0
```

[52]:
```
log_reg = LogisticRegression(penalty = "l1", solver = "liblinear" )
scores = cross_validate(log_reg, selected_train_data, train_labels, cv= 10,␣
 ↪scoring=('accuracy','precision', 'recall','f1'),n_jobs = -1,verbose = 1)
print(log_reg)
print("Average accuracy, " , scores['test_accuracy'].mean())
print("Average precision, " , scores['test_precision'].mean())
print("Average recall, " , scores['test_recall'].mean())
print("Average f1, " , scores['test_f1'].mean())
```

```
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 20 concurrent workers.
[Parallel(n_jobs=-1)]: Done   4 out of  10 | elapsed:   21.0s remaining:   31.6s
[Parallel(n_jobs=-1)]: Done  10 out of  10 | elapsed:   25.6s finished
```

```
LogisticRegression(penalty='l1', solver='liblinear')
Average accuracy,  0.8918605853820962
Average precision,  0.8797562942581578
Average recall,  0.8584709965164272
Average f1,  0.8689619382188193
```

[53]:
```
from sklearn import tree
clf_tree = tree.DecisionTreeClassifier()
scores = cross_validate(clf_tree, selected_train_data, train_labels, cv= 10,␣
 ↪scoring=('accuracy','precision', 'recall','f1'),n_jobs = -1,verbose = 1)
print(clf_tree)
print("Average accuracy, " , scores['test_accuracy'].mean())
print("Average precision, " , scores['test_precision'].mean())
print("Average recall, " , scores['test_recall'].mean())
print("Average f1, " , scores['test_f1'].mean())
```

```
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 20 concurrent workers.
[Parallel(n_jobs=-1)]: Done   4 out of  10 | elapsed:    1.2s remaining:    1.8s
[Parallel(n_jobs=-1)]: Done  10 out of  10 | elapsed:    1.2s finished
```

```
DecisionTreeClassifier()
Average accuracy,  0.9993228876789964
Average precision,  0.9992847603902637
Average recall,  0.9990939664589616
Average f1,  0.9991891814476951
```

9 9. Experiment with 1 Ensemble Method

[54]:
```
# Ensemble Methods: https://scikit-learn.org/stable/modules/ensemble.html
from sklearn.ensemble import RandomForestClassifier
clf_random_forest = RandomForestClassifier(random_state= 42)
scores = cross_validate(clf_random_forest, selected_train_data, train_labels,␣
 ↪cv= 10, scoring=('accuracy','precision', 'recall','f1'),n_jobs = -1,verbose␣
 ↪= 1)
print(clf_random_forest)
```

```
print("Average accuracy, " , scores['test_accuracy'].mean())
print("Average precision, " , scores['test_precision'].mean())
print("Average recall, " , scores['test_recall'].mean())
print("Average f1, " , scores['test_f1'].mean())
```

```
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 20 concurrent workers.
[Parallel(n_jobs=-1)]: Done   4 out of  10 | elapsed:    9.4s remaining:   14.2s
[Parallel(n_jobs=-1)]: Done  10 out of  10 | elapsed:    9.6s finished
```

```
RandomForestClassifier(random_state=42)
Average accuracy,  0.9999800836486756
Average precision,  0.9999523355576739
Average recall,  1.0
Average f1,  0.9999761620977354
```

[55]:
```
from sklearn.ensemble import GradientBoostingClassifier
clf_gb = GradientBoostingClassifier(random_state=42)
scores = cross_validate(clf_gb, selected_train_data, train_labels, cv= 10,␣
 ↪scoring=('accuracy','precision', 'recall','f1'),n_jobs = -1,verbose = 1)
print(clf_gb)
print("Average accuracy, " , scores['test_accuracy'].mean())
print("Average precision, " , scores['test_precision'].mean())
print("Average recall, " , scores['test_recall'].mean())
print("Average f1, " , scores['test_f1'].mean())
```

```
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 20 concurrent workers.
[Parallel(n_jobs=-1)]: Done   4 out of  10 | elapsed:   48.8s remaining:  1.2min
[Parallel(n_jobs=-1)]: Done  10 out of  10 | elapsed:   49.0s finished
```

```
GradientBoostingClassifier(random_state=42)
Average accuracy,  0.9472445636728766
Average precision,  0.9428335573540858
Average recall,  0.9301417931922357
Average f1,  0.9364181130299158
```

[56]:
```
from sklearn.ensemble import AdaBoostClassifier
clf_ab = AdaBoostClassifier(random_state=42)
scores = cross_validate(clf_ab, selected_train_data, train_labels, cv= 10,␣
 ↪scoring=('accuracy','precision', 'recall','f1'),n_jobs = -1,verbose = 1)
print(clf_ab)
print("Average accuracy, " , scores['test_accuracy'].mean())
print("Average precision, " , scores['test_precision'].mean())
print("Average recall, " , scores['test_recall'].mean())
print("Average f1, " , scores['test_f1'].mean())
```

```
[Parallel(n_jobs=-1)]: Using backend LokyBackend with 20 concurrent workers.
[Parallel(n_jobs=-1)]: Done   4 out of  10 | elapsed:   12.3s remaining:   18.5s
[Parallel(n_jobs=-1)]: Done  10 out of  10 | elapsed:   12.4s finished
```

```
AdaBoostClassifier(random_state=42)
```

```
Average accuracy,  0.8349630159463268
Average precision,  0.8011544890461046
Average recall,  0.8046344294109383
Average f1,  0.8028209259631545
```

10 10. Cross-Validation & Hyperparameter Tuning for All 3 Models

[57]:
```
# Cross-Validation: https://scikit-learn.org/stable/modules/cross_validation.
↪html
# Hyperparameter Tuning: https://scikit-learn.org/stable/modules/grid_search.
↪html
with open('data.npy', 'wb') as f:
    np.save(f, selected_train_data)
    np.save(f, selected_test_data)
    np.save(f, train_labels)
    np.save(f, test_labels)
```

[58]:
```
import numpy as np
from sklearn.metrics import *
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
with open('data.npy', 'rb') as f:
    selected_train_data = np.load(f)
    selected_test_data = np.load(f)
    train_labels = np.load(f)
    test_labels = np.load(f)
train_data = selected_train_data.copy()
test_data  = selected_test_data.copy()
```

[59]:
```
clf1 = DecisionTreeClassifier(random_state=42)
clf2 = LogisticRegression(random_state=42)
clf3 = RandomForestClassifier(random_state=42)
```

[60]:
```
#Decision Tree
param1 = {}
param1['classifier__criterion'] = ["gini","entropy"]
param1['classifier__splitter'] = ["best","random"]
param1['classifier__max_depth'] = [3,5,10,15,20]
param1['classifier__min_samples_split'] = [2,5,7,10]
param1['classifier__min_samples_leaf'] = [5,20]
param1['classifier__max_leaf_nodes'] = [5,10,100]
param1['classifier__min_impurity_decrease'] = [0.001,0.01]
#param1['classifier__class_weight'] = ["balanced","balanced_subsample",None]
param1['classifier__ccp_alpha'] = [0.001,0.01]
```

```
param1['classifier'] = [clf1]

#Logistic Regression
param2 = {}
param2['classifier__penalty'] = ['l1','l2']
param2['classifier__C'] = [1e-3,1e-2,1e-1,1e-0,1e1,1e2,1e3]
param2['classifier__max_iter'] = [100000]
param2['classifier__solver'] =␣
↪["lbfgs","liblinear","newton-cg","newton-cholesky","sag","saga"]
param2['classifier'] = [clf2]

#Random Forest

param3 = {}
param3['classifier__n_estimators'] = [100]
param3['classifier__criterion'] = ["gini","entropy"]
param3['classifier__max_depth'] = [3,5,10,15,20]
param3['classifier__min_samples_split'] = [2,5,7,10]
param3['classifier__min_samples_leaf'] = [5,20]
#param3['classifier__max_features'] = ["sqrt","log2",None]
param3['classifier__max_leaf_nodes'] = [5,10,100]
param3['classifier__min_impurity_decrease'] = [0.001,0.01]
param3['classifier__n_jobs'] = [-1]
param3['classifier__warm_start'] = [True,False]
#param3['classifier__class_weight'] = ["balanced","balanced_subsample",None]
param1['classifier__ccp_alpha'] = [0.001,0.01]
param3['classifier'] = [clf3]
```

[61]:
```
from sklearn.base import TransformerMixin, BaseEstimator
from sklearn.pipeline import Pipeline
from sklearn.model_selection import GridSearchCV
from sklearn import model_selection
import joblib
```

[62]:
```
kfold = model_selection.KFold(n_splits = 10, random_state = 42, shuffle = True)
pipeline = Pipeline([('classifier', clf1)])

grid_search = GridSearchCV(pipeline, cv= kfold, n_jobs=-1, param_grid=param1,␣
↪scoring='f1',verbose=10)
grid_search.fit(train_data, train_labels)

#save your model or results
joblib.dump(grid_search, 'tree.pkl')

#load your model for further usage
joblib.load("tree.pkl")
```

```
Fitting 10 folds for each of 1920 candidates, totalling 19200 fits
```

[62]:
```
GridSearchCV(cv=KFold(n_splits=10, random_state=42, shuffle=True),
             estimator=Pipeline(steps=[('classifier',
                                        DecisionTreeClassifier(ccp_alpha=0.001,
criterion='entropy',
                                                               max_depth=20,
max_leaf_nodes=100,
min_impurity_decrease=0.001,
min_samples_leaf=5,
random_state=42))]),
             n_jobs=-1,
             param_grid={'classifier': [DecisionTreeClassifier(ccp_alpha=0.001,
                                                               criterion='en…
                         'classifier__ccp_alpha': [0.001, 0.01],
                         'classifier__criterion': ['gini', 'entropy'],
                         'classifier__max_depth': [3, 5, 10, 15, 20],
                         'classifier__max_leaf_nodes': [5, 10, 100],
                         'classifier__min_impurity_decrease': [0.001, 0.01],
                         'classifier__min_samples_leaf': [5, 20],
                         'classifier__min_samples_split': [2, 5, 7, 10],
                         'classifier__splitter': ['best', 'random']},
             scoring='f1', verbose=10)
```

[63]:
```
#Logistic

kfold = model_selection.KFold(n_splits = 10, random_state = 42, shuffle = True)
pipeline = Pipeline([('classifier', clf2)])

grid_search = GridSearchCV(pipeline, cv= kfold, n_jobs=-1, param_grid=param2,␣
 ↪scoring='f1',verbose=10)
grid_search.fit(train_data, train_labels)

#save your model or results
joblib.dump(grid_search, 'logistic.pkl')

#load your model for further usage
joblib.load("logistic.pkl")
```

```
Fitting 10 folds for each of 84 candidates, totalling 840 fits
```

[63]:
```
GridSearchCV(cv=KFold(n_splits=10, random_state=42, shuffle=True),
             estimator=Pipeline(steps=[('classifier',
                                        LogisticRegression(C=1000.0,
                                                           max_iter=100000,
                                                           random_state=42,
solver='liblinear'))]),
             n_jobs=-1,
             param_grid={'classifier': [LogisticRegression(C=1000.0,
                                                           max_iter=100000,
```

```
                                                        random_state=42,
                                                        solver='liblinear')],
                         'classifier__C': [0.001, 0.01, 0.1, 1.0, 10.0, 100.0,
                                           1000.0],
                         'classifier__max_iter': [100000],
                         'classifier__penalty': ['l1', 'l2'],
                         'classifier__solver': ['lbfgs', 'liblinear',
                                                'newton-cg', 'newton-cholesky',
                                                'sag', 'saga']},
             scoring='f1', verbose=10)
```

[64]:
```
kfold = model_selection.KFold(n_splits = 10, random_state = 42, shuffle = True)
pipeline = Pipeline([('classifier', clf3)])

grid_search = GridSearchCV(pipeline, cv= kfold, n_jobs=-1, param_grid=param3,␣
 ↪scoring='f1',verbose=10)
grid_search.fit(train_data, train_labels)

#save your model or results
joblib.dump(grid_search, 'forest.pkl')

#load your model for further usage
joblib.load("forest.pkl")
```

```
Fitting 10 folds for each of 960 candidates, totalling 9600 fits
```

[64]:
```
GridSearchCV(cv=KFold(n_splits=10, random_state=42, shuffle=True),
             estimator=Pipeline(steps=[('classifier',
RandomForestClassifier(criterion='entropy',
                                                              max_depth=20,
max_leaf_nodes=100,
min_impurity_decrease=0.001,
min_samples_leaf=20,
                                                              n_jobs=-1,
                                                              random_state=42,
warm_start=True))]),
             n_jobs=-1,
             param_grid={'classifier':
[RandomForestClassifier(criterion='entropy…
                         'classifier__criterion': ['gini', 'entropy'],
                         'classifier__max_depth': [3, 5, 10, 15, 20],
                         'classifier__max_leaf_nodes': [5, 10, 100],
                         'classifier__min_impurity_decrease': [0.001, 0.01],
                         'classifier__min_samples_leaf': [5, 20],
                         'classifier__min_samples_split': [2, 5, 7, 10],
                         'classifier__n_estimators': [100],
                         'classifier__n_jobs': [-1],
                         'classifier__warm_start': [True, False]},
```

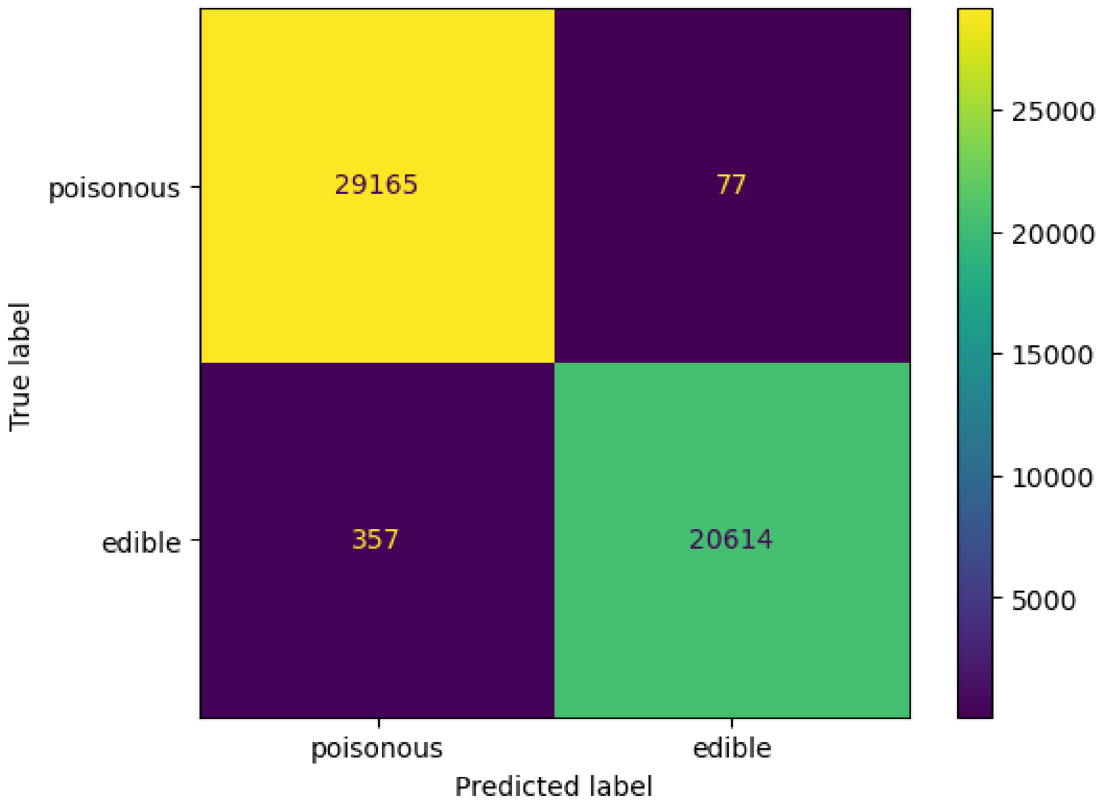
```
scoring='f1', verbose=10)
```

11 11. Report Final Results

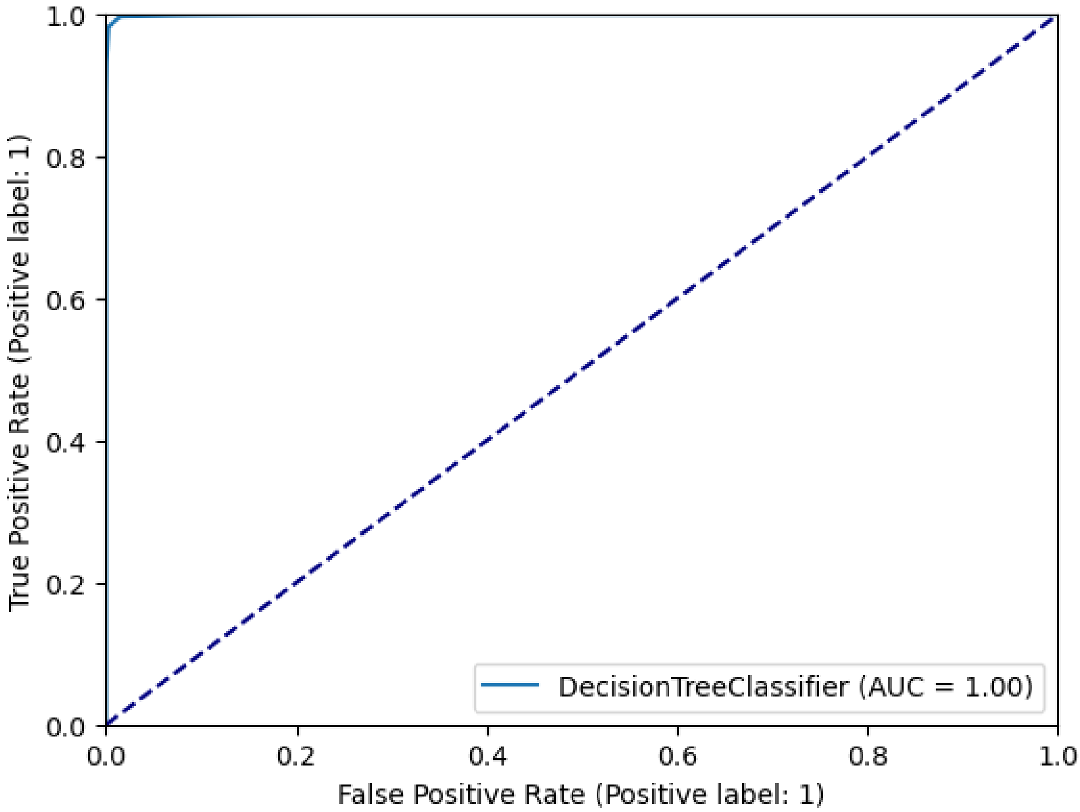
[65]:
```
# e.g. Accuracy, Precision etc.
```

[66]:
```
#Tree best performance
gs = joblib.load("tree.pkl")
print("Decision Tree with best param ", gs.best_params_)
print("Best validation score: ", gs.best_score_)

# PERFORMANCE ON TRAINING DATASET
best_clf = gs.best_params_["classifier"]
report_classifier_performance(best_clf,train_data,train_data,train_labels,train_labels)
# PERFORMANCE ON TEST DATASET
report_classifier_performance(best_clf,train_data,test_data,train_labels,test_labels)
```

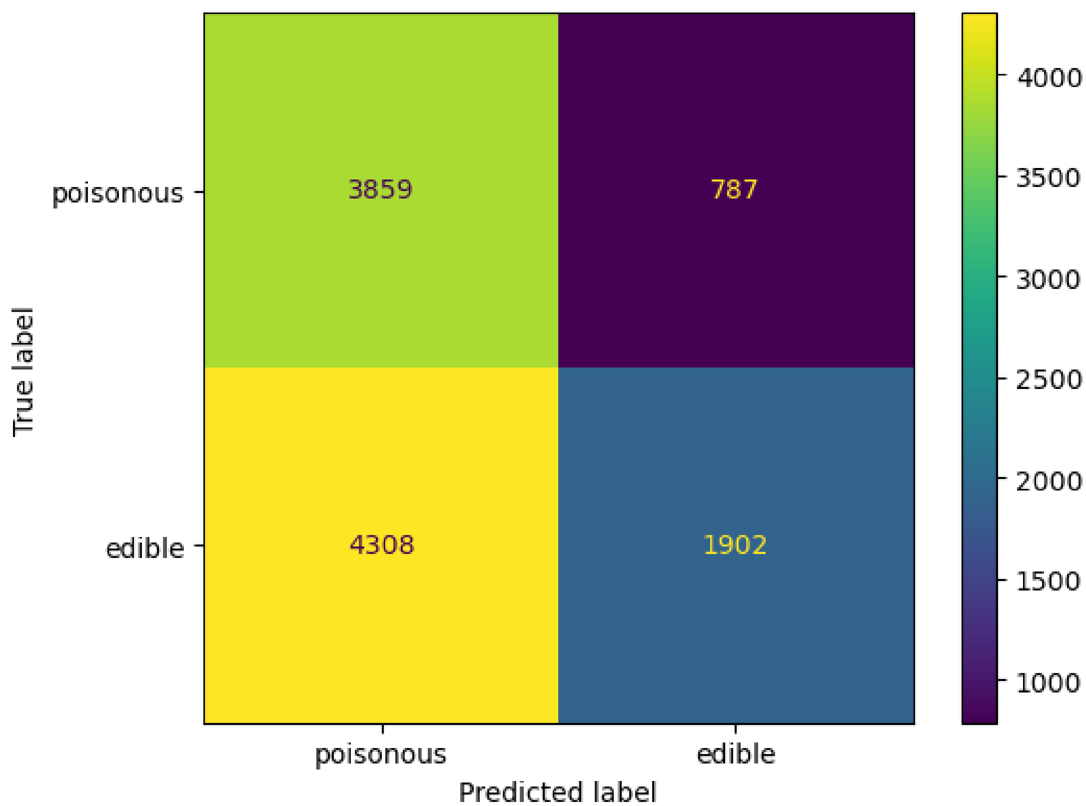
```
Decision Tree with best param  {'classifier':
DecisionTreeClassifier(ccp_alpha=0.001, criterion='entropy', max_depth=20,
                       max_leaf_nodes=100, min_impurity_decrease=0.001,
                       min_samples_leaf=5, random_state=42),
'classifier__ccp_alpha': 0.001, 'classifier__criterion': 'entropy',
'classifier__max_depth': 20, 'classifier__max_leaf_nodes': 100,
'classifier__min_impurity_decrease': 0.001, 'classifier__min_samples_leaf': 5,
'classifier__min_samples_split': 2, 'classifier__splitter': 'best'}
Best validation score:  0.9899072609584103
DecisionTreeClassifier(ccp_alpha=0.001, criterion='entropy', max_depth=20,
                       max_leaf_nodes=100, min_impurity_decrease=0.001,
                       min_samples_leaf=5, random_state=42)
Accuracy with transformed data:  0.9913568199470256
Precision with transformed data:  0.9962785752259437
Recall with transformed data:  0.9829764913451909
F1 score with transformed data:  0.989582833277327
```

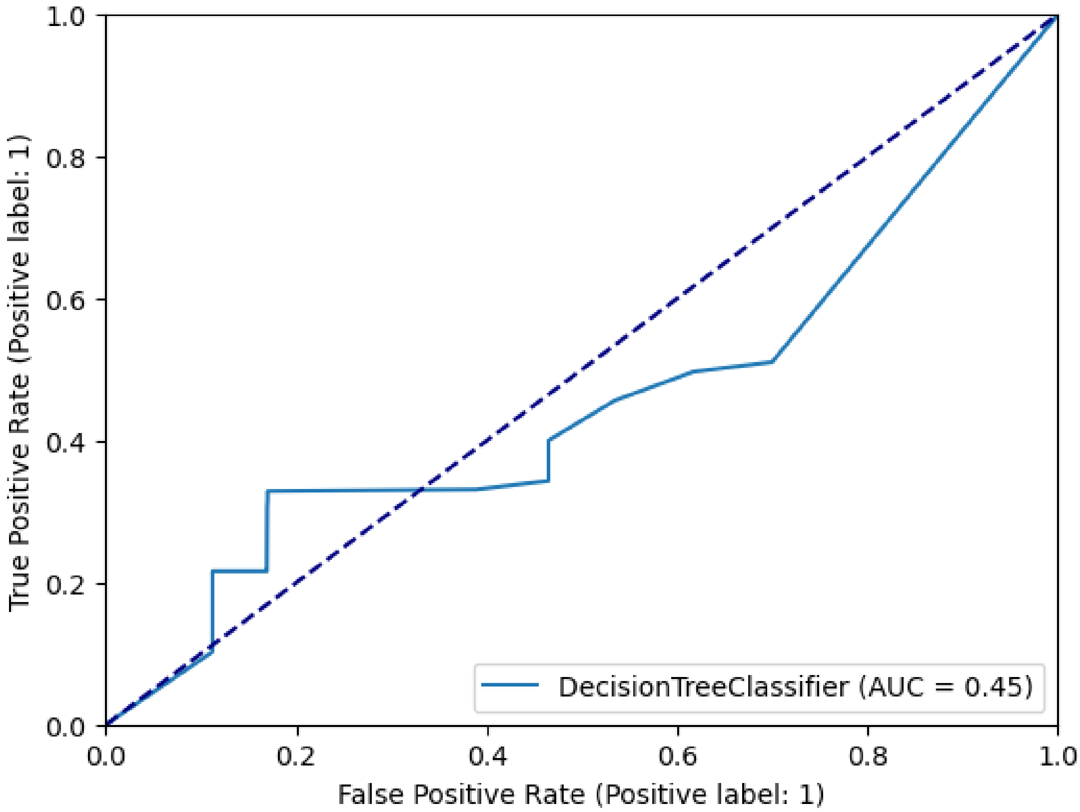


29165
77
357
20614
poisonous
edible
True label
poisonous
edible
Predicted label
25000
20000
15000
10000
5000




```
DecisionTreeClassifier(ccp_alpha=0.001, criterion='entropy', max_depth=20,
                       max_leaf_nodes=100, min_impurity_decrease=0.001,
                       min_samples_leaf=5, random_state=42)
Accuracy with transformed data:  0.5306742815033162
Precision with transformed data:  0.7073261435477873
Recall with transformed data:  0.30628019323671496
F1 score with transformed data:  0.42746375997303065
```

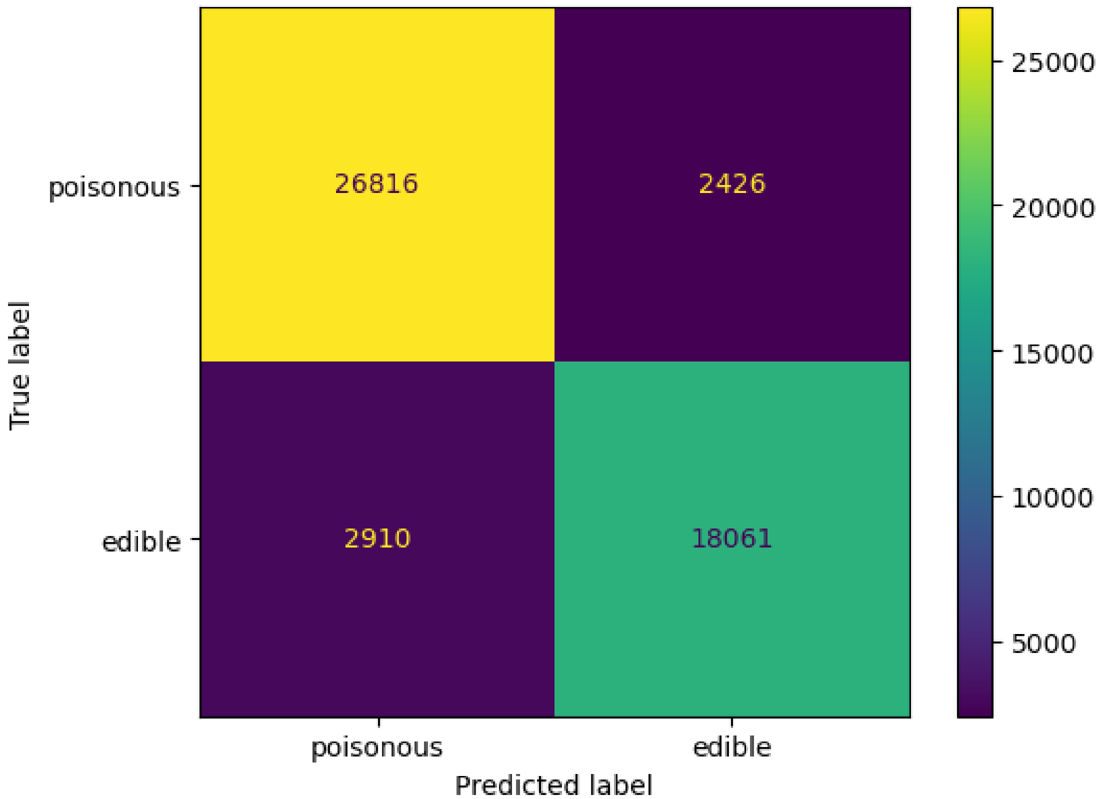

3859
787
4308
1902
poisonous
edible
True label
poisonous
edible
Predicted label
4000
3500
3000
2500
2000
1500
1000

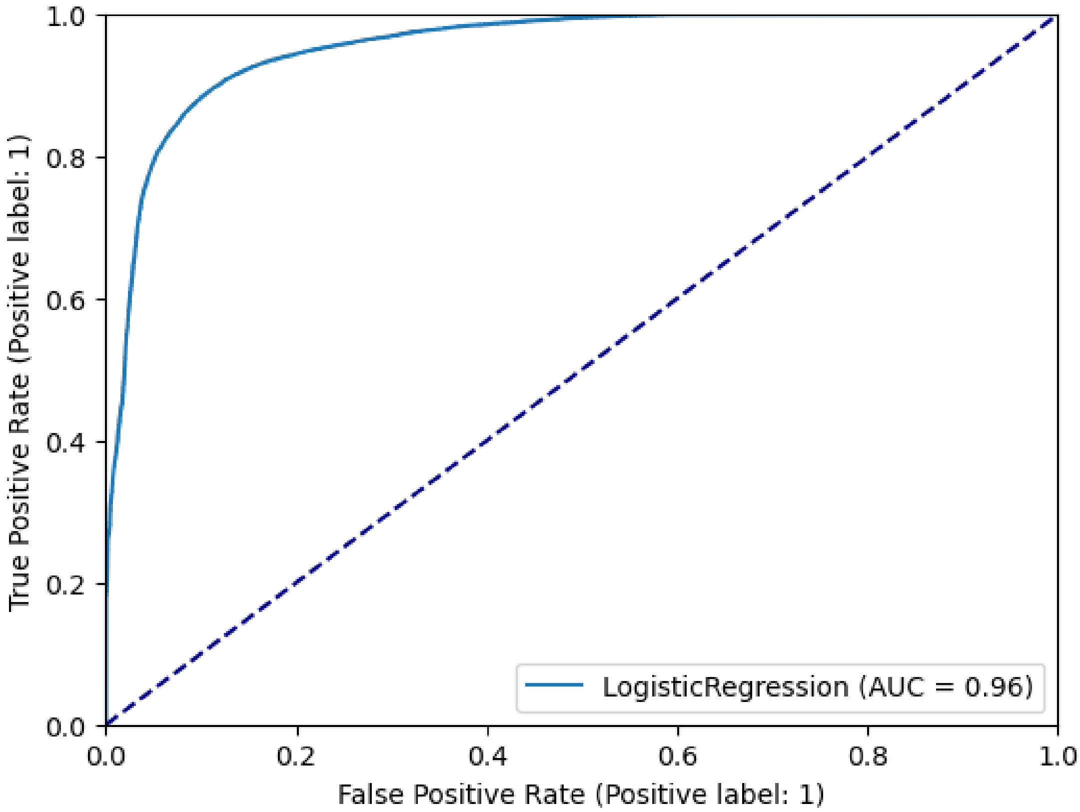


[67]:
```
#Tree best performance
gs = joblib.load("logistic.pkl")
print("Logistic Regression with best param ", gs.best_params_)
print("Best validation score: ", gs.best_score_)

# PERFORMANCE ON TRAINING DATASET
best_clf = gs.best_params_["classifier"]
report_classifier_performance(best_clf,train_data,train_data,train_labels,train_labels)
# PERFORMANCE ON TEST DATASET
report_classifier_performance(best_clf,train_data,test_data,train_labels,test_labels)
```

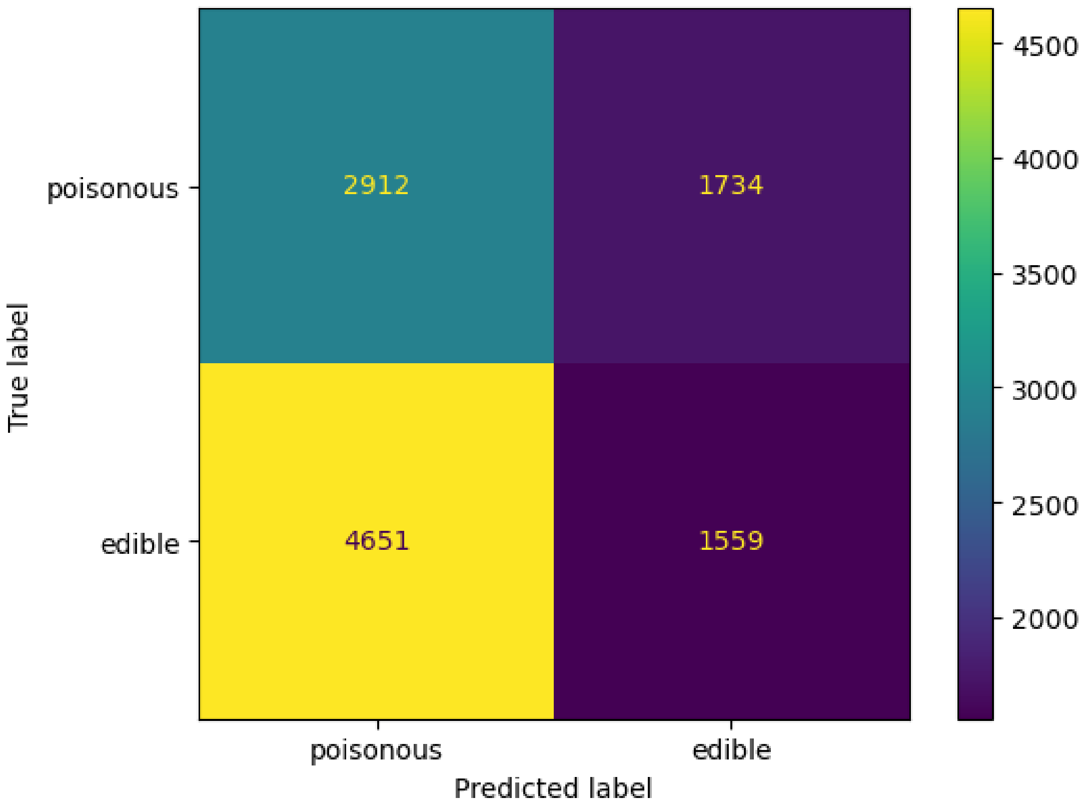
```
Logistic Regression with best param  {'classifier': LogisticRegression(C=1000.0,
max_iter=100000, random_state=42,
                   solver='liblinear'), 'classifier__C': 1000.0,
'classifier__max_iter': 100000, 'classifier__penalty': 'l2',
'classifier__solver': 'liblinear'}
Best validation score:  0.8702077774540855
LogisticRegression(C=1000.0, max_iter=100000, random_state=42,
                   solver='liblinear')
Accuracy with transformed data:  0.893732698703523
Precision with transformed data:  0.8815834431590764
```

```
Recall with transformed data:  0.8612369462591197
F1 score with transformed data:  0.8712914274687635
```

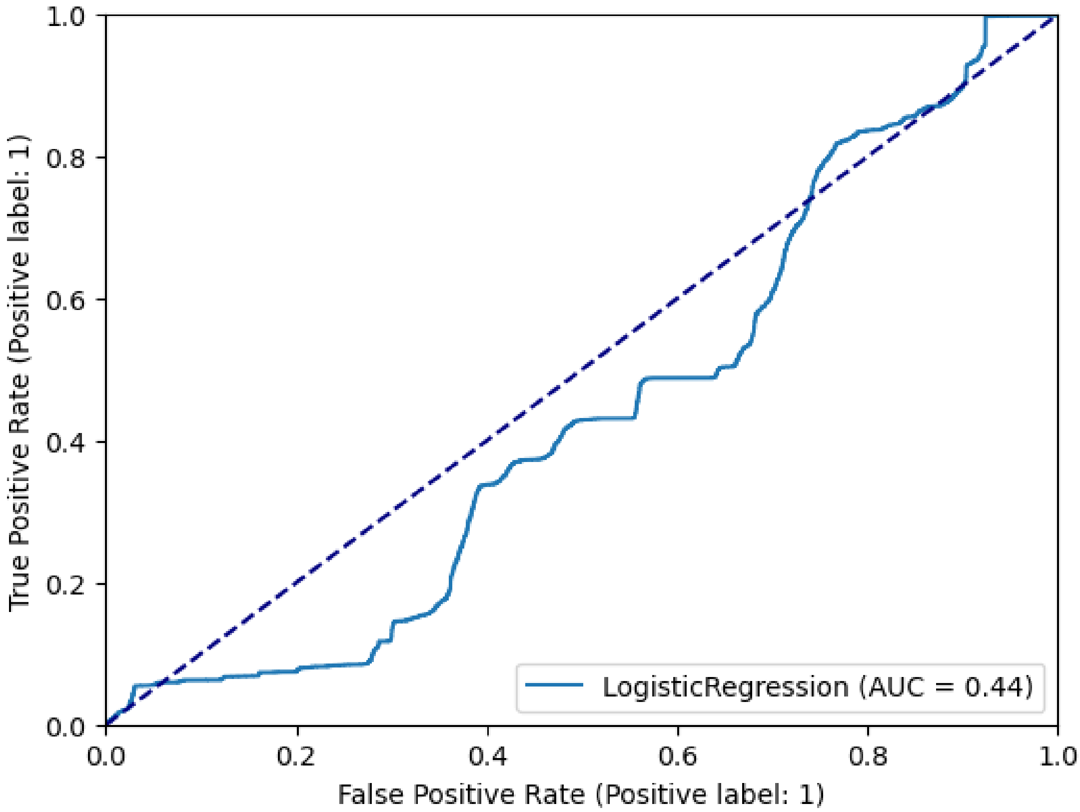





```
LogisticRegression(C=1000.0, max_iter=100000, random_state=42,
                   solver='liblinear')
Accuracy with transformed data:  0.41184598378776716
Precision with transformed data:  0.4734284846644397
Recall with transformed data:  0.25104669887278586
F1 score with transformed data:  0.3281069136062296
```



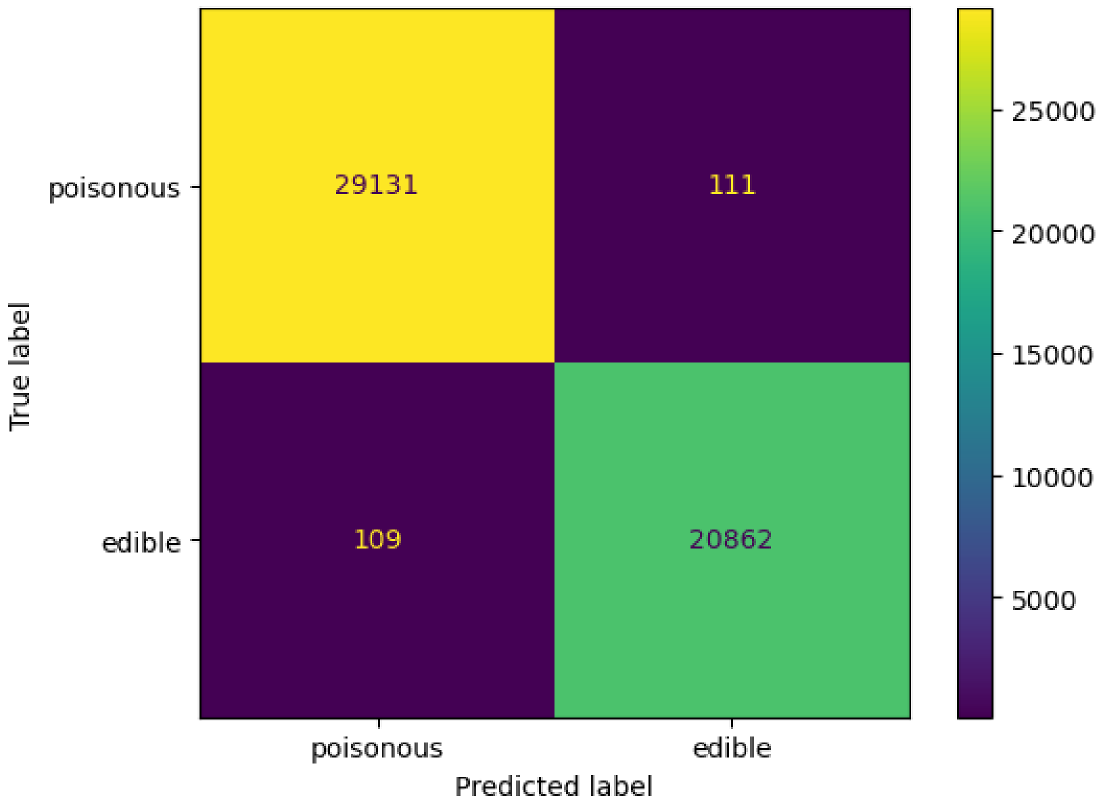
poisonous
edible
True label
2912
1734
4651
1559
poisonous
edible
Predicted label
4500
4000
3500
3000
2500
2000

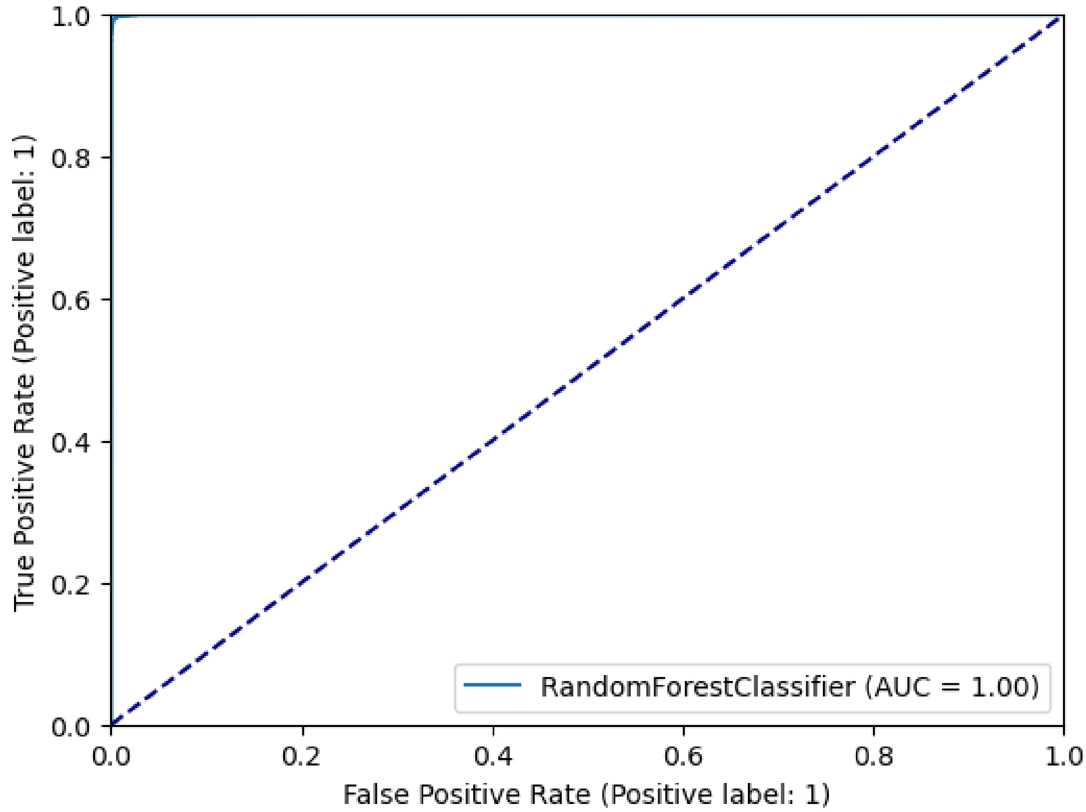


[68]:
```
#Tree best performance
gs = joblib.load("forest.pkl")
print("Random Forest with best param ", gs.best_params_)
print("Best validation score: ", gs.best_score_)

# PERFORMANCE ON TRAINING DATASET
best_clf = gs.best_params_["classifier"]
report_classifier_performance(best_clf,train_data,train_data,train_labels,train_labels)
# PERFORMANCE ON TEST DATASET
report_classifier_performance(best_clf,train_data,test_data,train_labels,test_labels)
```

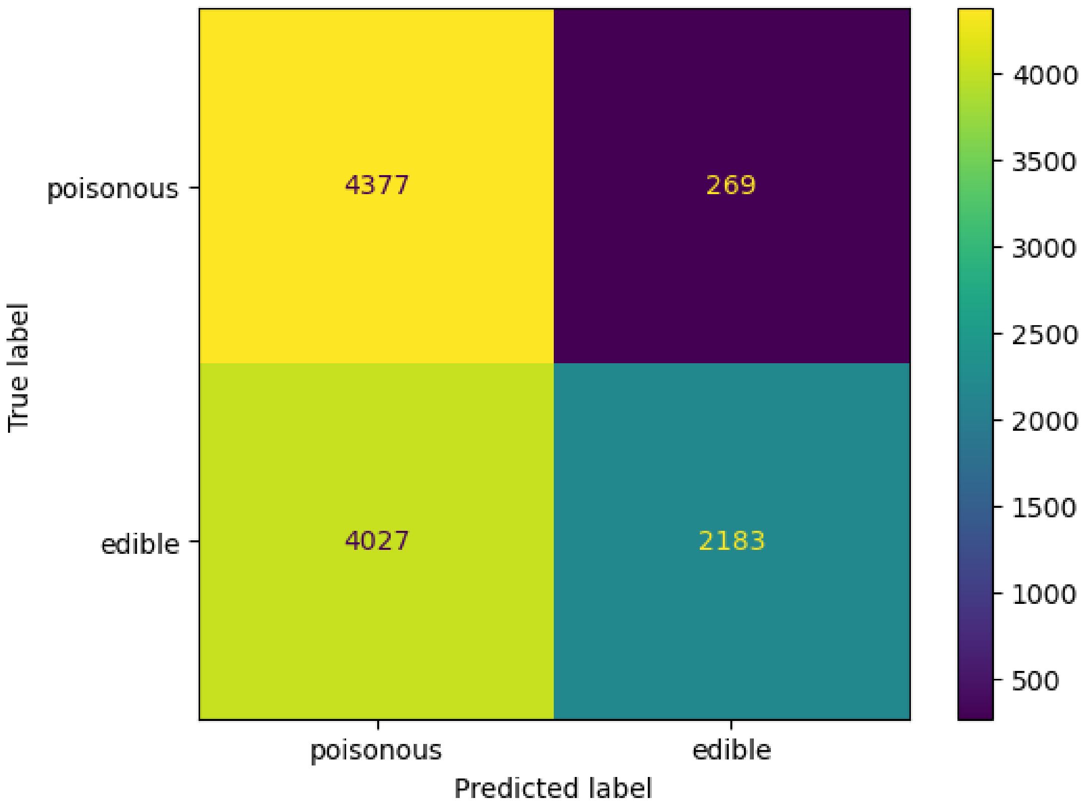
```
Random Forest with best param  {'classifier':
RandomForestClassifier(criterion='entropy', max_depth=20, max_leaf_nodes=100,
                       min_impurity_decrease=0.001, min_samples_leaf=20,
                       n_jobs=-1, random_state=42, warm_start=True),
'classifier__criterion': 'entropy', 'classifier__max_depth': 20,
'classifier__max_leaf_nodes': 100, 'classifier__min_impurity_decrease': 0.001,
'classifier__min_samples_leaf': 20, 'classifier__min_samples_split': 2,
'classifier__n_estimators': 100, 'classifier__n_jobs': -1,
'classifier__warm_start': True}
Best validation score:  0.9945308061458794
```

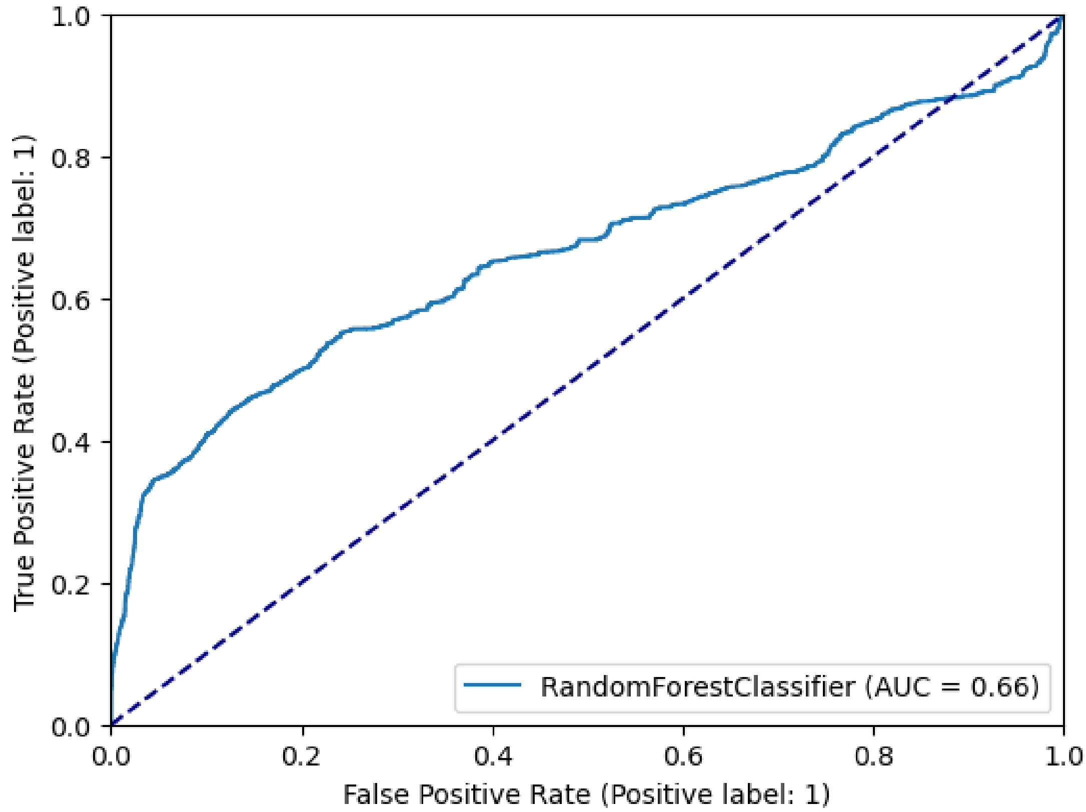
```
RandomForestClassifier(criterion='entropy', max_depth=20, max_leaf_nodes=100,
                       min_impurity_decrease=0.001, min_samples_leaf=20,
                       n_jobs=-1, random_state=42, warm_start=True)
Accuracy with transformed data:  0.9956186644892757
Precision with transformed data:  0.9947074810470605
Recall with transformed data:  0.994802346096991
F1 score with transformed data:  0.9947549113103186
```






```
RandomForestClassifier(criterion='entropy', max_depth=20, max_leaf_nodes=100,
                       min_impurity_decrease=0.001, min_samples_leaf=20,
                       n_jobs=-1, random_state=42, warm_start=True)
Accuracy with transformed data:  0.604274134119381
Precision with transformed data:  0.8902936378466558
Recall with transformed data:  0.35152979066022544
F1 score with transformed data:  0.5040406372662203
```


True label
poisonous
edible
4377
269
4027
2183
poisonous
edible
Predicted label
4000
3500
3000
2500
2000
1500
1000
500


1.0
0.8
0.6
0.4
0.2
0.0
True Positive Rate (Positive label: 1)
RandomForestClassifier (AUC = 0.66)
0.0
0.2
0.4
0.6
0.8
1.0
False Positive Rate (Positive label: 1)

[ ]: