Mushroom Database

In [1]:

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as pl
```

In [2]:

```
features = ["class","cap-shape","cap-surface","cap-color","bruises","odor","gill-

agri = pd.read_csv('agaricus-lepiota.data', names=features)
agri
```

Out[2]:

	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	gill-color	...	stalk surface below rin
0	p	x	s	n	t	p	f	c	n	k	...	
1	e	x	s	y	t	a	f	c	b	k	...	
2	e	b	s	w	t	l	f	c	b	n	...	
3	p	x	y	w	t	p	f	c	n	n	...	
4	e	x	s	g	f	n	f	w	b	k	...	
...	...	...	...	...	...	...	...	...	...	...	...	.
8119	e	k	s	n	f	n	a	c	b	y	...	
8120	e	x	s	n	f	n	a	c	b	y	...	
8121	e	f	s	n	f	n	a	c	b	n	...	
8122	p	k	y	n	f	y	f	c	n	b	...	
8123	e	x	s	n	f	n	a	c	b	y	...	

8124 rows × 23 columns

In [3]:

```
agri.shape
```

Out[3]:

```
(8124, 23)
```

Basic Information of Data type:

In [4]:

```
agri.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 8124 entries, 0 to 8123
Data columns (total 23 columns):
 #   Column                    Non-Null Count  Dtype 
---  ------                    --------------  ----- 
 0   class                     8124 non-null   object
 1   cap-shape                 8124 non-null   object
 2   cap-surface               8124 non-null   object
 3   cap-color                 8124 non-null   object
 4   bruises                   8124 non-null   object
 5   odor                      8124 non-null   object
 6   gill-attachment           8124 non-null   object
 7   gill-spacing              8124 non-null   object
 8   gill-size                 8124 non-null   object
 9   gill-color                8124 non-null   object
 10  stalk-shape               8124 non-null   object
 11  stalk-root                8124 non-null   object
 12  stalk-surface-above-ring  8124 non-null   object
 13  stalk-surface-below-ring  8124 non-null   object
 14  stalk-color-above-ring    8124 non-null   object
 15  stalk-color-below-ring    8124 non-null   object
 16  veil-type                 8124 non-null   object
 17  veil-color                8124 non-null   object
 18  ring-number               8124 non-null   object
 19  ring-type                 8124 non-null   object
 20  spore-print-color         8124 non-null   object
 21  population                8124 non-null   object
 22  habitat                   8124 non-null   object
dtypes: object(23)
memory usage: 1.4+ MB
```

Overview of all attributes at dataset:

In [5]:

```python
agri.describe()
```

Out[5]:

	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	gill-color	...	st surfa bel
count	8124	8124	8124	8124	8124	8124	8124	8124	8124	8124	...	8
unique	2	6	4	10	2	9	2	2	2	12	...	
top	e	x	y	n	f	n	f	c	b	b	...	
freq	4208	3656	3244	2284	4748	3528	7914	6812	5612	1728	...	4

4 rows × 23 columns

In [6]:

```python
agri["class"].value_counts()
```

Out[6]:

```
e    4208
p    3916
Name: class, dtype: int64
```

In [7]:

```python
agri.isnull().sum()
```

Out[7]:
```
class                       0
cap-shape                   0
cap-surface                 0
cap-color                   0
bruises                     0
odor                        0
gill-attachment             0
gill-spacing                0
gill-size                   0
gill-color                  0
stalk-shape                 0
stalk-root                  0
stalk-surface-above-ring    0
stalk-surface-below-ring    0
stalk-color-above-ring      0
stalk-color-below-ring      0
veil-type                   0
veil-color                  0
ring-number                 0
ring-type                   0
spore-print-color           0
population                  0
habitat                     0
dtype: int64
```

In [8]:
```
agri["class"].unique()
```

Out[8]:
```
array(['p', 'e'], dtype=object)
```

Analysis relation between CLASS & ODOR

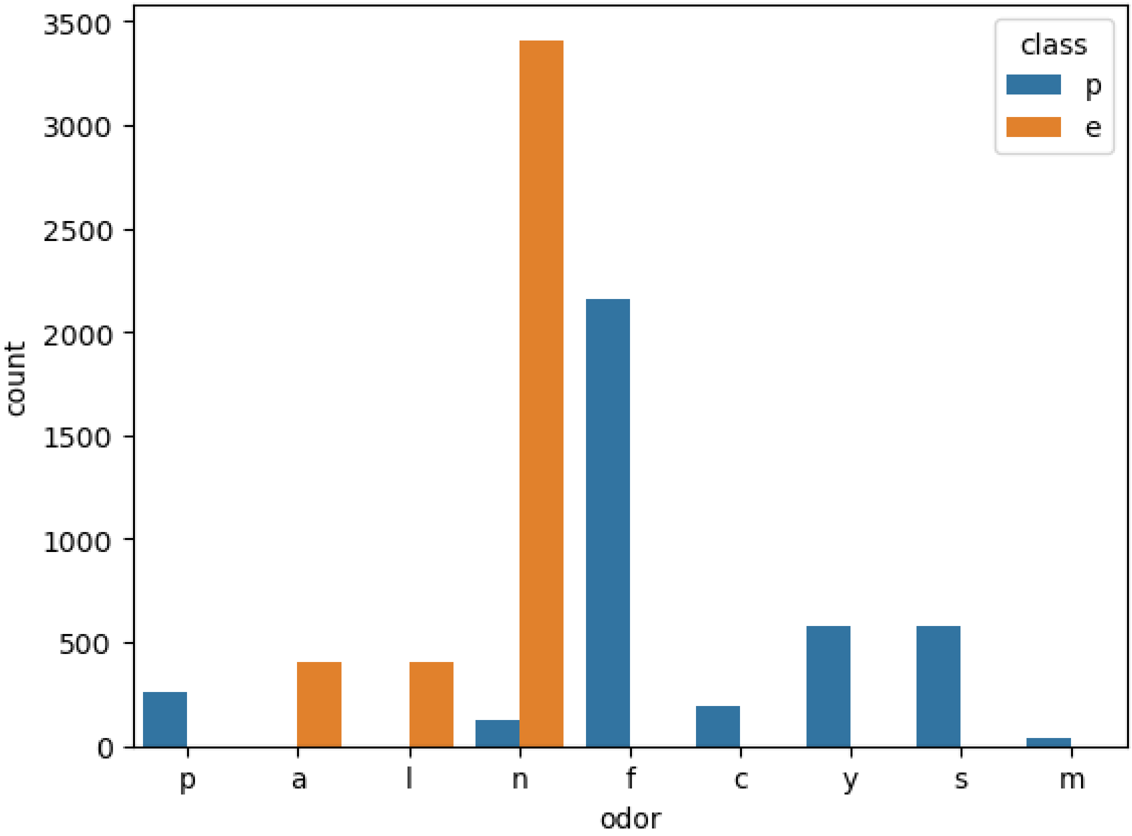
In [9]:
```
pd.crosstab(agri["class"], agri["odor"],margins=True)
```

Out[9]:

odor	**a**	**c**	**f**	**l**	**m**	**n**	**p**	**s**	**y**	**All**
class										
e	400	0	0	400	0	3408	0	0	0	4208
p	0	192	2160	0	36	120	256	576	576	3916
All	400	192	2160	400	36	3528	256	576	576	8124

In [10]:
```
sns.countplot(data=agri, x="odor", hue="class")
```

Out[10]:
```
<Axes: xlabel='odor', ylabel='count'>
```



Analysis relation between CLASS & SPORE PRINT COLOR

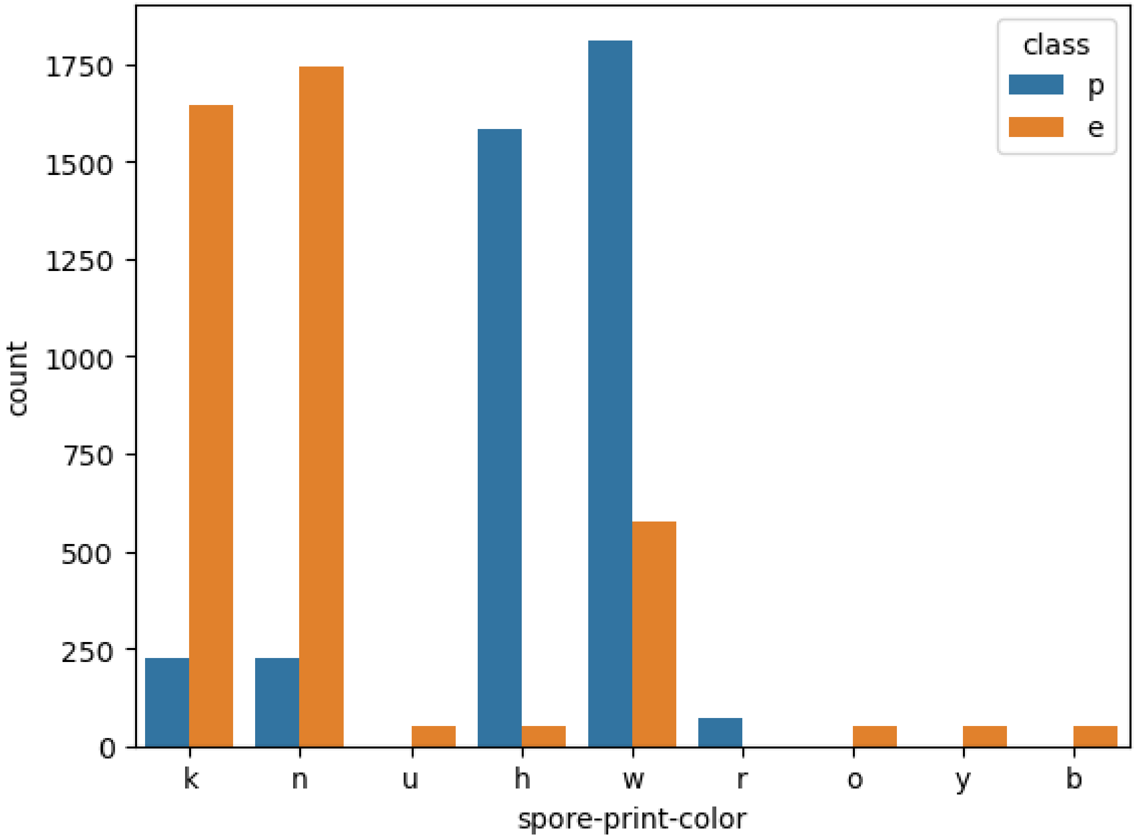
```
In [11]: pd.crosstab(agri["class"], agri["spore-print-color"],margins=True)
```

Out[11]:

spore-print-color	b	h	k	n	o	r	u	w	y	All
class										
e	48	48	1648	1744	48	0	48	576	48	4208
p	0	1584	224	224	0	72	0	1812	0	3916
All	48	1632	1872	1968	48	72	48	2388	48	8124

```
In [12]: sns.countplot(data=agri, x="spore-print-color", hue="class")
```

```
Out[12]: <Axes: xlabel='spore-print-color', ylabel='count'>
```



Analysis relation between CLASS & POPULATION

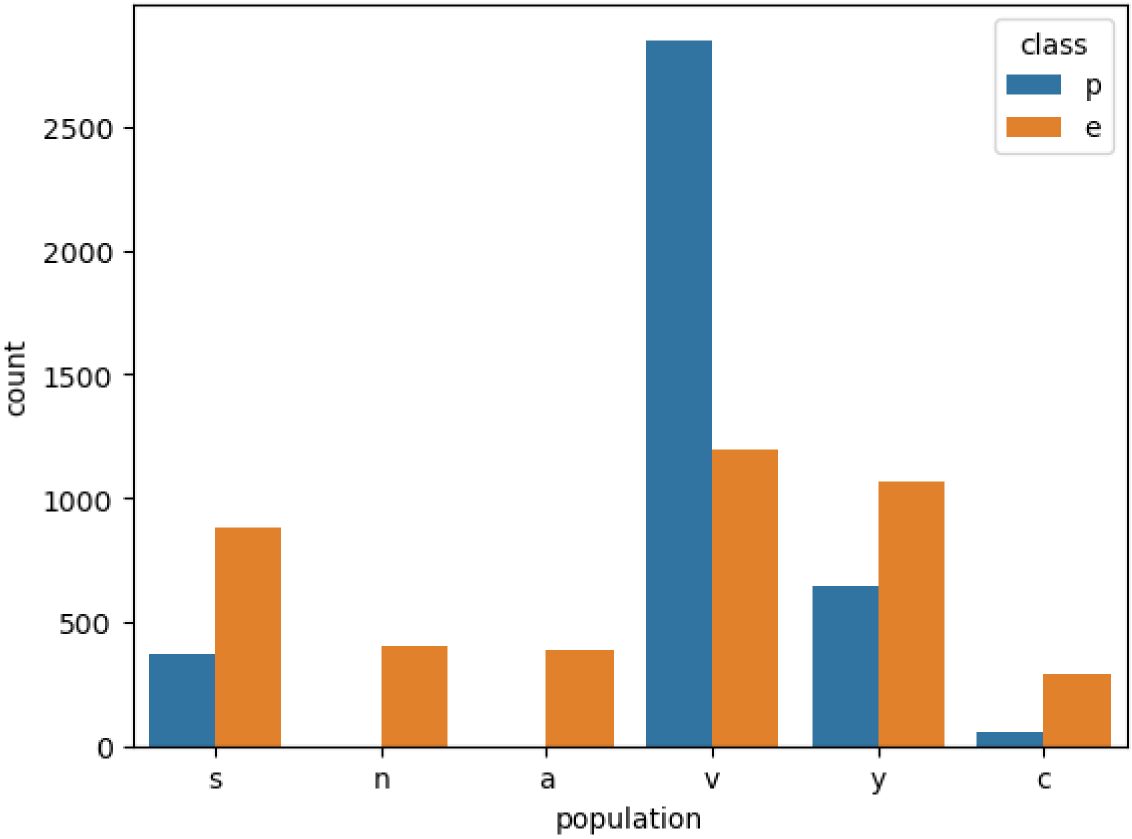
In [13]:
```
pd.crosstab(agri["class"], agri["population"],margins=True)
```

Out[13]:

population	a	c	n	s	v	y	All
class							
e	384	288	400	880	1192	1064	4208
p	0	52	0	368	2848	648	3916
All	384	340	400	1248	4040	1712	8124

In [14]:
```
sns.countplot(data=agri, x="population", hue="class")
```

Out[14]:
```
<Axes: xlabel='population', ylabel='count'>
```



Analysis relation between CLASS & HABITAT

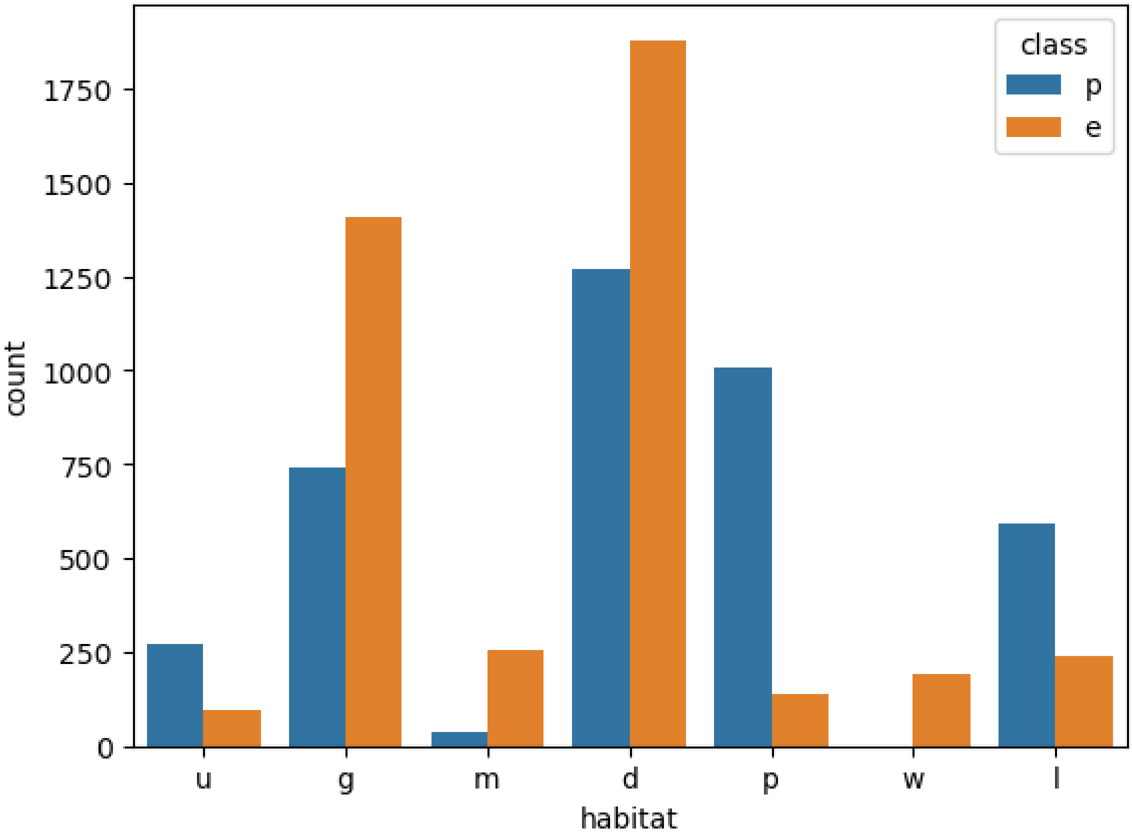
In [15]:
```
pd.crosstab(agri["class"], agri["habitat"],margins=True)
```

Out[15]:

habitat	d	g	l	m	p	u	w	All
class								
e	1880	1408	240	256	136	96	192	4208
p	1268	740	592	36	1008	272	0	3916
All	3148	2148	832	292	1144	368	192	8124

In [16]:
```
sns.countplot(data=agri, x="habitat", hue="class")
```

Out[16]:
```
<Axes: xlabel='habitat', ylabel='count'>
```



Dropping Veil-type attribute as unique categorical values is '1' only.

In [17]:

```
agri1 = agri.drop(["veil-type"], axis = 1)
agri1
```

Out[17]:

	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	gill-color	...	stalk surface above rin
0	p	x	s	n	t	p	f	c	n	k	...	
1	e	x	s	y	t	a	f	c	b	k	...	
2	e	b	s	w	t	l	f	c	b	n	...	
3	p	x	y	w	t	p	f	c	n	n	...	
4	e	x	s	g	f	n	f	w	b	k	...	
...	...	...	...	...	...	...	...	...	...	...	...	.
8119	e	k	s	n	f	n	a	c	b	y	...	
8120	e	x	s	n	f	n	a	c	b	y	...	
8121	e	f	s	n	f	n	a	c	b	n	...	
8122	p	k	y	n	f	y	f	c	n	b	...	
8123	e	x	s	n	f	n	a	c	b	y	...	

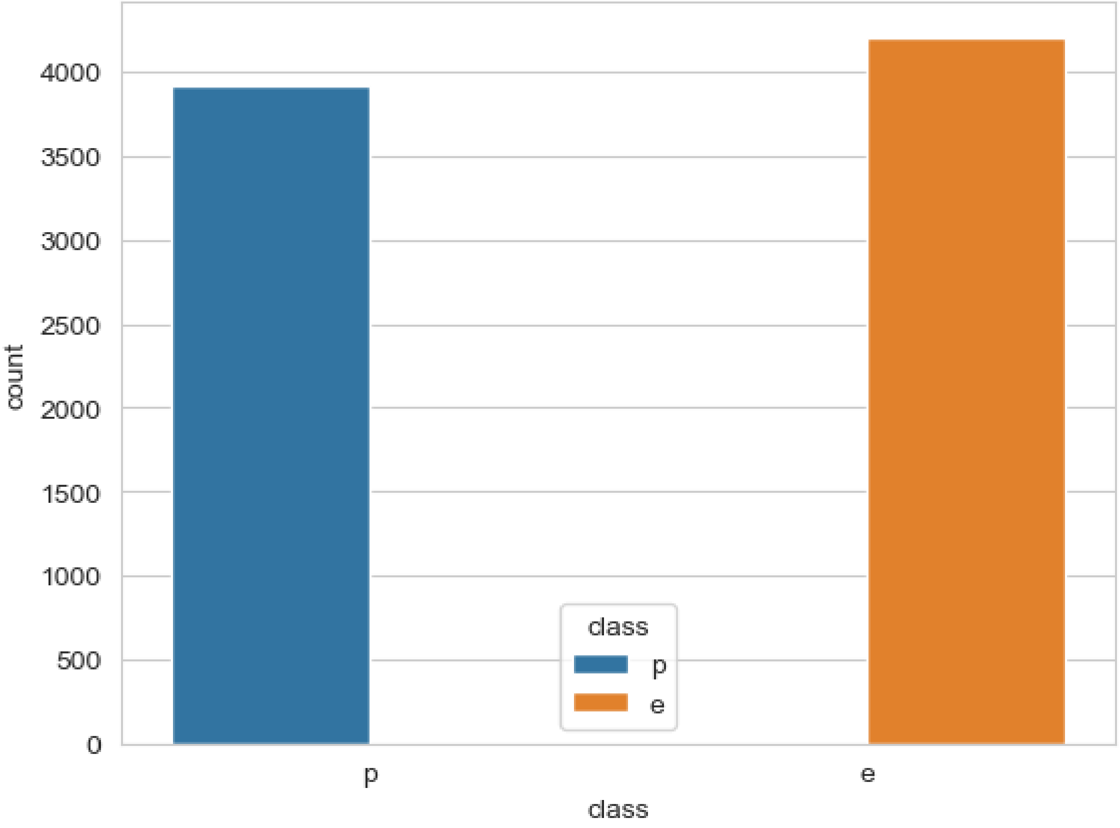
8124 rows × 22 columns

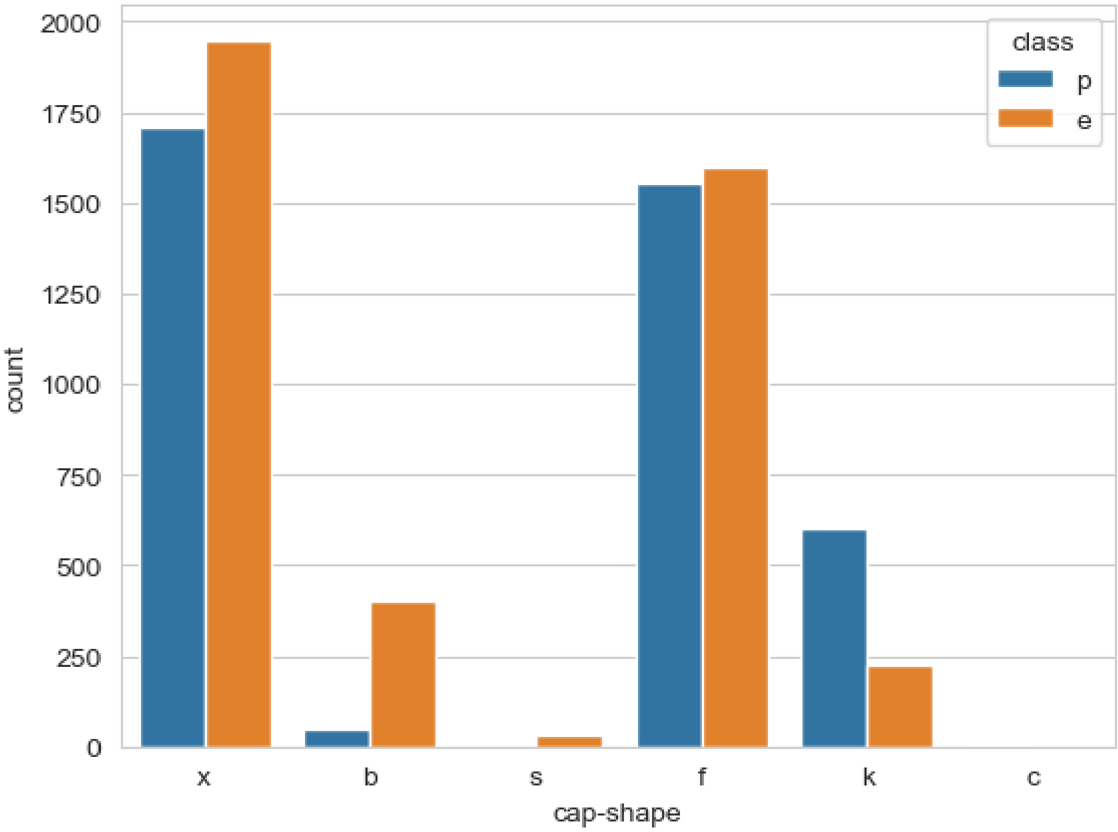
Generating countplot with each feature comparing with Class

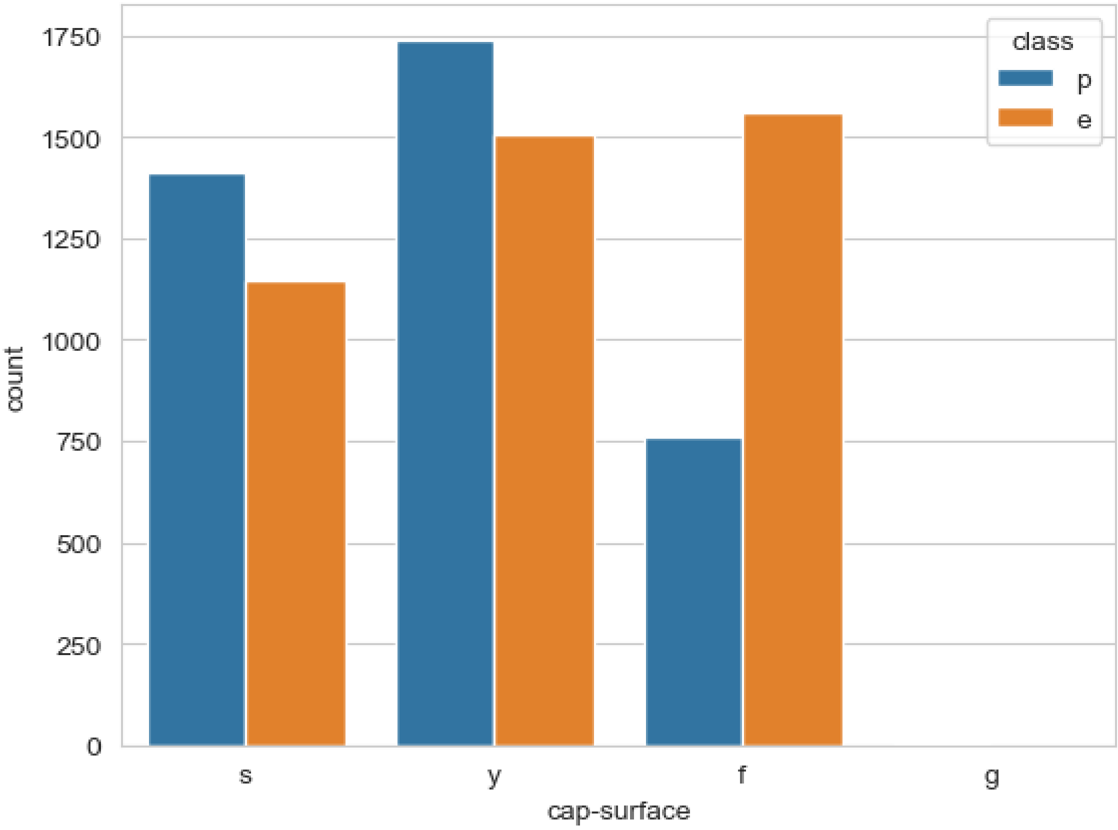
In [18]:

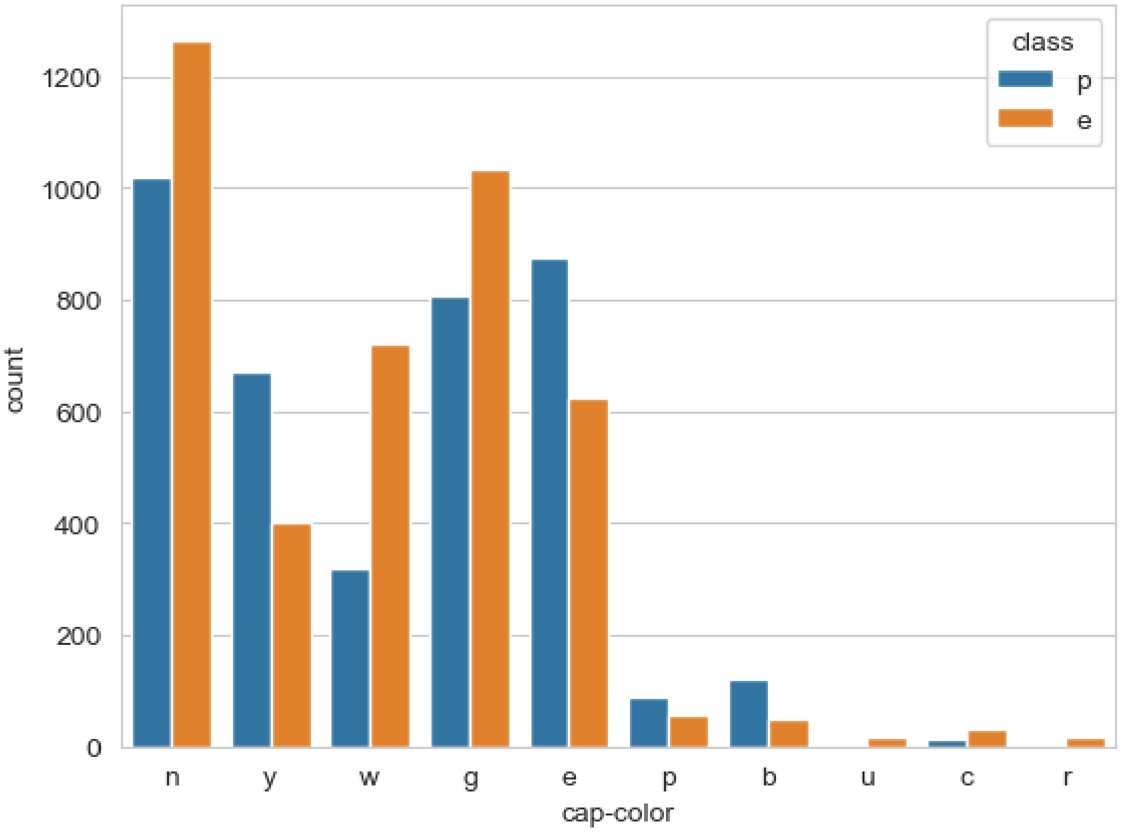
```
sns.set_style('whitegrid')
for i, col in enumerate(agri1.columns):
    pl.figure(i)
    sns_plot = sns.countplot(x=col, hue='class', data=agri)
    sns_plot.figure.savefig("{} countplot.png".format(col))
```

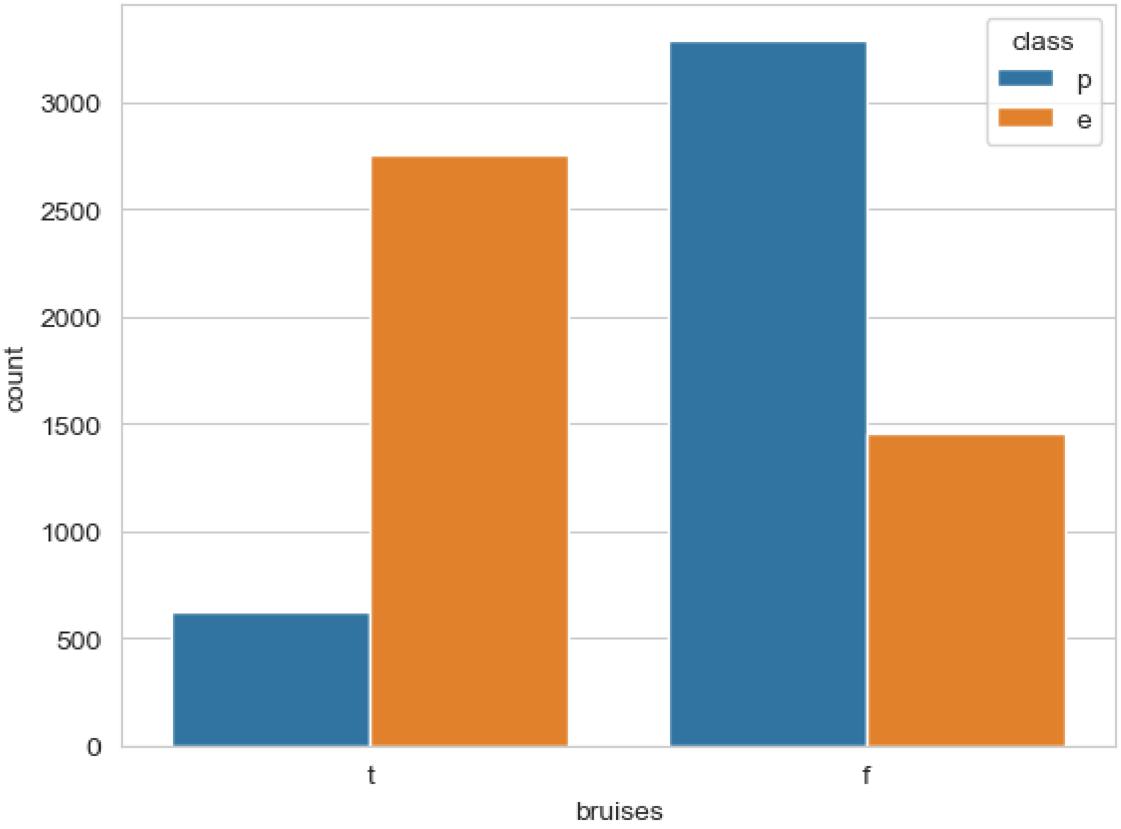
```
C:\Users\santh\AppData\Local\Temp\ipykernel_20332\2902536500.py:3: RuntimeWarnin
g: More than 20 figures have been opened. Figures created through the pyplot int
erface (`matplotlib.pyplot.figure`) are retained until explicitly closed and may
consume too much memory. (To control this warning, see the rcParam `figure.max_o
pen_warning`). Consider using `matplotlib.pyplot.close()`.
  pl.figure(i)
```

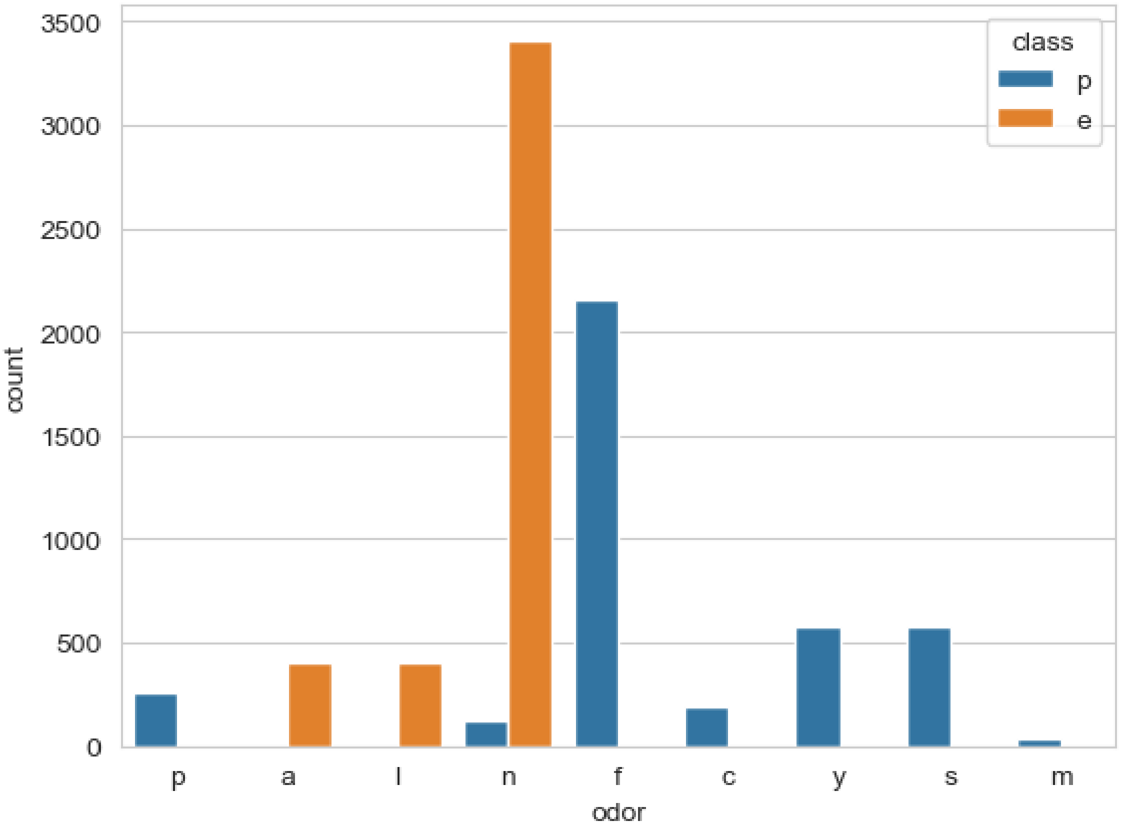


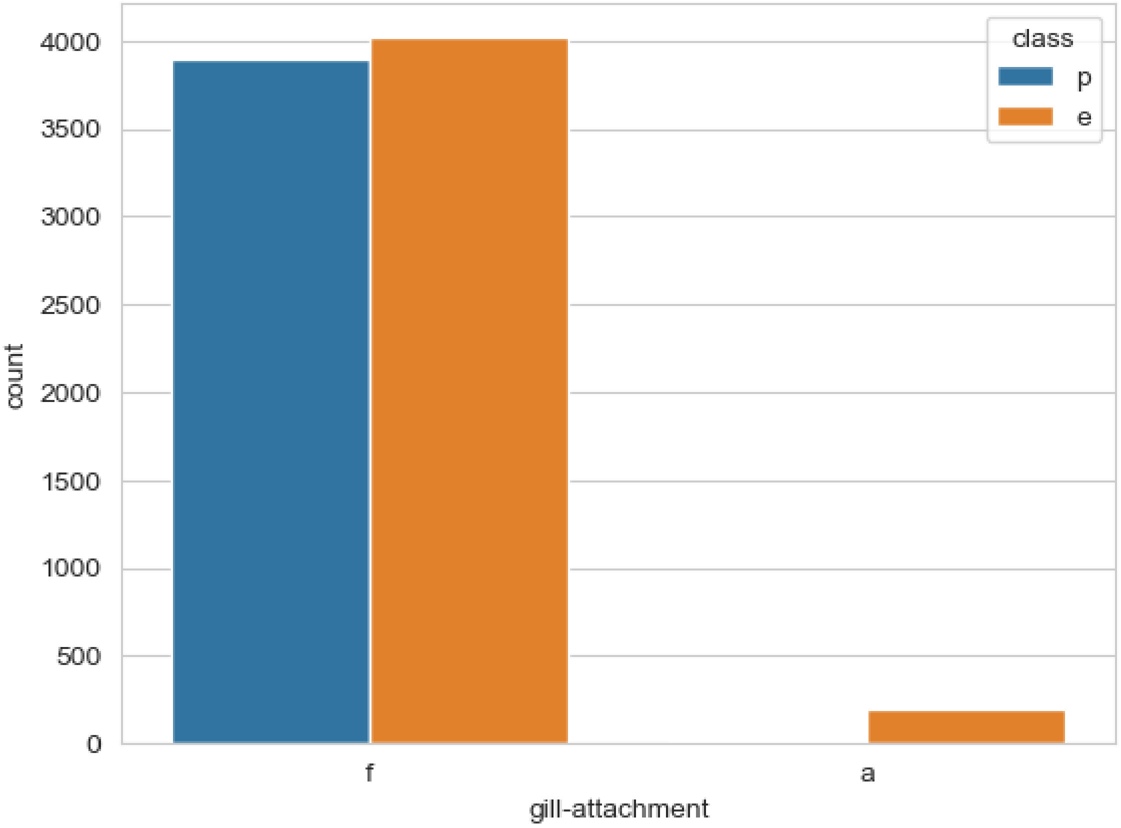

2000
1750
1500
1250
1000
750
500
250
0
count
x
b
s
f
k
c
cap-shape
class
p
e

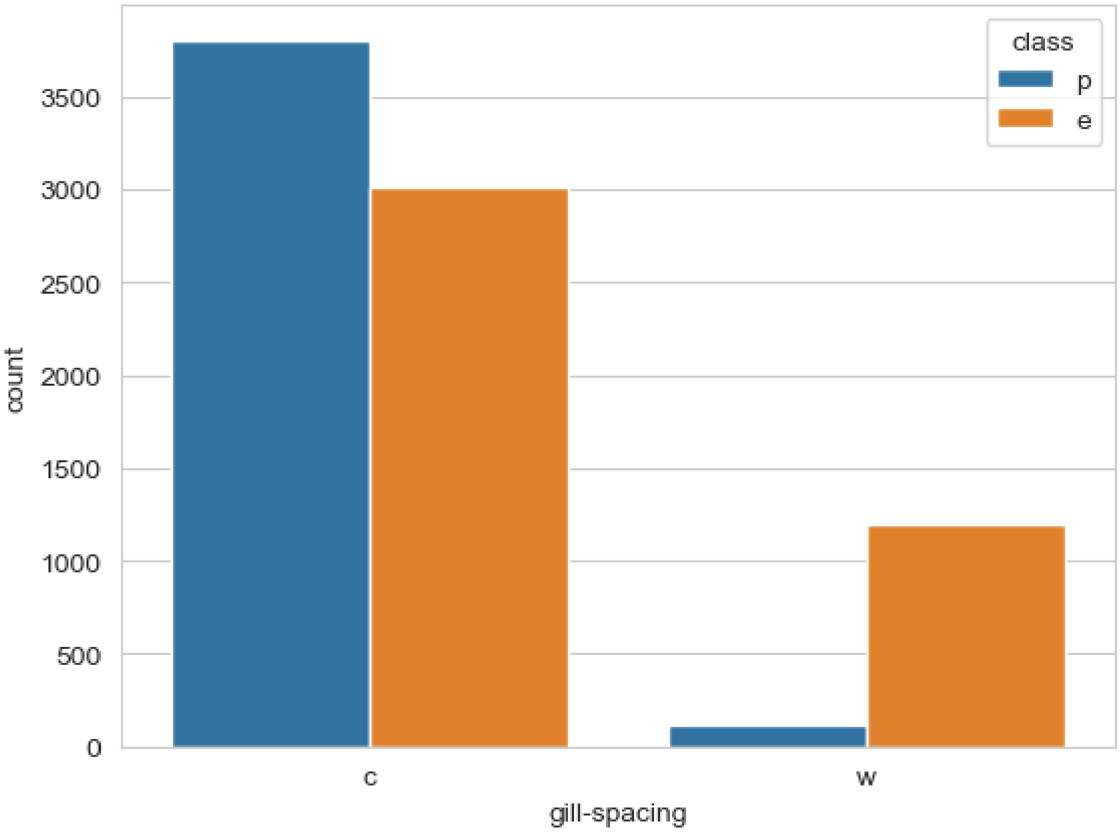

1750
1500
1250
1000
750
500
250
0
count
s
y
f
g
cap-surface
class
p
e

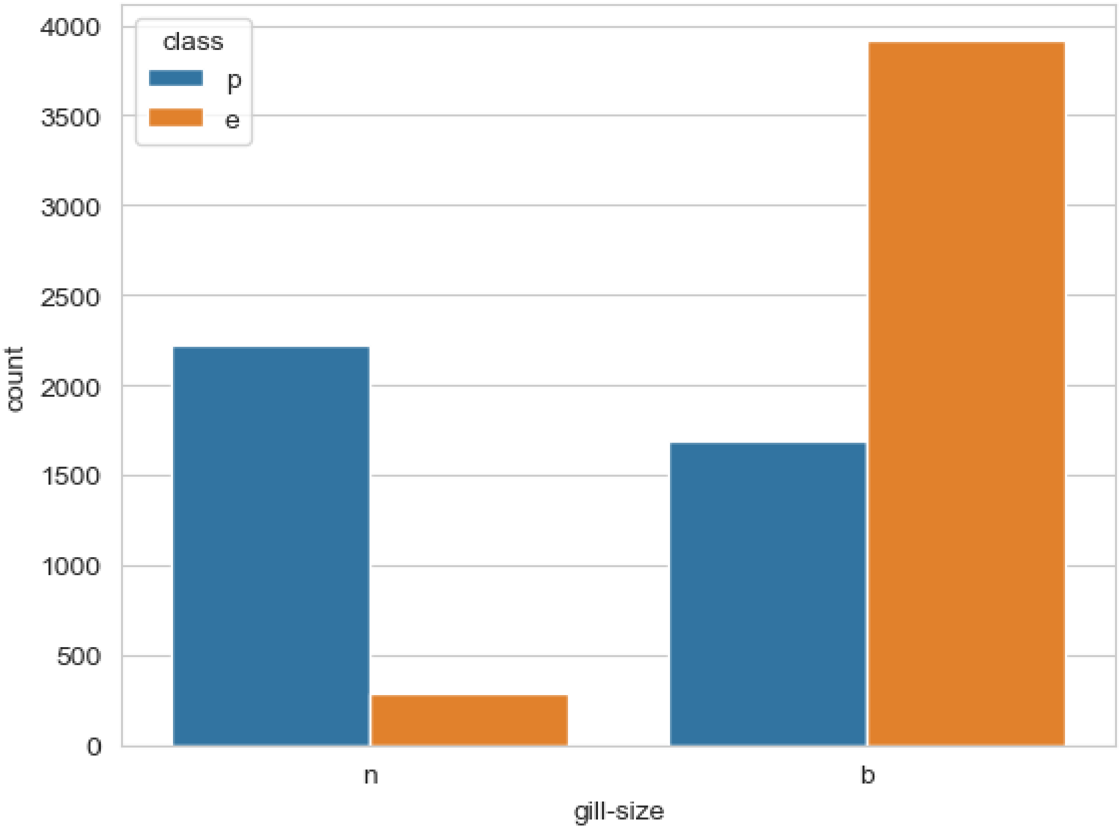

class
p
e
1200
1000
800
600
400
200
0
count
n
y
w
g
e
p
b
u
c
r
cap-color

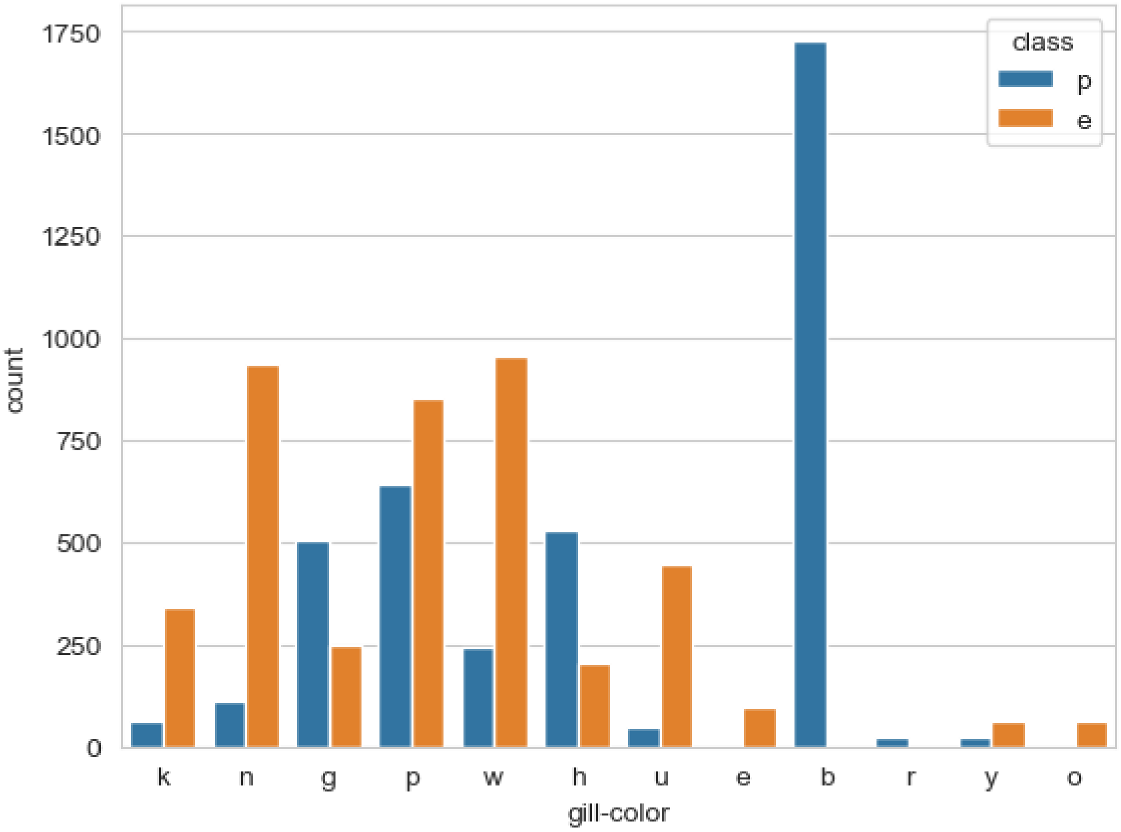

class
p
e
3000
2500
2000
1500
1000
500
0
count
t
f
bruises

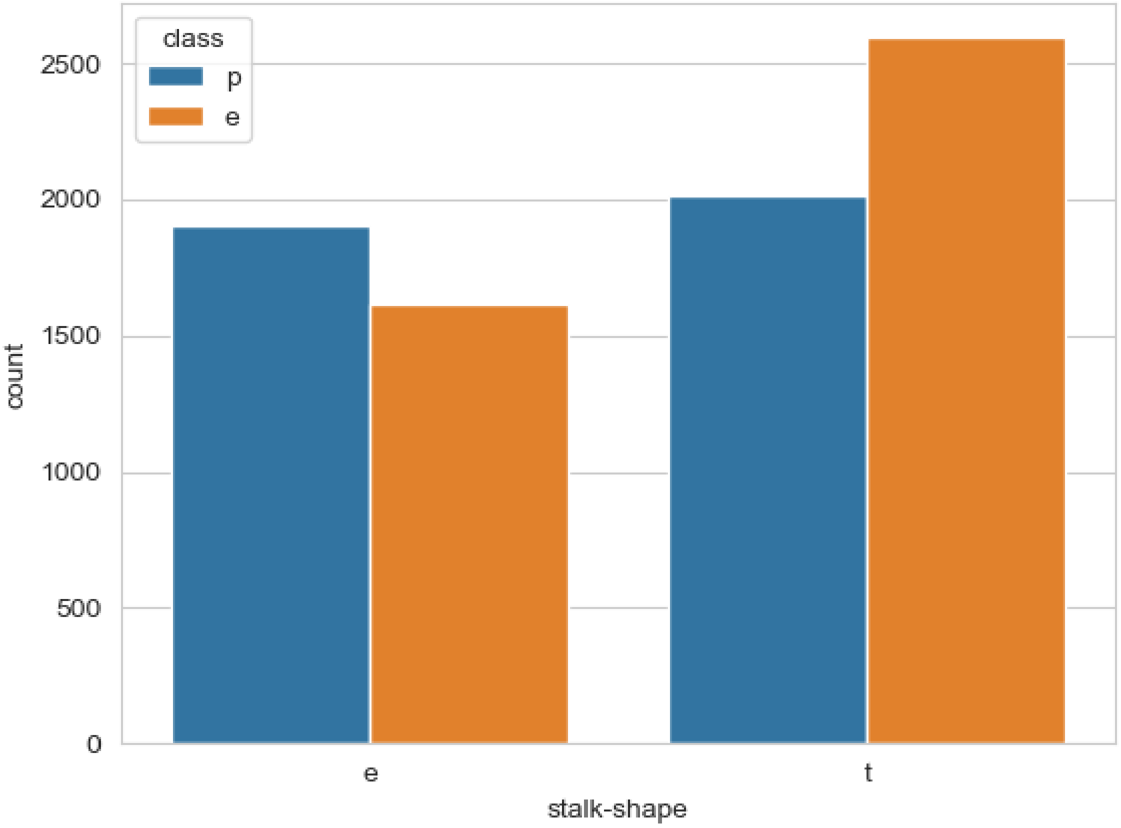

class
p
e
count
3500
3000
2500
2000
1500
1000
500
0
p
a
l
n
f
c
y
s
m
odor

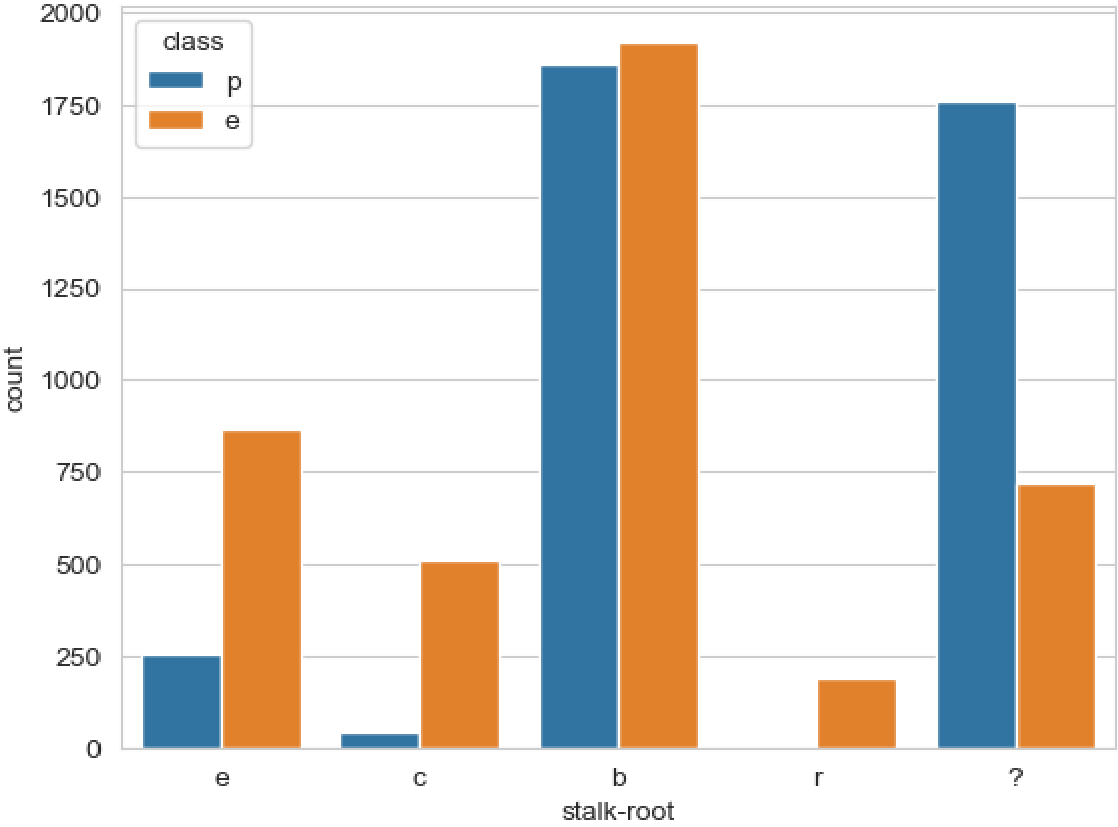

class
p
e
count
4000
3500
3000
2500
2000
1500
1000
500
0
f
a
gill-attachment

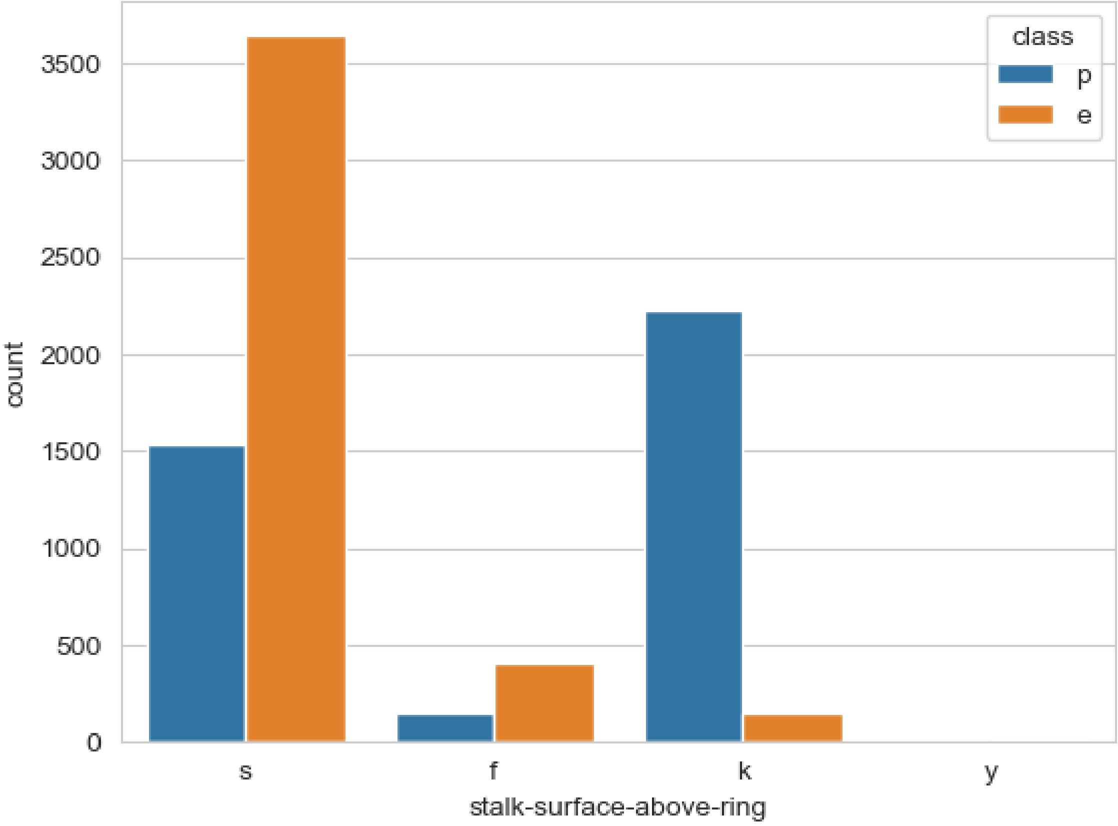

class
p
e
count
3500
3000
2500
2000
1500
1000
500
0
c
w
gill-spacing

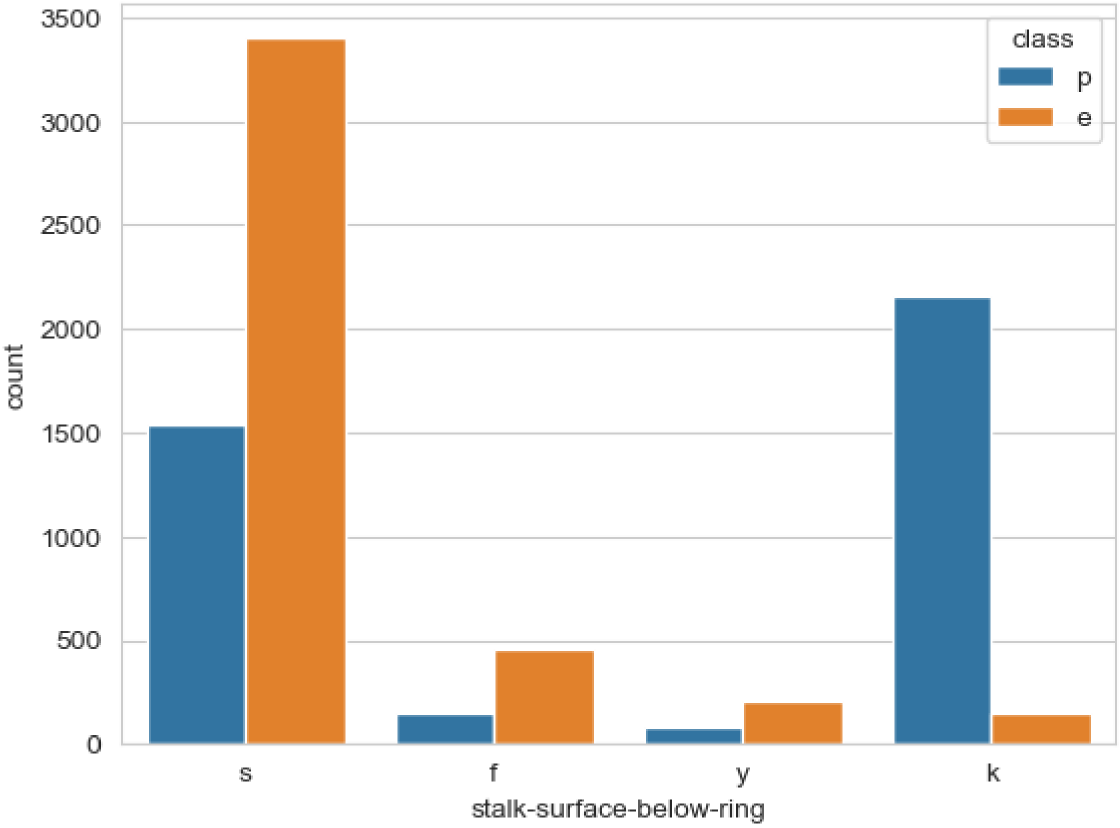

class
p
e
count
4000
3500
3000
2500
2000
1500
1000
500
0
n
b
gill-size

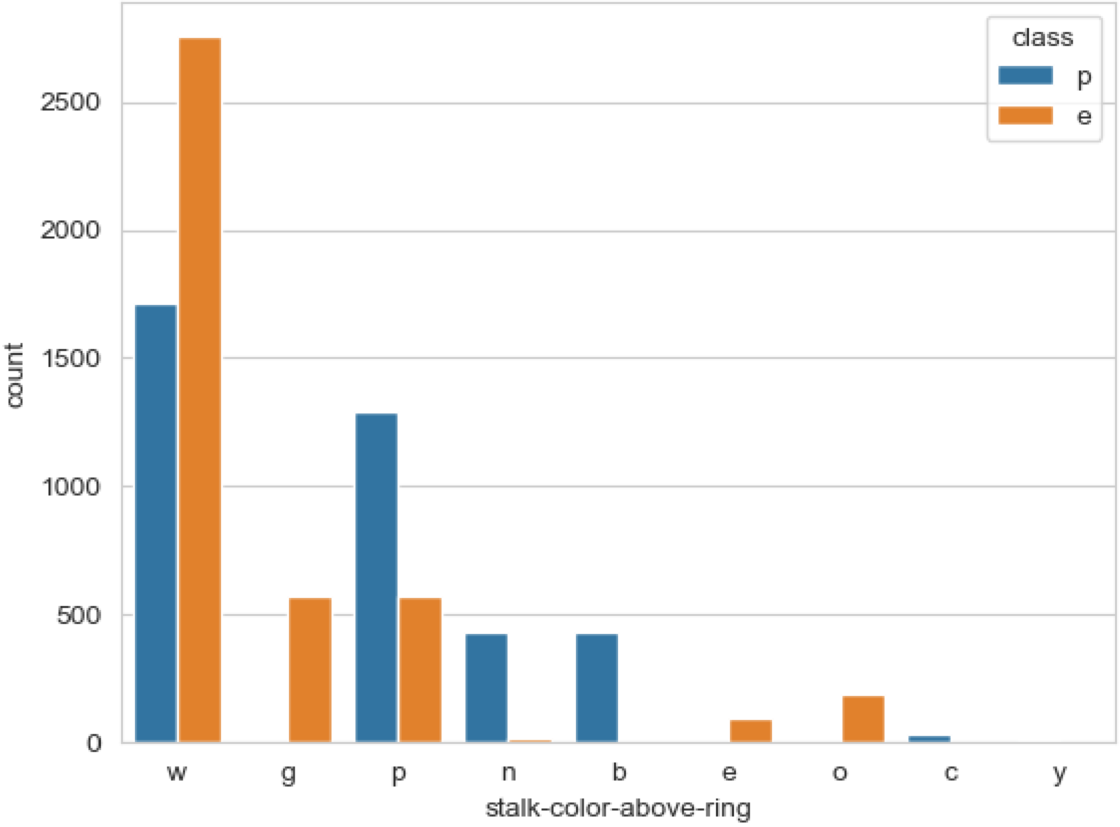

class
p
e
1750
1500
1250
1000
750
500
250
0
count
k
n
g
p
w
h
u
e
b
r
y
o
gill-color

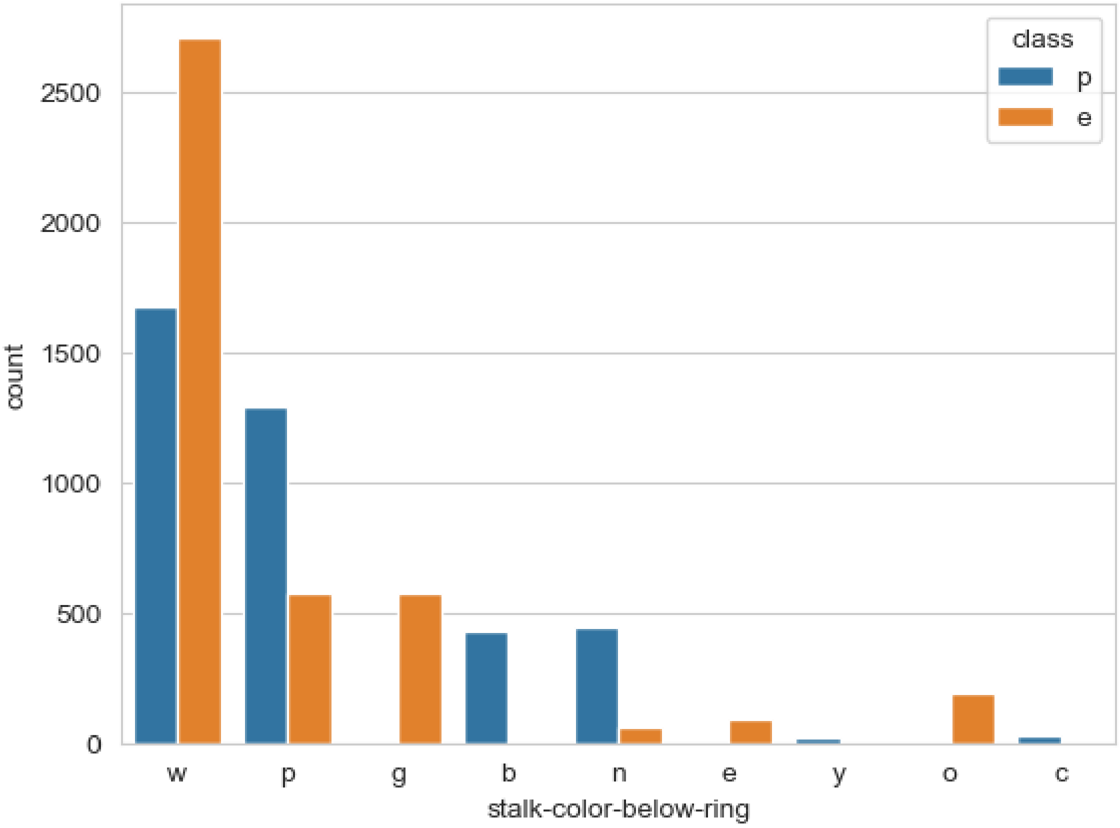

class
p
e
2500
2000
1500
1000
500
0
count
e
t
stalk-shape

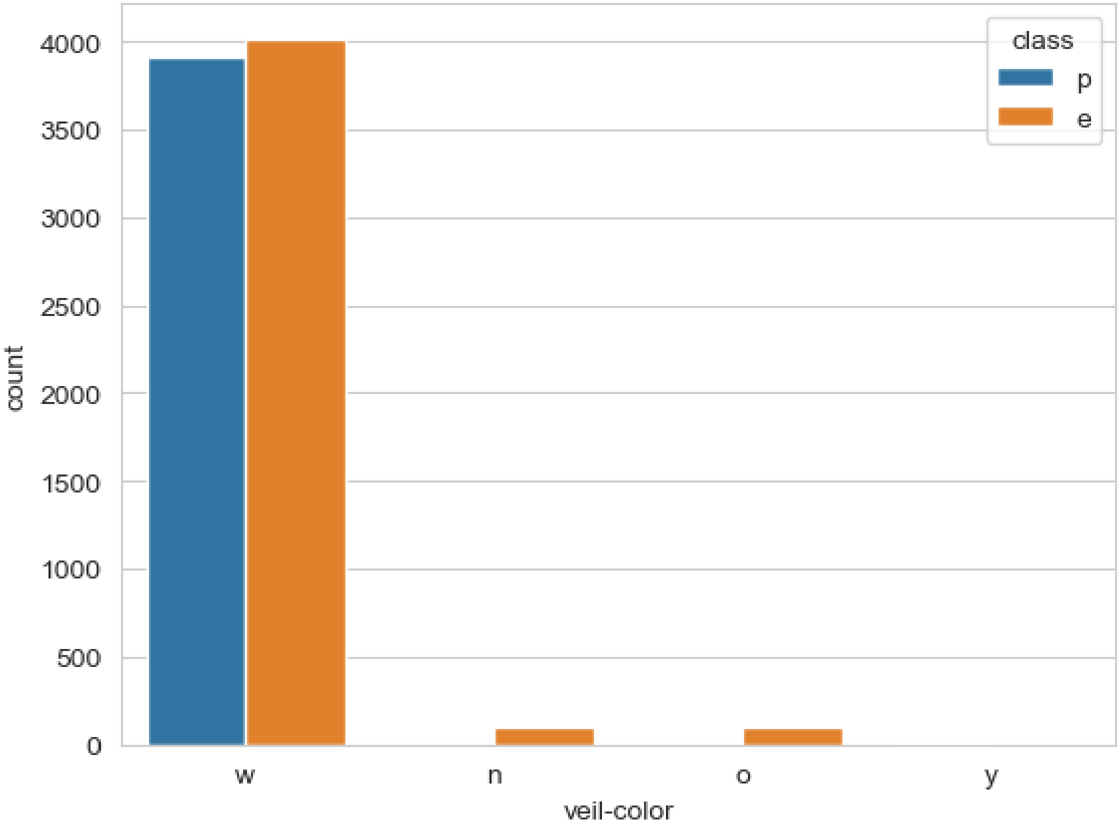

class
p
e
count
2000
1750
1500
1250
1000
750
500
250
0
e
c
b
r
?
stalk-root

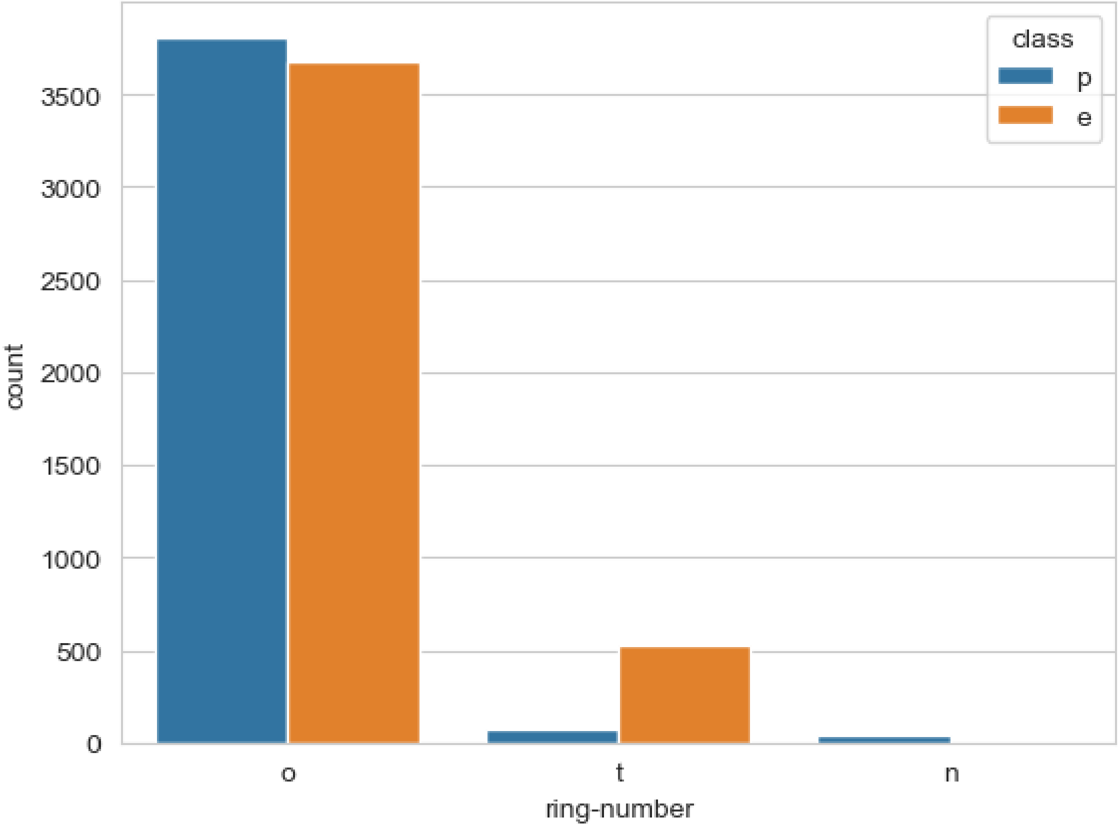

class
p
e
count
3500
3000
2500
2000
1500
1000
500
0
s
f
k
y
stalk-surface-above-ring

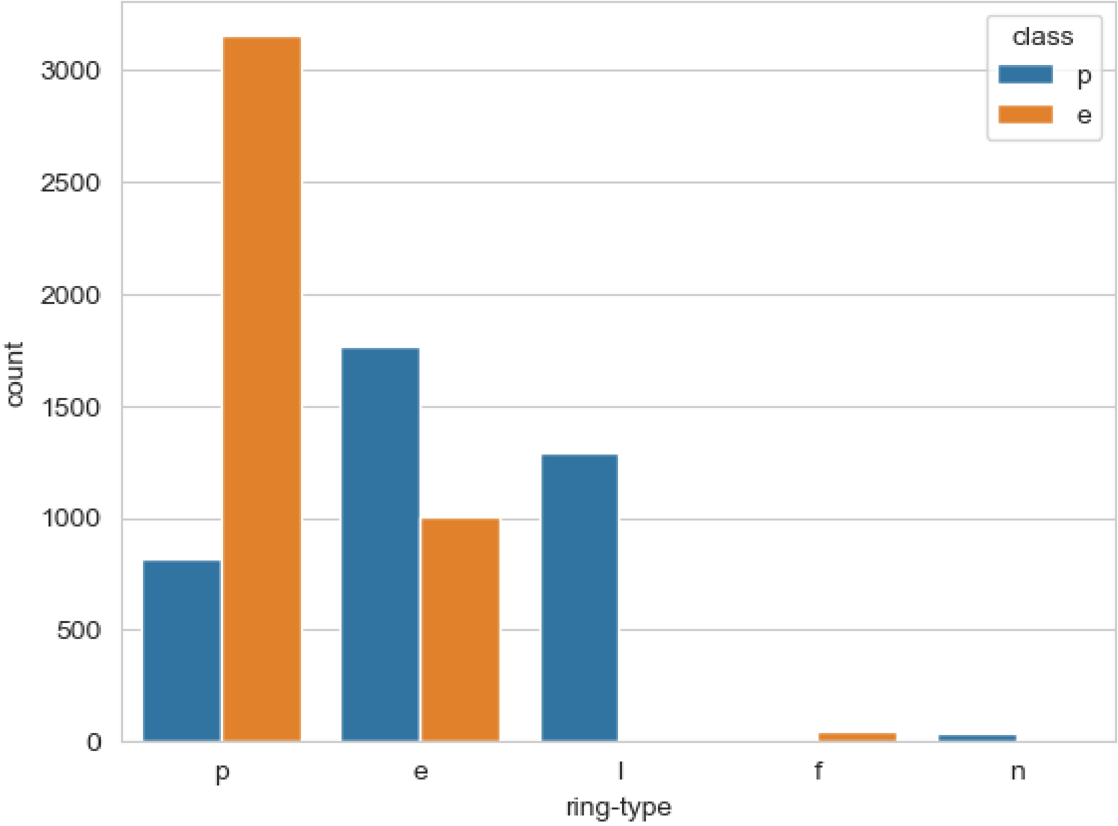

count
0
500
1000
1500
2000
2500
3000
3500
class
p
e
s
f
y
k
stalk-surface-below-ring

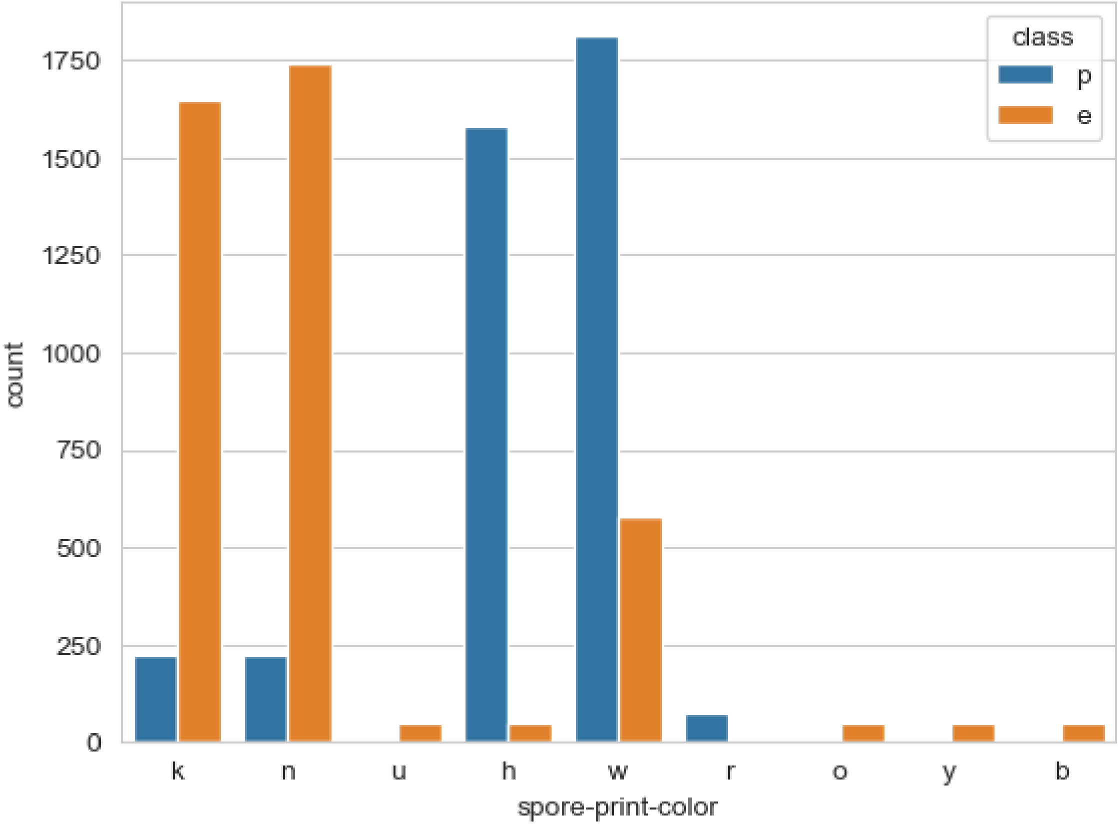

count
0
500
1000
1500
2000
2500
class
p
e
w
g
p
n
b
e
o
c
y
stalk-color-above-ring

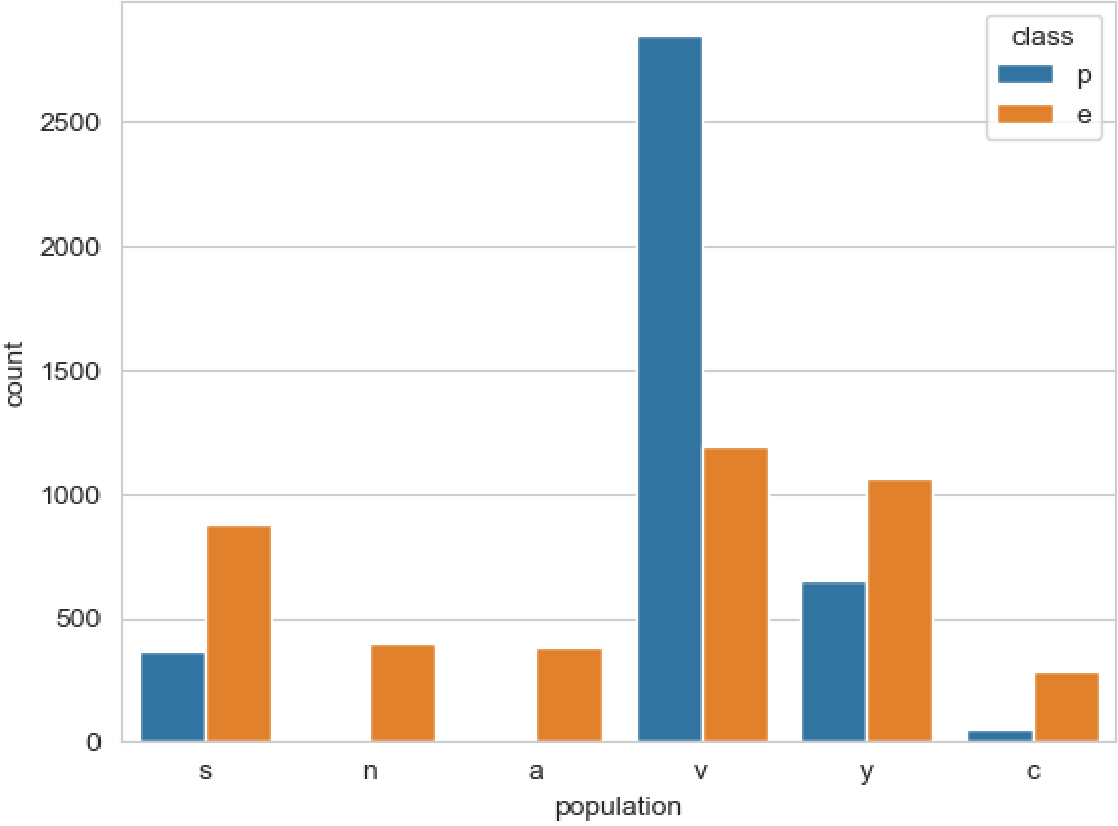

class
p
e
count
2500
2000
1500
1000
500
0
w
p
g
b
n
e
y
o
c
stalk-color-below-ring

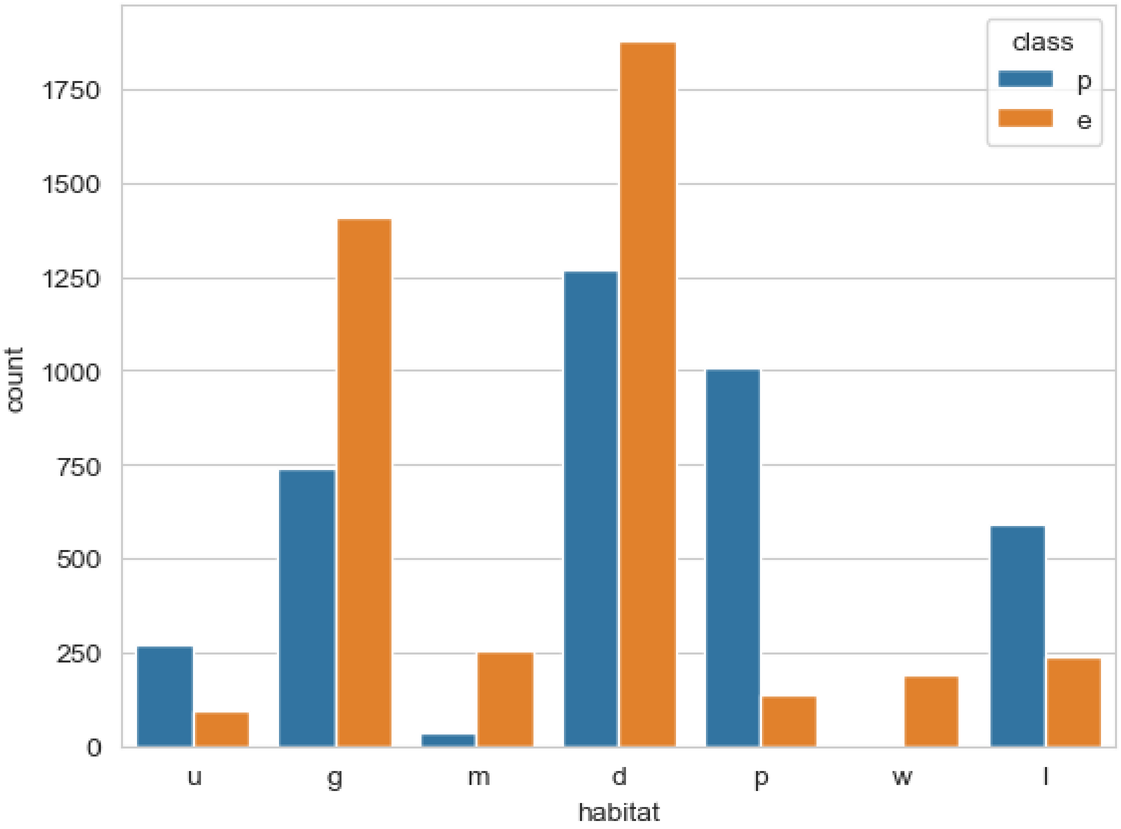

class
p
e
count
4000
3500
3000
2500
2000
1500
1000
500
0
w
n
o
y
veil-color


class
p
e
count
3500
3000
2500
2000
1500
1000
500
0
o
t
n
ring-number


class
p
e
count
3000
2500
2000
1500
1000
500
0
p
e
l
f
n
ring-type


class
p
e
count
1750
1500
1250
1000
750
500
250
0
k
n
u
h
w
r
o
y
b
spore-print-color


class
p
e
count
2500
2000
1500
1000
500
0
s
n
a
v
y
c
population


class
p
e
count
1750
1500
1250
1000
750
500
250
0
u
g
m
d
p
w
l
habitat