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Course:	CS 5402
Week03: Example:	1R Mushroom Example
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In [1]:
```
# Imported for data management (dataframes)
import pandas as pd

# This package needs part of anaconda and needs to be installed
#    conda install -c conda-forge wordcloud

# Imported to allow for the display of word clouds
import matplotlib.pyplot as plt

# Imported to create train/test partitioning of the data.
from sklearn.model_selection import train_test_split

# Imported to get frequency counts
import collections

# Imported to use confusion matrix.
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score
from sklearn.metrics import classification_report
```

Concept Description:

Train a system from existing data to classify mushrooms as either edible or inedible.

Data Collection:

The data has been provided by Perry B. Koob, not professor or doctor. It is a modified version of the UCI Mushroom data set found here: [https://archive.ics.uci.edu/ml/datasets/mushroom (https://archive.ics.uci.edu/ml/datasets/mushroom)](https://archive.ics.uci.edu/ml/datasets/mushroom)

Example Description:

Mushroom Diagram

edible.poisonous

This is the class label.

cap.shape

Nominal attribute that describes the cap shape of the mushroom as:

bell
conical
convex
flat
knobbed
sunken

cap.surface

Nominal attribute that describes the cap surface of the mushroom as:

fibrous
grooves
scaly
smooth

cap.color

Nominal attribute that describes the cap color of the mushroom as:

brown
buff
cinnamon
green
grey
pink
purple
red
white
yellow

bruises

Nominal attribute, boolean in nature, that describes if the mushroom has bruises.

odor

Nominal attribute that describes the odor of the mushroom as:

almond
anise
creosote
fishy
foul
musty
none
pungent
spicy

colony

Interval attribute that describes the approximate size of the mushroom colony:

edible

This is a binary class label generated from the edible.poisonous class label. It is a transformation of a nominal Class label, so it is also nominal.The labels are now edible or inedible.

There are no missing values.

Data Import and Wrangling:

The results of each search is read from the respective comma separated value file (csv) into separate dataframes. Careful attention is paid to make sure the data is read in as character strings.

In [2]:
```
df = pd.read_csv("../src-data/mushroom.csv", dtype=str)
```

In [3]:
```
df.columns
```

Out[3]:
```
Index(['edible-poisonous', 'cap-shape', 'cap-surface', 'cap-color', 'bruise
s',
       'odor', 'colony'],
      dtype='object')
```

In [4]:
```
df.loc[(df['edible-poisonous'] == 'edible'),'edible'] = 'edible'
df.loc[(df['edible-poisonous'] == 'poisonous'),'edible'] = 'inedible'
```

In [5]:
```
df.columns
```

Out[5]:
```
Index(['edible-poisonous', 'cap-shape', 'cap-surface', 'cap-color', 'bruise
s',
       'odor', 'colony', 'edible'],
      dtype='object')
```

Partition the data into a training set and a test set using a 80/20 split.

In [6]:
```
X = df.drop(columns=['edible','edible-poisonous'])
Y = df[['edible']]
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, train_size = 0.80,ra
ndom_state=123)
```

In [7]:
```
Y
```

Out[7]:

	edible
0	inedible
1	edible
2	edible
3	inedible
4	edible
...	...
8119	inedible
8120	edible
8121	inedible
8122	edible
8123	edible

8124 rows × 1 columns

Exploratory Data Analysis:

Looking into what type of measure the attributes are.

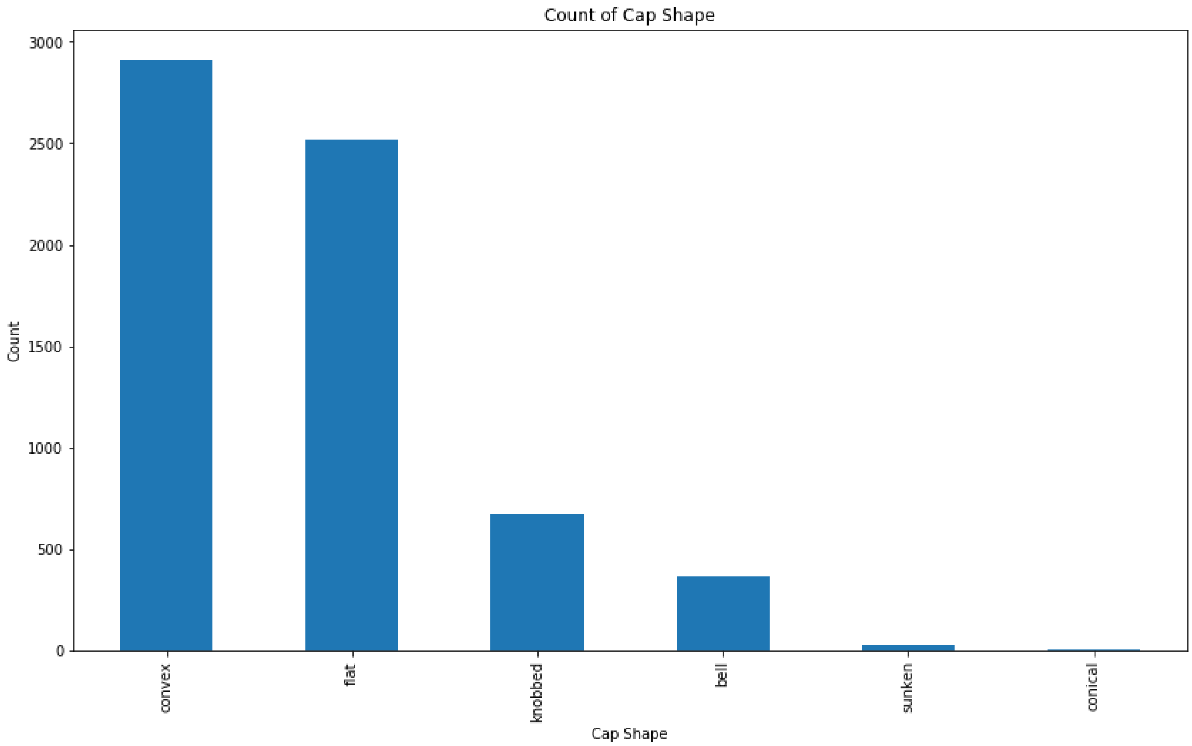
In [8]:
```
df.describe()
```

Out[8]:

	edible-poisonous	cap-shape	cap-surface	cap-color	bruises	odor	colony	edible
count	8124	8124	8124	8124	8124	8124	8124	8124
unique	2	6	4	10	2	9	410	2
top	edible	convex	scaly	brown	no	none	1	edible
freq	4208	3656	3244	2284	4748	3528	3768	4208

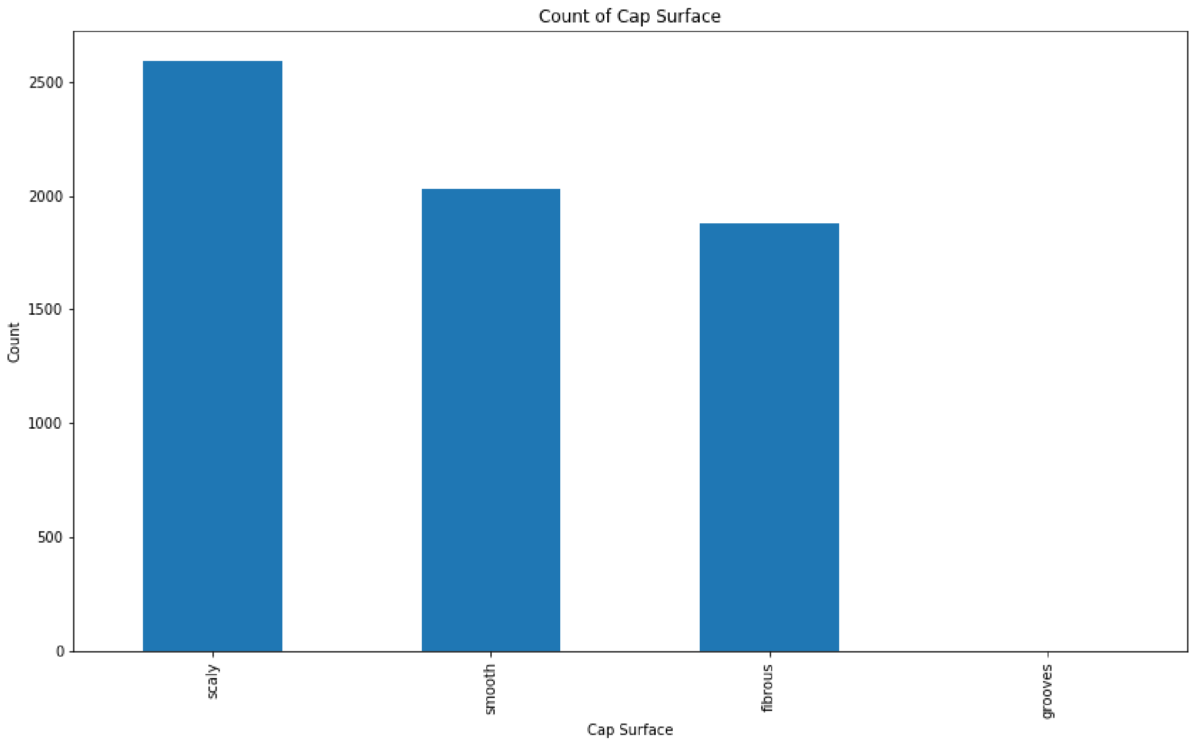
In [9]:
```
#Cap Shape
plot = X_train['cap-shape'].value_counts().plot(kind='bar',
                                   figsize=(14,8),
                                   title="Count of Cap Shape")
plot.set_xlabel("Cap Shape")
plot.set_ylabel("Count")
```

Out[9]:
```
Text(0, 0.5, 'Count')
```



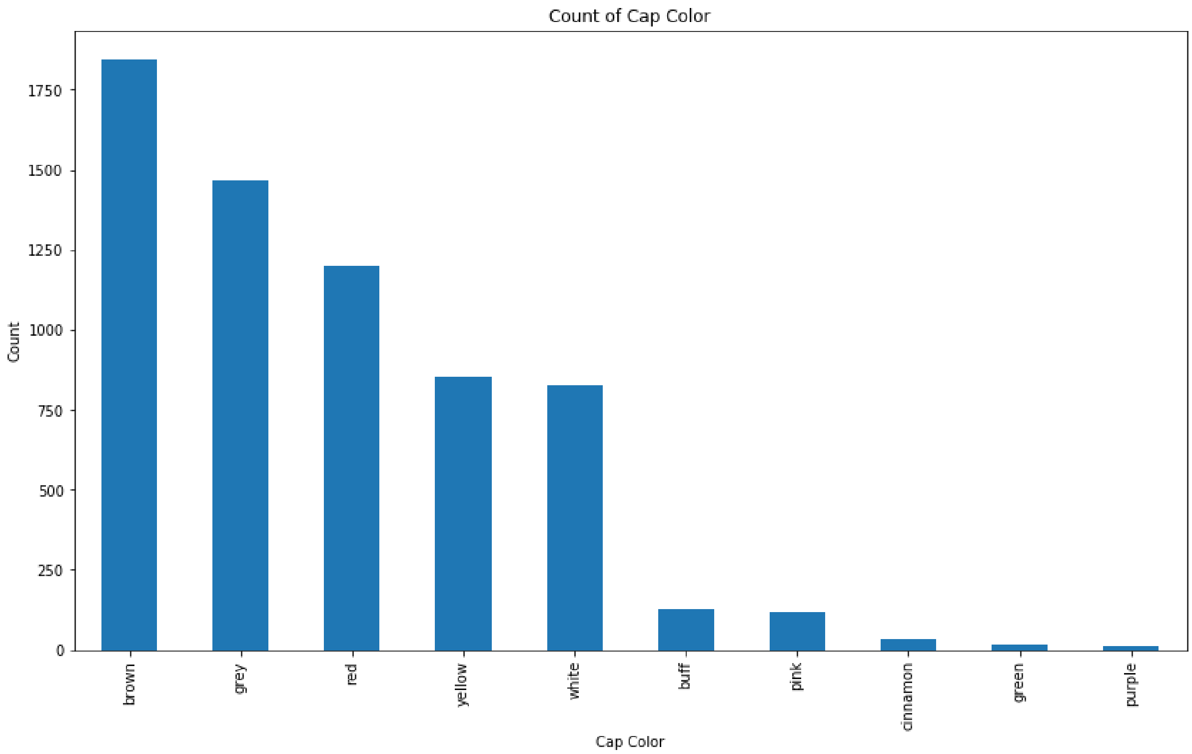
In [10]:
```
#Cap Surface
plot = X_train['cap-surface'].value_counts().plot(kind='bar',
                                                   figsize=(14,8),
                                                   title="Count of Cap Surface")
plot.set_xlabel("Cap Surface")
plot.set_ylabel("Count")
```

Out[10]:
```
Text(0, 0.5, 'Count')
```



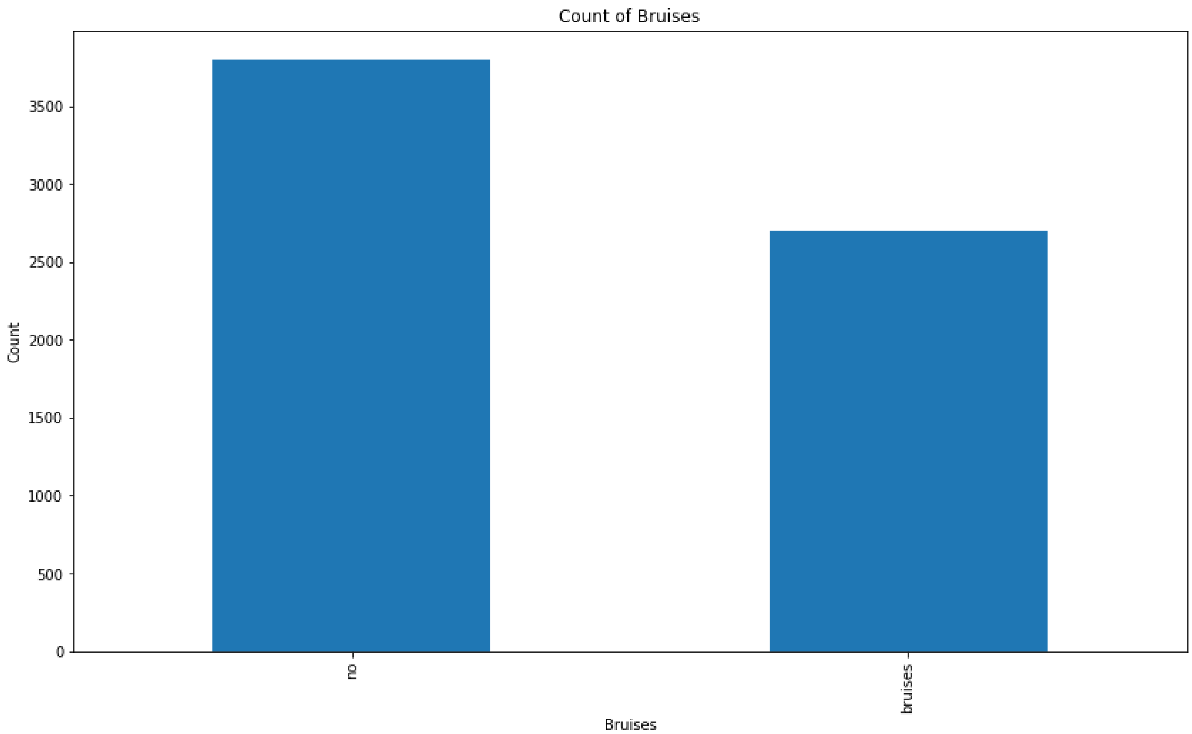
In [11]:
```
#Cap Color
plot = X_train['cap-color'].value_counts().plot(kind='bar',
                                                figsize=(14,8),
                                                title="Count of Cap Color")
plot.set_xlabel("Cap Color")
plot.set_ylabel("Count")
```

Out[11]:
```
Text(0, 0.5, 'Count')
```



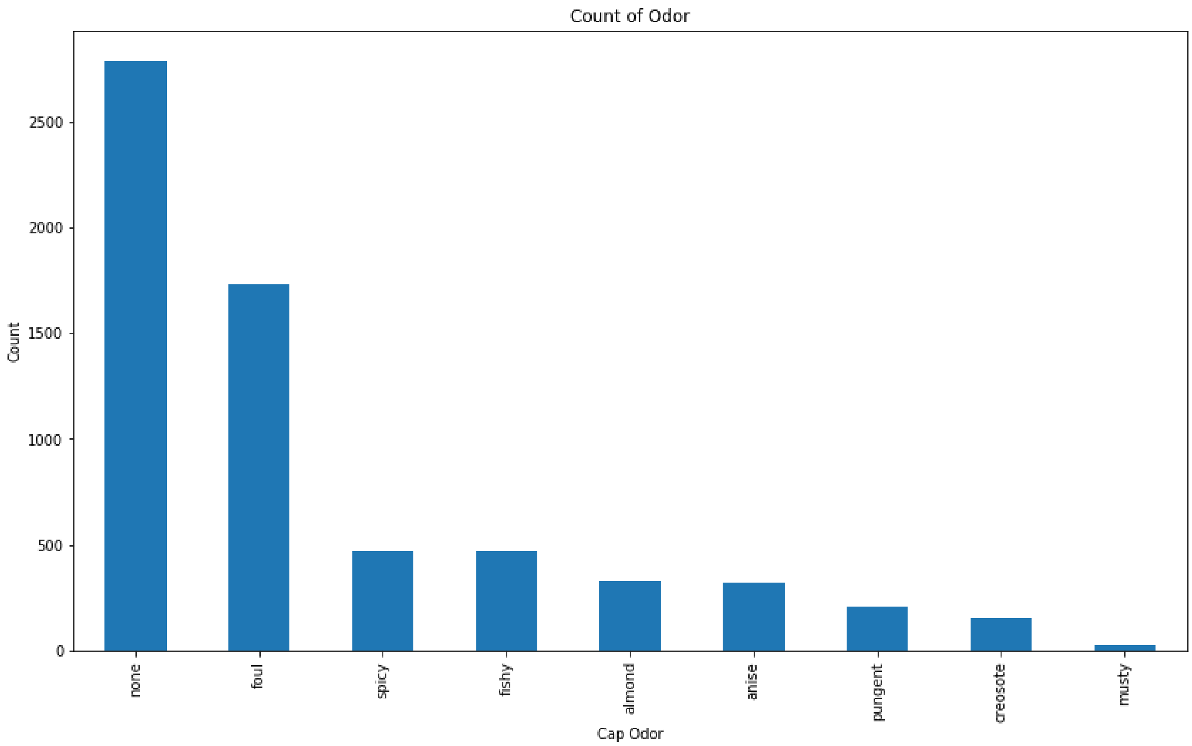
In [12]:
```
#Bruises
plot = X_train['bruises'].value_counts().plot(kind='bar',
                                    figsize=(14,8),
                                    title="Count of Bruises")
plot.set_xlabel("Bruises")
plot.set_ylabel("Count")
```

Out[12]: Text(0, 0.5, 'Count')



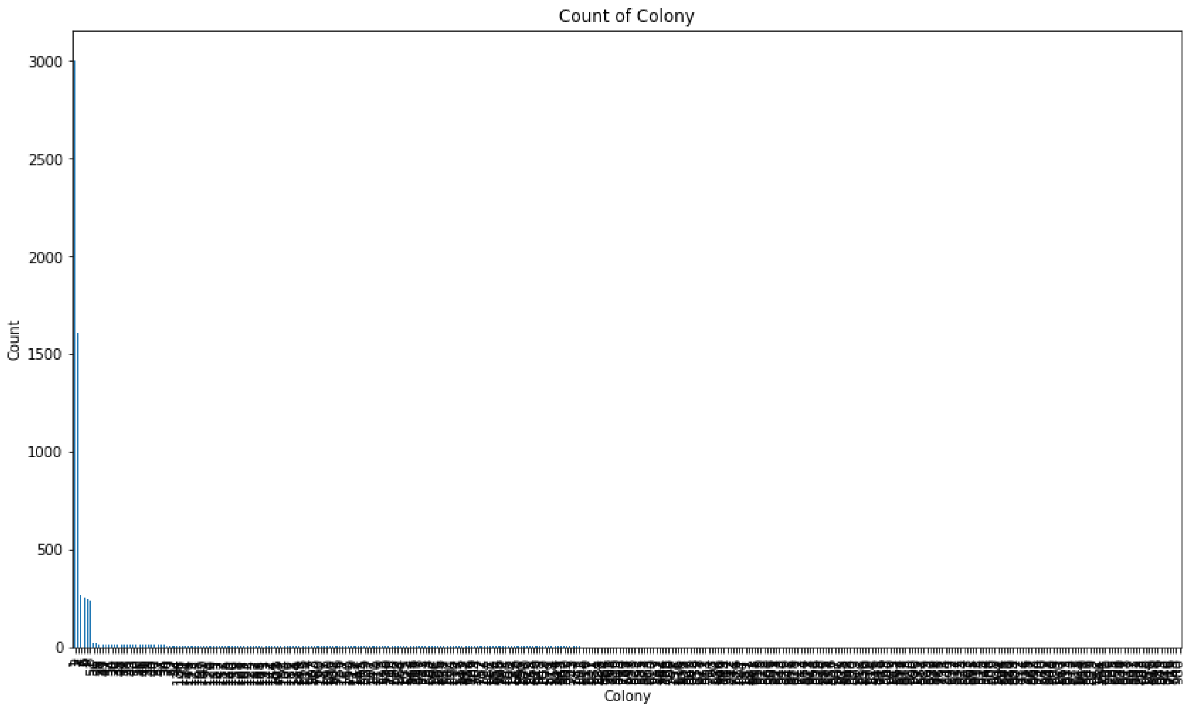
In [13]:
```
#Cap Shape
plot = X_train['odor'].value_counts().plot(kind='bar',
                                            figsize=(14,8),
                                            title="Count of Odor")
plot.set_xlabel("Cap Odor")
plot.set_ylabel("Count")
```

Out[13]: `Text(0, 0.5, 'Count')`



In [14]:
```
#Colony
plot = X_train['colony'].value_counts().plot(kind='bar',
                                    figsize=(14,8),
                                    title="Count of Colony")
plot.set_xlabel("Colony")
plot.set_ylabel("Count")
```

Out[14]: `Text(0, 0.5, 'Count')`



In [15]:
```
X_train['colony'].describe()
```

Out[15]:
```
count     6499
unique     360
top          1
freq      3007
Name: colony, dtype: object
```

In [16]:
```
X_train['colony'] = X_train['colony'].astype('int')
X_train.loc[(X_train['colony'] <=2 ),'dcolony'] = 'single'
X_train.loc[(X_train['colony'] > 2 ),'dcolony'] = 'colony'
X_train = X_train.drop(columns=['colony'])

X_test['colony'] = X_test['colony'].astype('int')
X_test.loc[(X_test['colony'] <=2 ),'dcolony'] = 'single'
X_test.loc[(X_test['colony'] >2 ),'dcolony'] = 'colony'
X_test = X_test.drop(columns=['colony'])
```

```
C:\ProgramData\Anaconda3\lib\site-packages\ipykernel_launcher.py:1: SettingWi
thCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/st
able/user_guide/indexing.html#returning-a-view-versus-a-copy
  """Entry point for launching an IPython kernel.
C:\ProgramData\Anaconda3\lib\site-packages\pandas\core\indexing.py:376: Setti
ngWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/st
able/user_guide/indexing.html#returning-a-view-versus-a-copy
  self.obj[key] = _infer_fill_value(value)
C:\ProgramData\Anaconda3\lib\site-packages\pandas\core\indexing.py:494: Setti
ngWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/st
able/user_guide/indexing.html#returning-a-view-versus-a-copy
  self.obj[item] = s
C:\ProgramData\Anaconda3\lib\site-packages\ipykernel_launcher.py:6: SettingWi
thCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/st
able/user_guide/indexing.html#returning-a-view-versus-a-copy
```

Mining or Analytics:

Using two way tables to get frequency of attribute per class.

In [17]:
```
cap_shape = pd.crosstab(index=X_train["cap-shape"],columns=Y_train["edible"],m
argins=True)
cap_shape
```

Out[17]:

edible	edible	inedible	All
cap-shape			
bell	329	37	366
conical	0	4	4
convex	1534	1381	2915
flat	1287	1233	2520
knobbed	177	494	671
sunken	23	0	23
All	3350	3149	6499

Base on the frequency of edible and inedible, we would generate the following rule set for the Cap Shape attribute:

bell -> Edible
conical -> Inedible
convex -> Edible
flat -> Edible
knobbed -> Inedible
sunken -> Edible

Now we determine the error rate of the Cap Shape rules.

In [18]:
```
errors = 0
errors += cap_shape.loc['bell','inedible']
errors += cap_shape.loc['conical','edible']
errors += cap_shape.loc['convex','inedible']
errors += cap_shape.loc['flat','inedible']
errors += cap_shape.loc['knobbed','edible']
errors += cap_shape.loc['sunken','inedible']

error_rate = errors/cap_shape.loc['All','All']
error_rate
```

Out[18]: 0.43514386828742885

In [19]:
```
cap_surface = pd.crosstab(index=X_train["cap-surface"],columns=Y_train["edible"],margins=True)
cap_surface
```

Out[19]:

edible	edible	inedible	All
cap-surface			
fibrous	1264	612	1876
grooves	0	2	2
scaly	1196	1397	2593
smooth	890	1138	2028
All	3350	3149	6499

Base on the frequency of edible and inedible, we would generate the following rule set for the Cap Surface attribute:

fibrous -> Edible
grooves -> Inedible
scaly -> Inedible
smooth -> Inedible

Now we determine the error rate of the Cap Surface rules.

In [20]:
```
errors = 0
errors += cap_surface.loc['fibrous','inedible']
errors += cap_surface.loc['grooves','edible']
errors += cap_surface.loc['scaly','edible']
errors += cap_surface.loc['smooth','edible']

error_rate = errors/cap_surface.loc['All','All']
error_rate
```

Out[20]: 0.4151407908909063

In [21]:
```
cap_color = pd.crosstab(index=X_train["cap-color"],columns=Y_train["edible"],margins=True)
cap_color
```

Out[21]:

edible	edible	inedible	All
cap-color			
brown	1024	820	1844
buff	35	92	127
cinnamon	23	10	33
green	15	0	15
grey	824	645	1469
pink	49	70	119
purple	12	0	12
red	482	720	1202
white	562	262	824
yellow	324	530	854
All	3350	3149	6499

Base on the frequency of edible and inedible, we would generate the following rule set for the Cap Color attribute:

brown -> Edible
buff -> Inedible
cinnamon -> Edible
green -> Edible
grey -> Edible
pink -> Inedible
purple -> Edible
red -> Inedible
white -> Edible
yellow -> Inedible

Now we determine the error rate of the Cap Color rules.

In [22]:
```
errors = 0
errors += cap_color.loc['brown','inedible']
errors += cap_color.loc['buff','edible']
errors += cap_color.loc['cinnamon','inedible']
errors += cap_color.loc['green','inedible']
errors += cap_color.loc['grey','inedible']
errors += cap_color.loc['pink','edible']
errors += cap_color.loc['purple','inedible']
errors += cap_color.loc['red','edible']
errors += cap_color.loc['white','inedible']
errors += cap_color.loc['yellow','edible']


error_rate = errors/cap_color.loc['All','All']
error_rate
```

Out[22]: 0.40421603323588245

In [23]:
```
bruises= pd.crosstab(index=X_train["bruises"],columns=Y_train["edible"],margin
s=True)
bruises
```

Out[23]:

edible bruises	edible	inedible	All
bruises	2206	497	2703
no	1144	2652	3796
All	3350	3149	6499

Base on the frequency of edible and inedible, we would generate the following rule set for the Cap Color attribute:

bruises -> Edible
no -> Inedible

Now we determine the error rate of the Bruises rules.

In [24]:
```
errors = 0
errors += bruises.loc['bruises','inedible']
errors += bruises.loc['no','edible']


error_rate = errors/bruises.loc['All','All']
error_rate
```

Out[24]: 0.2525003846745653

In [25]:
```
odor = pd.crosstab(index=X_train["odor"],columns=Y_train["edible"],margins=True)
odor
```

Out[25]:

edible	edible	inedible	All
odor			
almond	329	0	329
anise	324	0	324
creosote	0	153	153
fishy	0	470	470
foul	0	1729	1729
musty	0	25	25
none	2697	93	2790
pungent	0	209	209
spicy	0	470	470
All	3350	3149	6499

Base on the frequency of edible and inedible, we would generate the following rule set for the Odor attribute:

almond -> edible
anise -> edible
creosote -> inedible
fishy -> inedible
foul -> inedible
musty -> inedible
none -> edible
pungent -> inedible
spicy -> inedible

Now we determine the error rate of the Odor rules.

In [26]:
```
errors = 0
errors += odor.loc['almond','inedible']
errors += odor.loc['anise','inedible']
errors += odor.loc['creosote','edible']
errors += odor.loc['fishy','edible']
errors += odor.loc['foul','edible']
errors += odor.loc['musty','edible']
errors += odor.loc['none','inedible']
errors += odor.loc['pungent','edible']
errors += odor.loc['spicy','edible']


error_rate = errors/odor.loc['All','All']
error_rate
```

Out[26]: 0.014309893829819972

In [27]:
```
dcolony = pd.crosstab(index=X_train["dcolony"],columns=Y_train["edible"],margi
ns=True)
dcolony
```

Out[27]:

edible	edible	inedible	All
dcolony			
colony	1553	332	1885
single	1797	2817	4614
All	3350	3149	6499

Base on the frequency of edible and inedible, we would generate the following rule set for the Discretized Colony attribute:

colony -> edible single -> inedible

Now we determine the error rate of the Colony rules.

In [28]:
```
errors = 0
errors += dcolony.loc['colony','inedible']
errors += dcolony.loc['single','edible']

error_rate = errors/dcolony.loc['All','All']
error_rate
```

Out[28]: 0.3275888598245884

The Rule Set with the best error rate is the Odor Rules Set, which has an error rate of 0.0143.

So we choose the the Odor Rules Set as out One Rule.

Evaluation:

After selecting the Odor Rules Set we want to evalues the model with our test data set to see if our model could be generalizable.

almond -> edible
anise -> edible
creosote -> inedible
fishy -> inedible
foul -> inedible
musty -> inedible
none -> edible
pungent -> inedible
spicy -> inedible

In [29]:
```
# Determine predicted values
prediction = pd.DataFrame(X_test['odor'])
prediction = prediction.rename(columns={'odor': 'prediction'})

prediction[prediction['prediction'] ==  'almond'] = 'edible'
prediction[prediction['prediction'] ==  'anise'] = 'edible'
prediction[prediction['prediction'] ==  'creosote'] = 'inedible'
prediction[prediction['prediction'] ==  'fishy'] = 'inedible'
prediction[prediction['prediction'] ==  'foul'] = 'inedible'
prediction[prediction['prediction'] ==  'musty'] = 'inedible'
prediction[prediction['prediction'] ==  'none'] = 'edible'
prediction[prediction['prediction'] ==  'pungent'] = 'inedible'
prediction[prediction['prediction'] ==  'spicy'] = 'inedible'
```

In [30]:
```
Y_test
```

Out[30]:

	edible
186	edible
2883	edible
5769	inedible
4363	inedible
2889	edible
...	...
5129	inedible
4895	inedible
6744	inedible
896	edible
3646	edible

1625 rows × 1 columns

In [31]:
```
# Confusion Matrix

cm = confusion_matrix(Y_test['edible'], prediction['prediction'])
print(cm)
```

```
[[858   0]
 [ 27 740]]
```

In [32]:
```
print("Accuracy Score :")
print(accuracy_score(Y_test['edible'], prediction['prediction']))
print("\n")
print("Report :")
print(classification_report(Y_test['edible'], prediction['prediction']))
```

```
Accuracy Score :
0.9833846153846154


Report :
              precision    recall  f1-score   support

      edible       0.97      1.00      0.98       858
    inedible       1.00      0.96      0.98       767

    accuracy                           0.98      1625
   macro avg       0.98      0.98      0.98      1625
weighted avg       0.98      0.98      0.98      1625
```

After validating the model against the test data, we found the accuracy of the model to be 0.98. This is enough to make us comfortable with models.

Results:

After a successfull validation, we feel that the Odor Rules Set would make a good model to determine whether a mushroom is edible or non-edible. The Odor Rules Set are as follows:

almond -> edible
anise -> edible
creosote -> inedible
fishy -> inedible
foul -> inedible
musty -> inedible
none -> edible
pungent -> inedible
spicy -> inedible

References:

Stack Overflow. (2015). Pandas DataFrame: replace all values in a column, based on condition. Retrieved (2020, June 22) from https://stackoverflow.com/questions/31511997/pandas-dataframe-replace-all-values-in-a-column-based-on-condition (https://stackoverflow.com/questions/31511997/pandas-dataframe-replace-all-values-in-a-column-based-on-condition)

https://stackoverflow.com/questions/2161752/how-to-count-the-frequency-of-the-elements-in-an-unordered-list (https://stackoverflow.com/questions/2161752/how-to-count-the-frequency-of-the-elements-in-an-unordered-list)

https://stackoverflow.com/questions/48939795/how-to-plot-a-count-bar-chart-with-a-pandas-df-grouping-by-one-categorical-colu (https://stackoverflow.com/questions/48939795/how-to-plot-a-count-bar-chart-with-a-pandas-df-grouping-by-one-categorical-colu)

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https://www.geeksforgeeks.org/creating-a-dataframe-from-pandas-series/ (https://www.geeksforgeeks.org/creating-a-dataframe-from-pandas-series/)

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