Business Problem

Goal here is to see if we can harness the power of machine learning and boosting to help create not just a predictive model, but a general guideline for features people should look out for when picking mushrooms.

In [1]:
```
import numpy as np
import pandas as pd

import matplotlib.pyplot as plt
import seaborn as sns
```

In [2]:
```
df = pd.read_csv("mushrooms.csv")
df.head()
```

Out[2]:

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

5 rows × 23 columns

Data

Mushroom : Edible or Poisonous?

Data Source: https://archive.ics.uci.edu/ml/datasets/Mushroom (https://archive.ics.uci.edu/ml/datasets/Mushroom)

This data set includes descriptions of hypothetical samples corresponding to 23 species of gilled mushrooms in the Agaricus and Lepiota Family (pp. 500-525). Each species is identified as definitely edible, definitely poisonous, or of unknown edibility and not recommended. This latter class was combined with the poisonous one. The Guide clearly states that there is no simple rule for determining the edibility of a mushroom; no rule like ``leaflets three, let it be'' for Poisonous Oak and Ivy.

Attribute Information:

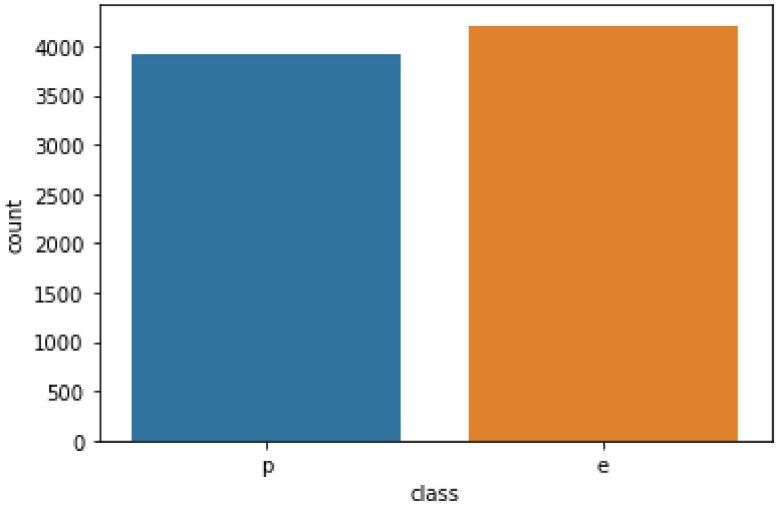
1. cap-shape: bell=b,conical=c,convex=x,flat=f, knobbed=k,sunken=s
2. cap-surface: fibrous=f,grooves=g,scaly=y,smooth=s
3. cap-color: brown=n,buff=b,cinnamon=c,gray=g,green=r, pink=p,purple=u,red=e,white=w,yellow=y
4. bruises?: bruises=t,no=f
5. odor: almond=a,anise=l,creosote=c,fishy=y,foul=f, musty=m,none=n,pungent=p,spicy=s
6. gill-attachment: attached=a,descending=d,free=f,notched=n
7. gill-spacing: close=c,crowded=w,distant=d
8. gill-size: broad=b,narrow=n
9. gill-color: black=k,brown=n,buff=b,chocolate=h,gray=g, green=r,orange=o,pink=p,purple=u,red=e, white=w,yellow=y
10. stalk-shape: enlarging=e,tapering=t
11. stalk-root: bulbous=b,club=c,cup=u,equal=e, rhizomorphs=z,rooted=r,missing=?
12. stalk-surface-above-ring: fibrous=f,scaly=y,silky=k,smooth=s
13. stalk-surface-below-ring: fibrous=f,scaly=y,silky=k,smooth=s
14. stalk-color-above-ring: brown=n,buff=b,cinnamon=c,gray=g,orange=o, pink=p,red=e,white=w,yellow=y
15. stalk-color-below-ring: brown=n,buff=b,cinnamon=c,gray=g,orange=o, pink=p,red=e,white=w,yellow=y
16. veil-type: partial=p,universal=u
17. veil-color: brown=n,orange=o,white=w,yellow=y
18. ring-number: none=n,one=o,two=t
19. ring-type: cobwebby=c,evanescent=e,flaring=f,large=l, none=n,pendant=p,sheathing=s,zone=z
20. spore-print-color: black=k,brown=n,buff=b,chocolate=h,green=r, orange=o,purple=u,white=w,yellow=y
21. population: abundant=a,clustered=c,numerous=n, scattered=s,several=v,solitary=y
22. habitat: grasses=g,leaves=l,meadows=m,paths=p, urban=u,waste=w,woods=d

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

EDA

In [4]:
```
sns.countplot(data=df,x='class')
plt.show()
```



In [5]:
```
df.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]:
```
df.describe().transpose()
```

Out[6]:

	count	unique	top	freq
class	8124	2	e	4208
cap-shape	8124	6	x	3656
cap-surface	8124	4	y	3244
cap-color	8124	10	n	2284
bruises	8124	2	f	4748
odor	8124	9	n	3528
gill-attachment	8124	2	f	7914
gill-spacing	8124	2	c	6812
gill-size	8124	2	b	5612
gill-color	8124	12	b	1728
stalk-shape	8124	2	t	4608
stalk-root	8124	5	b	3776
stalk-surface-above-ring	8124	4	s	5176
stalk-surface-below-ring	8124	4	s	4936
stalk-color-above-ring	8124	9	w	4464
stalk-color-below-ring	8124	9	w	4384
veil-type	8124	1	p	8124
veil-color	8124	4	w	7924
ring-number	8124	3	o	7488
ring-type	8124	5	p	3968
spore-print-color	8124	9	w	2388
population	8124	6	v	4040
habitat	8124	7	d	3148

X & y

In [7]:
```
X = pd.get_dummies(df.drop('class',axis=1),drop_first=True)
y = df['class']
```

In [8]:
```
X
```

Out[8]:

	cap-shape_c	cap-shape_f	cap-shape_k	cap-shape_s	cap-shape_x	cap-surface_g	cap-surface_s	cap-surface_y	cap-color_c
0	0	0	0	0	1	0	1	0	0
1	0	0	0	0	1	0	1	0	0
2	0	0	0	0	0	0	1	0	0
3	0	0	0	0	1	0	0	1	0
4	0	0	0	0	1	0	1	0	0
...	...	...	...	...	...	...	...	...	...
8119	0	0	1	0	0	0	1	0	0
8120	0	0	0	0	1	0	1	0	0
8121	0	1	0	0	0	0	1	0	0
8122	0	0	1	0	0	0	0	1	0
8123	0	0	0	0	1	0	1	0	0

8124 rows × 95 columns

In [9]:
```
X.shape,y.shape
```

Out[9]:
```
((8124, 95), (8124,))
```

Train/Test Split

In [10]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, rando
m_state=101)
```

Modeling

AdaBoost Classifier with default parameters

In [11]:
```
from sklearn.ensemble import AdaBoostClassifier
```

In [12]:
```
model = AdaBoostClassifier()
```

In [13]:
```
model.fit(X_train,y_train)
```

Out[13]:
```
AdaBoostClassifier()
```

Prediction

In [14]:
```
ypred_train=model.predict(X_train)
```

In [15]:
```
predictions = model.predict(X_test)
```

Evaluation

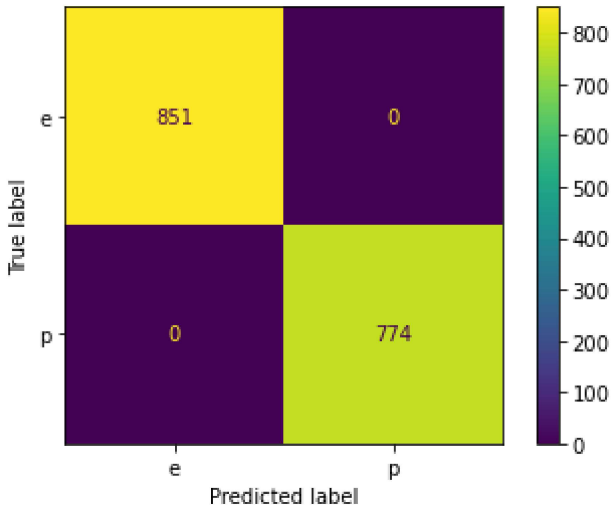
Accuracy

In [16]:
```
from sklearn.metrics import accuracy_score
print("Train accuracy:",accuracy_score(y_train,ypred_train))
print("Test accuracy:",accuracy_score(y_test,predictions))
```

```
Train accuracy: 1.0
Test accuracy: 1.0
```

Confusion Matrix

In [17]:
```
from sklearn.metrics import plot_confusion_matrix
plot_confusion_matrix(model,X_test,y_test)
plt.show()
```



Classification Report

'

In [18]:
```
from sklearn.metrics import classification_report
print(classification_report(y_test,predictions))
```

```
              precision    recall  f1-score   support

           e       1.00      1.00      1.00       851
           p       1.00      1.00      1.00       774

    accuracy                           1.00      1625
   macro avg       1.00      1.00      1.00      1625
weighted avg       1.00      1.00      1.00      1625
```

Cross validation Score

In [19]:
```
from sklearn.model_selection import cross_val_score
scores = cross_val_score(model,X,y,cv=5)
print("Cross Validation Score:",scores.mean())
```

```
Cross Validation Score: 0.9251425539977264
```

Importance of each feature given by this model

In [20]:
```
model.feature_importances_
```

Out[20]:
```
array([0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.02, 0.  , 0.  ,
       0.02, 0.  , 0.  , 0.  , 0.02, 0.  , 0.04, 0.04, 0.04, 0.  , 0.  ,
       0.04, 0.02, 0.  , 0.  , 0.  , 0.12, 0.08, 0.  , 0.  , 0.  , 0.  ,
       0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  ,
       0.  , 0.06, 0.  , 0.  , 0.  , 0.  , 0.02, 0.  , 0.  , 0.  , 0.  ,
       0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.08, 0.  , 0.  , 0.  ,
       0.  , 0.  , 0.  , 0.  , 0.  , 0.02, 0.  , 0.  , 0.  , 0.  , 0.  ,
       0.  , 0.  , 0.  , 0.04, 0.  , 0.18, 0.  , 0.08, 0.  , 0.  , 0.06,
       0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.02])
```

In [21]:
```
f_imp = pd.DataFrame(index=X.columns,data=model.feature_importances_,columns=[
'Feature Importance'])
```

In [22]:
```
f_imp[f_imp['Feature Importance'] > 0]
```

Out[22]:

	Feature Importance
cap-color_c	0.02
cap-color_n	0.02
cap-color_w	0.02
bruises_t	0.04
odor_c	0.04
odor_f	0.04
odor_n	0.04
odor_p	0.02
gill-spacing_w	0.12
gill-size_n	0.08
stalk-surface-above-ring_k	0.06
stalk-surface-below-ring_y	0.02
stalk-color-below-ring_n	0.08
ring-number_t	0.02
spore-print-color_r	0.04
spore-print-color_w	0.18
population_c	0.08
population_v	0.06
habitat_w	0.02

Hyperparameter Tuning

In [23]:
```
from sklearn.model_selection import GridSearchCV

estimator = AdaBoostClassifier()

param_grid = {"n_estimators":list(range(1,101))}

grid = GridSearchCV(estimator,  param_grid, cv=5,  scoring='accuracy')

grid.fit(X_train,y_train)

grid.best_params_
```

Out[23]:
```
{'n_estimators': 20}
```

Final Model

In [24]:
```
final_model = AdaBoostClassifier(n_estimators=20)
final_model.fit(X_train,y_train)

preds_train = final_model.predict(X_train)
preds_test = final_model.predict(X_test)

print("Train Accuracy Score: ", accuracy_score(y_train,preds_train))
print("Test Accuracy Score: ",accuracy_score(y_test,preds_test))
```

```
Train Accuracy Score:  1.0
Test Accuracy Score:  1.0
```

In [25]:
```
final_model.feature_importances_
```

Out[25]:
```
array([0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  ,
       0.  , 0.  , 0.  , 0.  , 0.05, 0.  , 0.05, 0.05, 0.05, 0.  , 0.  ,
       0.1 , 0.05, 0.  , 0.  , 0.  , 0.05, 0.15, 0.  , 0.  , 0.  , 0.  ,
       0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  ,
       0.  , 0.05, 0.  , 0.  , 0.  , 0.  , 0.  , 0.05, 0.  , 0.  , 0.  ,
       0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.05, 0.  , 0.  ,
       0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  ,
       0.  , 0.  , 0.  , 0.05, 0.  , 0.1 , 0.  , 0.05, 0.  , 0.  , 0.1 ,
       0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  , 0.  ])
```

In [26]:
```
feats = pd.DataFrame(index=X.columns,data=final_model.feature_importances_,col
umns=['Importance'])
feats
```

Out[26]:

	Importance
cap-shape_c	0.0
cap-shape_f	0.0
cap-shape_k	0.0
cap-shape_s	0.0
cap-shape_x	0.0
...	...
habitat_l	0.0
habitat_m	0.0
habitat_p	0.0
habitat_u	0.0
habitat_w	0.0

95 rows × 1 columns

In [27]:
```
imp_feats = feats[feats['Importance']>0]
```

In [28]:
```
imp_feats.sort_values("Importance")
```

Out[28]:

	Importance
cap-color_w	0.05
bruises_t	0.05
odor_c	0.05
odor_f	0.05
odor_p	0.05
gill-spacing_w	0.05
stalk-surface-above-ring_k	0.05
stalk-surface-below-ring_y	0.05
stalk-color-below-ring_n	0.05
spore-print-color_r	0.05
population_c	0.05
odor_n	0.10
spore-print-color_w	0.10
population_v	0.10
gill-size_n	0.15

In [29]:
```
plt.figure(figsize=(14,6),dpi=200)
sns.barplot(data=imp_feats.sort_values('Importance'),x=imp_feats.index,y='Importance')

plt.xticks(rotation=90)
plt.show()
```