Adaboost

The Data

Mushroom Hunting: Edible or Poisonous?

Data Source: 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**

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

Goal

THIS IS IMPORTANT, THIS IS NOT OUR TYPICAL PREDICTIVE MODEL!

Our general 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.

Import

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("D:\\Study\\Programming\\python\\Python course from udemy\\Udemy - 2022 Python for Machine Learning & Data Science Masterclass\\18 - Boosting Methods\\31286610-mushrooms.csv")
df.head()
```

Out[2]:

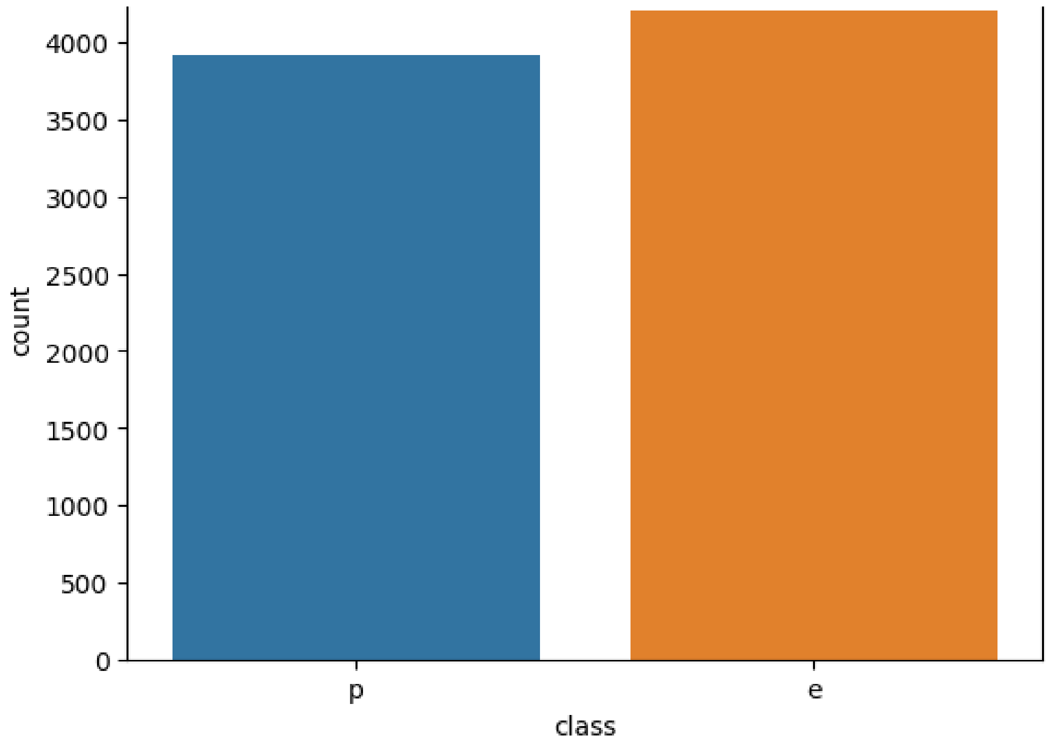
	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	gill-color	...	stalk-surface-below-ring	stalk-color-above-ring	stalk-color-below-ring	veil-type	veil-color	nu
0	p	x	s	n	t	p	f	c	n	k	...	s	w	w	p	w	
1	e	x	s	y	t	a	f	c	b	k	...	s	w	w	p	w	
2	e	b	s	w	t	l	f	c	b	n	...	s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

5 rows × 23 columns

EDA (Exploratory Data Analysis)

In [6]:

```
sns.countplot(data=df,x='class');
```



In [12]:

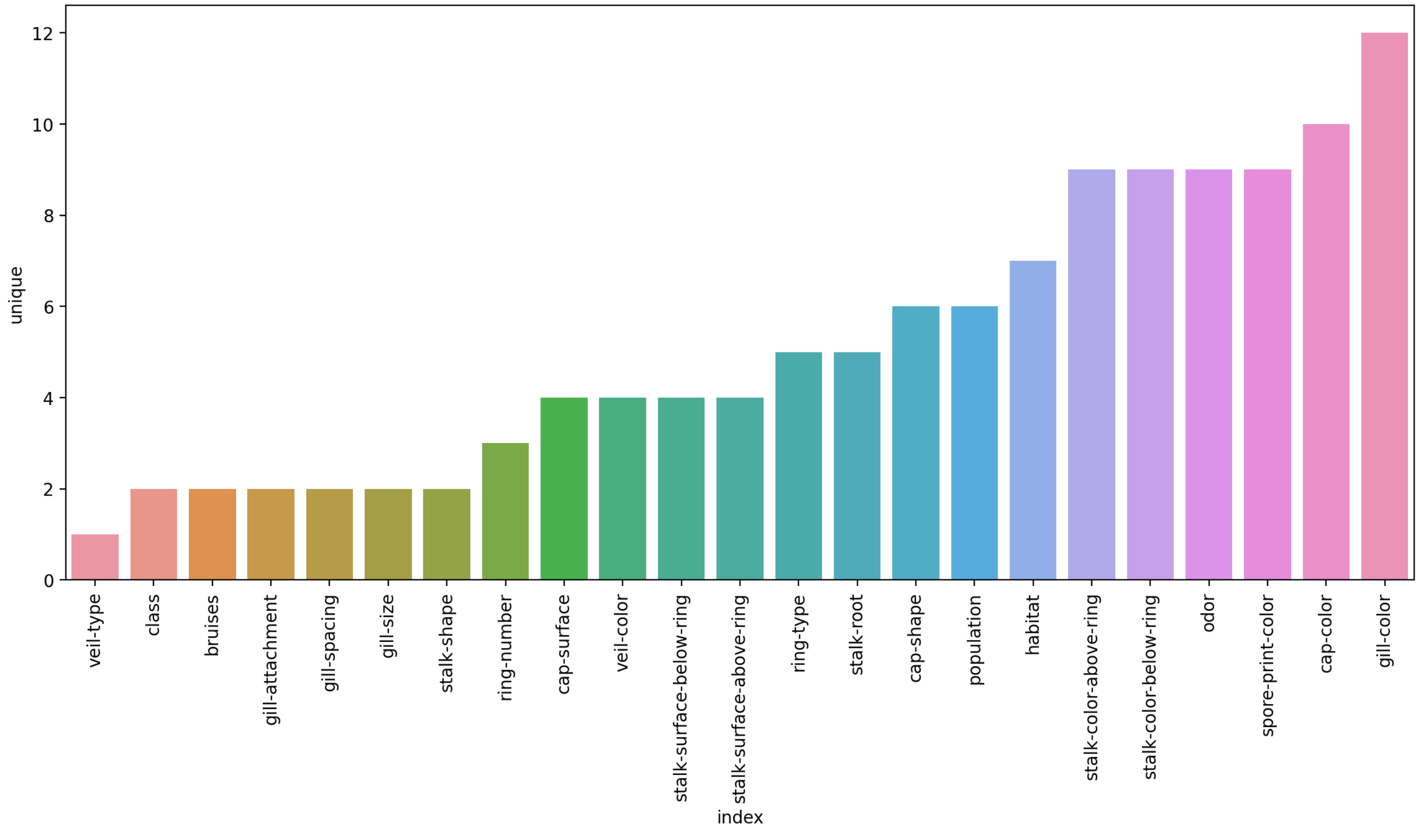
```
feat_uni = df.describe().transpose().reset_index().sort_values('unique')
feat_uni
```

Out[12]:

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

In [16]:

```
plt.figure(figsize=(14,6),dpi=200)
sns.barplot(x='index',y='unique',data=feat_uni)
plt.xticks(rotation=90);
```



In [19]:

```
df.isnull().sum()
```

Out[19]:

```
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
```

Train Test Split

In [20]:

```
X= pd.get_dummies(df.drop('class',axis=1),drop_first=True)
```

In [22]:

```
X.head()
```

Out[22]:

	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	cap-color_e	...	population_n	populat
0	0	0	0	0	1	0	1	0	0	0	...	0	
1	0	0	0	0	1	0	1	0	0	0	...	1	
2	0	0	0	0	0	0	1	0	0	0	...	1	
3	0	0	0	0	1	0	0	1	0	0	...	0	
4	0	0	0	0	1	0	1	0	0	0	...	0	

5 rows × 95 columns

In [23]:

```
y=df['class']
```

In [24]:

```
from sklearn.model_selection import train_test_split
```

In [25]:

```
X_train,X_test,y_train,y_test= train_test_split(X,y,test_size=0.15,random_state=101)
```

Modeling

In [26]:

```
from sklearn.ensemble import AdaBoostClassifier
```

In [45]:

```
# Here we set that n_estimators that will take only one feature and all other will be nul
l
model = AdaBoostClassifier(n_estimators=1)
```

In [48]:

```
model.fit(X_train,y_train)
```

Out[48]:

```
▾ AdaBoostClassifier
AdaBoostClassifier(n_estimators=1)
```

In [49]:

```
preds = model.predict(X_test)
```

Evaluation

In [50]:

```
from sklearn.metrics import classification_report, accuracy_score,confusion_matrix
```

In [51]:

```
from mlxtend.plotting import plot_confusion_matrix
```

In [52]:

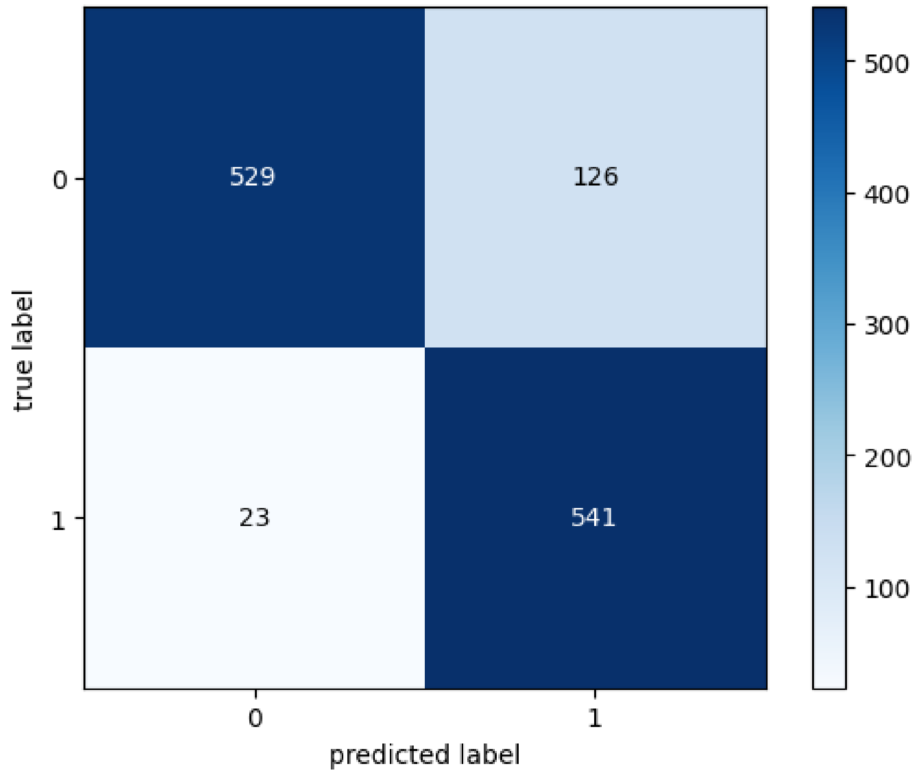
```
m=confusion_matrix(y_test,preds)
m
```

Out[52]:

```
array([[529, 126],
       [ 23, 541]], dtype=int64)
```

In [53]:

```
plot_confusion_matrix(m,colorbar=True);
```



In [54]:

```
print(classification_report(y_test,preds))
```

```
              precision    recall  f1-score   support

           e       0.96      0.81      0.88       655
           p       0.81      0.96      0.88       564

    accuracy                           0.88      1219
   macro avg       0.88      0.88      0.88      1219
weighted avg       0.89      0.88      0.88      1219
```

In [55]:

```
accuracy_score(y_test,preds)
```

Out[55]:

```
0.8777686628383922
```

In [56]:

```
# Here we can see all feature have 0 importance except one
model.feature_importances_
```

Out[56]:

```
array([0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 1., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0., 0.,
       0., 0., 0., 0., 0., 0., 0., 0., 0., 0.])
```

In [57]:

```
# Here we find that maximum value that is one to know the index id of that
model.feature_importances_.argmax()
```

Out[57]:

```
22
```

In [41]:

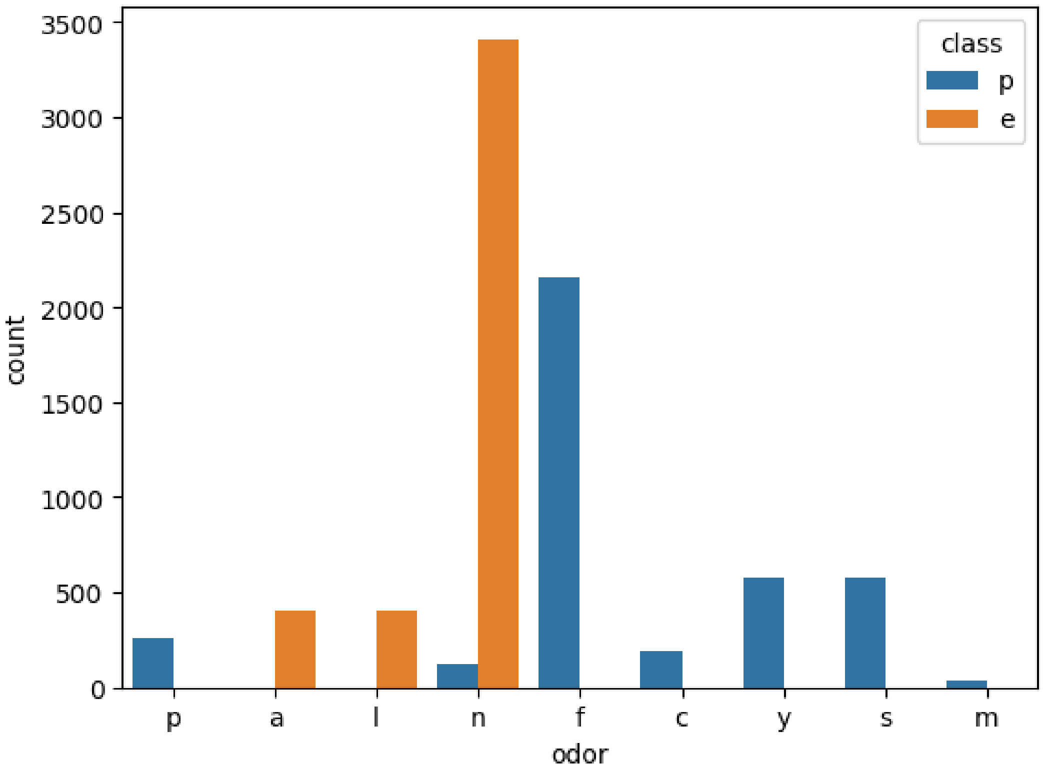
```
# Here is that one feature
X.columns[22]
```

Out[41]:

```
'odor_n'
```

In [44]:

```
sns.countplot(data=df,x='odor',hue='class');
```



Analyzing performance as more weak learners are added.

In [58]:

```
# Here to total number of columns after applying pd.get_dummies
len(X.columns)
```

Out[58]:

```
95
```

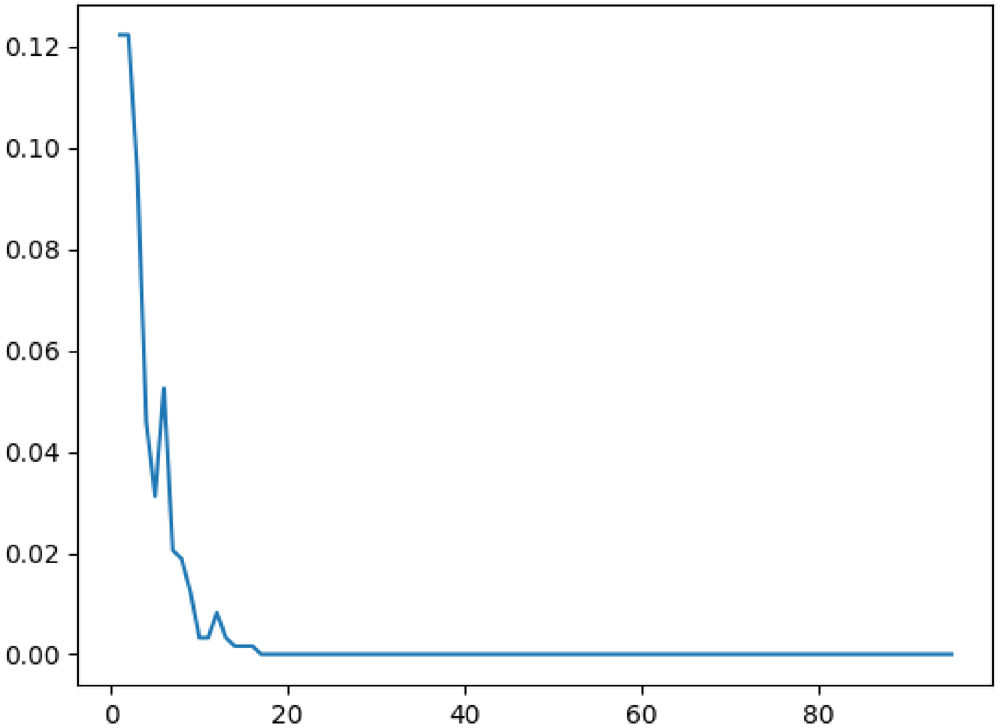
now developing model to check total number of features 1 to 95

In [59]:

```python
error_rates = []

for n in range(1,96):

    model = AdaBoostClassifier(n_estimators=n)
    model.fit(X_train,y_train)
    preds = model.predict(X_test)
    err = 1 - accuracy_score(y_test,preds)

    error_rates.append(err)
```

In [62]:

```python
plt.plot(range(1,96),error_rates);
```



In [63]:

```python
model
```

Out[63]:

```
▾ AdaBoostClassifier
AdaBoostClassifier(n_estimators=95)
```

In [64]:

```python
model.feature_importances_
```

Out[64]:

```
array([0.        , 0.        , 0.        , 0.        , 0.        ,
       0.        , 0.        , 0.        , 0.01052632, 0.        ,
       0.        , 0.01052632, 0.        , 0.        , 0.        ,
       0.01052632, 0.        , 0.05263158, 0.03157895, 0.03157895,
       0.        , 0.        , 0.06315789, 0.02105263, 0.        ,
       0.        , 0.        , 0.09473684, 0.09473684, 0.        ,
       0.        , 0.        , 0.        , 0.        , 0.        ,
       0.        , 0.        , 0.        , 0.        , 0.        ,
       0.01052632, 0.01052632, 0.        , 0.        , 0.        ,
       0.06315789, 0.        , 0.        , 0.        , 0.        ,
       0.03157895, 0.        , 0.        , 0.        , 0.        ,
       0.        , 0.        , 0.        , 0.        , 0.        ,
       0.        , 0.        , 0.06315789, 0.        , 0.        ,
       0.01052632, 0.        , 0.        , 0.        , 0.        ,
       0.        , 0.01052632, 0.        , 0.        , 0.        ,
       0.        , 0.        , 0.        , 0.        , 0.        ,
```

```
       0.05263158, 0.        , 0.16842105, 0.        , 0.10526316,
       0.        , 0.        , 0.04210526, 0.        , 0.        ,
       0.        , 0.        , 0.        , 0.        , 0.01052632])
```

In [70]:

```
feats = pd.DataFrame(index=X.columns , data=model.feature_importances_,columns=['Importance'])
feats
```

Out[70]:

	Importance
cap-shape_c	0.000000
cap-shape_f	0.000000
cap-shape_k	0.000000
cap-shape_s	0.000000
cap-shape_x	0.000000
...	...
habitat_l	0.000000
habitat_m	0.000000
habitat_p	0.000000
habitat_u	0.000000
habitat_w	0.010526

95 rows × 1 columns

In [72]:

```
imp_feats = feats[feats['Importance']>0]
imp_feats.sort_values('Importance')
```

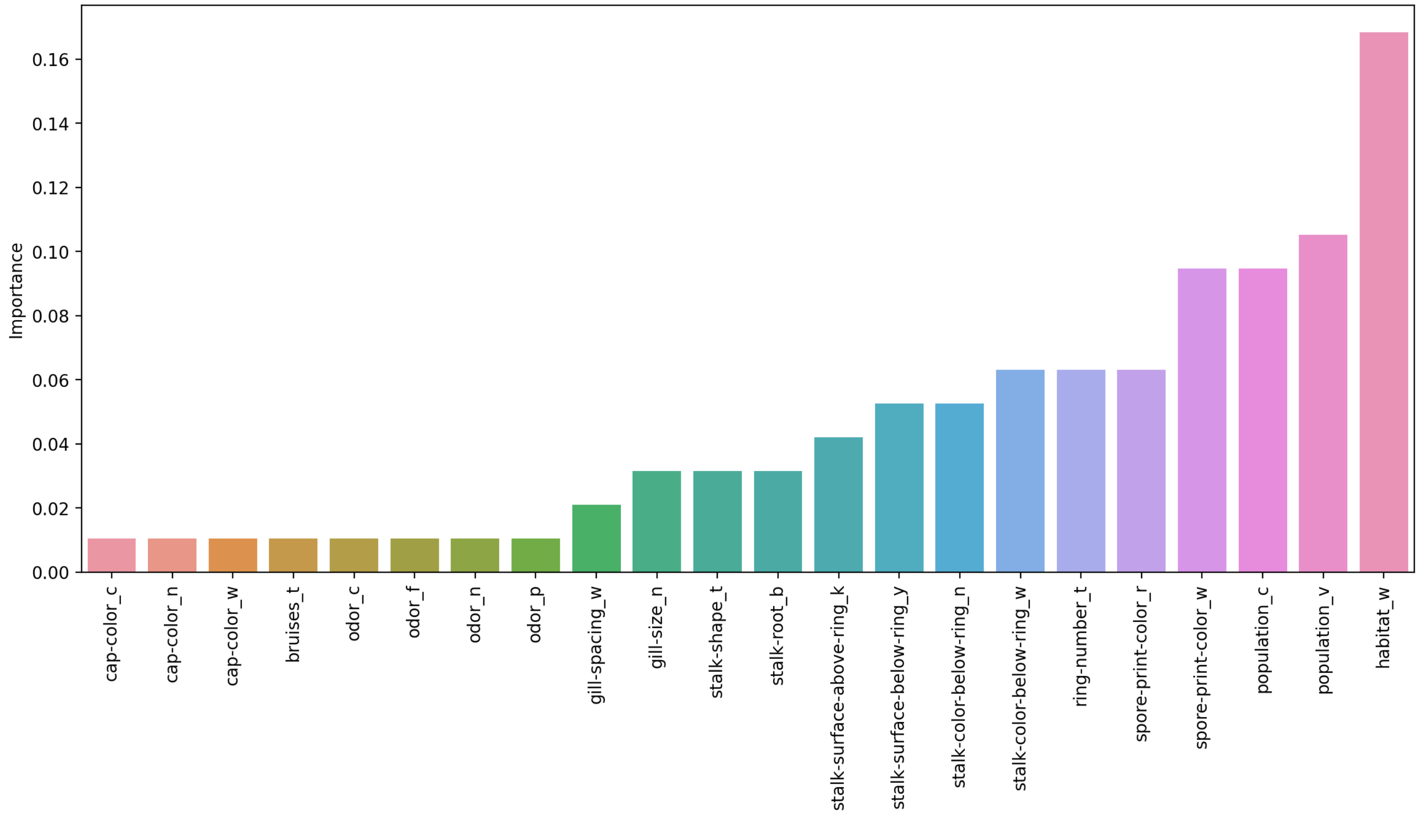
Out[72]:

	Importance
cap-color_c	0.010526
ring-number_t	0.010526
stalk-color-below-ring_w	0.010526
stalk-root_b	0.010526
stalk-shape_t	0.010526
habitat_w	0.010526
cap-color_n	0.010526
cap-color_w	0.010526
odor_p	0.021053
odor_c	0.031579
odor_f	0.031579
stalk-surface-below-ring_y	0.031579
population_v	0.042105
bruises_t	0.052632
spore-print-color_r	0.052632
stalk-surface-above-ring_k	0.063158
stalk-color-below-ring_n	0.063158
odor_n	0.063158

	Importance
gill-size_n	0.094737
gill-spacing_w	0.094737
population_c	0.105263
spore-print-color_w	0.168421

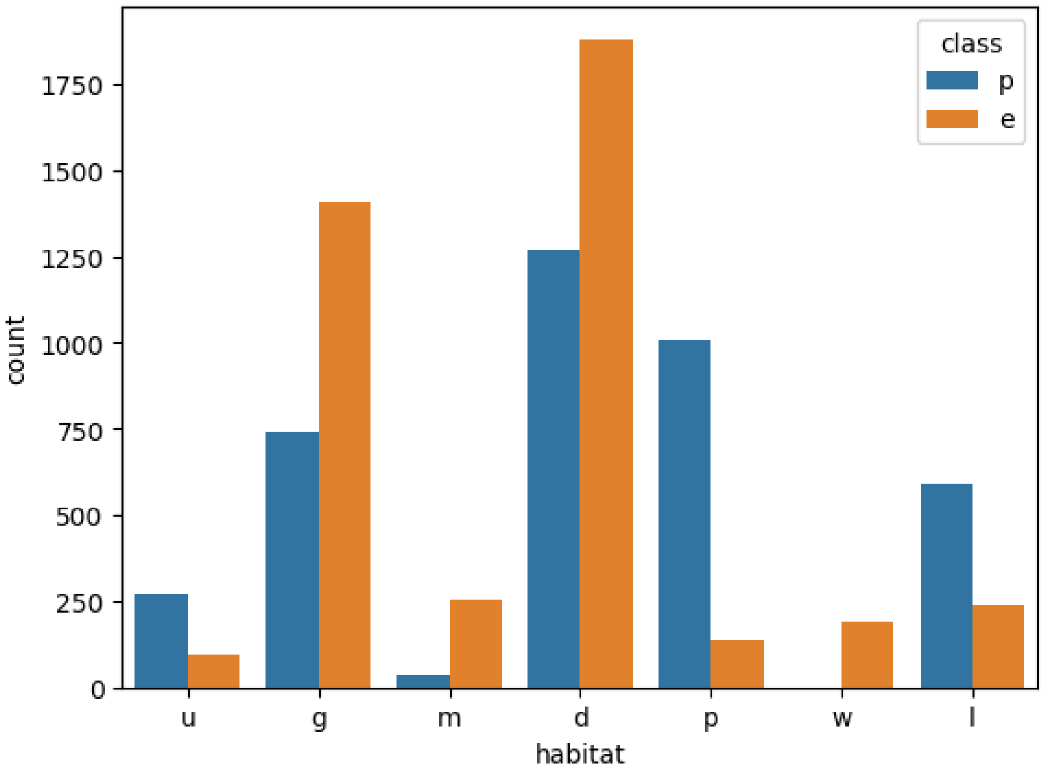
In [75]:

```
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);
```



In [76]:

```
sns.countplot(data=df,x='habitat',hue='class');
```



Interesting to see how the importance of the features shift as more are allowed to be added in! But remember these are all weak learner stumps, and feature importance is available for all the tree methods!

Gradient Boosting and GridSearch

In [117]:

```
df.head()
```

Out[117]:

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

5 rows × 23 columns

In [118]:

```
X = df.drop('class',axis=1)
y = df['class']
```

In [119]:

```
X = pd.get_dummies(X,drop_first=True)
```

In [120]:

```
X.head()
```

Out[120]:

	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	cap-color_e	...	population_n	populat
0	0	0	0	0	1	0	1	0	0	0	...	0	
1	0	0	0	0	1	0	1	0	0	0	...	1	
2	0	0	0	0	0	0	1	0	0	0	...	1	
3	0	0	0	0	1	0	0	1	0	0	...	0	
4	0	0	0	0	1	0	1	0	0	0	...	0	

5 rows × 95 columns

In [121]:

```
y.head()
```

Out[121]:

```
0    p
1    e
2    e
3    p
4    e
```

```
Name: class, dtype: object
```

Train Test Split

In [122]:

```
from sklearn.model_selection import train_test_split
```

In [123]:

```
X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.15,random_state=101)
```

Gradient Boosting and Grid Search with CV

In [124]:

```
from sklearn.ensemble import GradientBoostingClassifier
```

In [125]:

```
#help(GradientBoostingClassifier)
```

In [126]:

```
from sklearn.model_selection import GridSearchCV
```

In [135]:

```
param_grid = {'n_estimators':[1,5,10,20,40,100],'learning_rate':[0.1,0.05,0.2],'max_dept
h':[3,4,5,6]}
```

In [136]:

```
gb_model = GradientBoostingClassifier()
```

In [137]:

```
grid = GridSearchCV(gb_model,param_grid)
```

Fit to Training Data with CV Search

In [138]:

```
grid.fit(X_train,y_train)
```

Out[138]:

```
▸ GridSearchCV
▸ estimator: GradientBoostingClassifier
  ▸ GradientBoostingClassifier
```

In [139]:

```
grid.best_params_
```

Out[139]:

```
{'learning_rate': 0.1, 'max_depth': 3, 'n_estimators': 100}
```

Performance

In [140]:

```python
from sklearn.metrics import classification_report,accuracy_score
```

In [141]:

```python
from mlxtend.plotting import plot_confusion_matrix
```

In [142]:

```python
preds = grid.predict(X_test)
```

In [143]:

```python
preds
```

Out[143]:

```
array(['p', 'e', 'p', ..., 'p', 'p', 'e'], dtype=object)
```

In [144]:

```python
print(classification_report(y_test,preds))
```

```
              precision    recall  f1-score   support

           e       1.00      1.00      1.00       655
           p       1.00      1.00      1.00       564

    accuracy                           1.00      1219
   macro avg       1.00      1.00      1.00      1219
weighted avg       1.00      1.00      1.00      1219
```

In [145]:

```python
grid.best_estimator_.feature_importances_
```

Out[145]:

```
array([2.91150176e-04, 2.35156614e-16, 0.00000000e+00, 0.00000000e+00,
       7.85087530e-17, 1.04524302e-03, 5.93230609e-18, 5.06011038e-06,
       0.00000000e+00, 0.00000000e+00, 1.66104383e-17, 0.00000000e+00,
       3.79992913e-17, 0.00000000e+00, 0.00000000e+00, 1.66230685e-08,
       2.38800034e-03, 5.23897091e-02, 6.24175887e-04, 1.01346784e-02,
       1.82499853e-02, 1.23525717e-05, 6.14744334e-01, 9.20844491e-04,
       0.00000000e+00, 0.00000000e+00, 0.00000000e+00, 1.25278108e-02,
       1.06871727e-02, 0.00000000e+00, 1.62087258e-16, 4.11091114e-18,
       7.44589338e-18, 0.00000000e+00, 0.00000000e+00, 1.74744598e-17,
       2.95645628e-17, 0.00000000e+00, 6.24729829e-18, 0.00000000e+00,
       2.03408198e-04, 0.00000000e+00, 1.35980705e-01, 7.71855052e-03,
       5.39517537e-02, 4.64723214e-04, 2.59824622e-04, 4.95063766e-06,
       1.83319493e-05, 1.35380870e-07, 1.23189646e-02, 1.45243645e-04,
       0.00000000e+00, 0.00000000e+00, 3.91530504e-04, 0.00000000e+00,
       0.00000000e+00, 2.00413270e-03, 1.10295205e-04, 3.18498550e-03,
       0.00000000e+00, 0.00000000e+00, 5.33104127e-05, 0.00000000e+00,
       0.00000000e+00, 0.00000000e+00, 3.02342639e-03, 0.00000000e+00,
       0.00000000e+00, 0.00000000e+00, 1.64648274e-04, 3.67811493e-06,
       8.43895349e-05, 0.00000000e+00, 1.16617901e-03, 3.61581197e-03,
       1.12337177e-02, 2.14106022e-04, 2.09075840e-04, 0.00000000e+00,
       3.04953583e-02, 4.10000880e-03, 4.86768755e-04, 0.00000000e+00,
       3.25747891e-03, 0.00000000e+00, 7.26245568e-08, 4.27311240e-04,
       6.76540868e-04, 1.73564810e-16, 0.00000000e+00, 0.00000000e+00,
       0.00000000e+00, 1.00485103e-05, 0.00000000e+00])
```

In [146]:

```python
imp_feats = pd.DataFrame(index=X.columns,data=grid.best_estimator_.feature_importances_,
columns=['Importance'])
imp_feats
```

Out[146]:

	Importance
cap-shape_c	2.911502e-04
cap-shape_f	2.351566e-16
cap-shape_k	0.000000e+00
cap-shape_s	0.000000e+00
cap-shape_x	7.850875e-17
...	...
habitat_l	0.000000e+00
habitat_m	0.000000e+00
habitat_p	0.000000e+00
habitat_u	1.004851e-05
habitat_w	0.000000e+00

95 rows × 1 columns

In [147]:

```
imp_feats.sort_values('Importance',ascending=False)
```

Out[147]:

	Importance
odor_n	0.614744
stalk-root_c	0.135981
stalk-root_r	0.053952
bruises_t	0.052390
spore-print-color_r	0.030495
...	...
veil-color_o	0.000000
veil-color_w	0.000000
gill-color_y	0.000000
odor_y	0.000000
habitat_w	0.000000

95 rows × 1 columns

In [148]:

```
imp_feats.describe().transpose()
```

Out[148]:

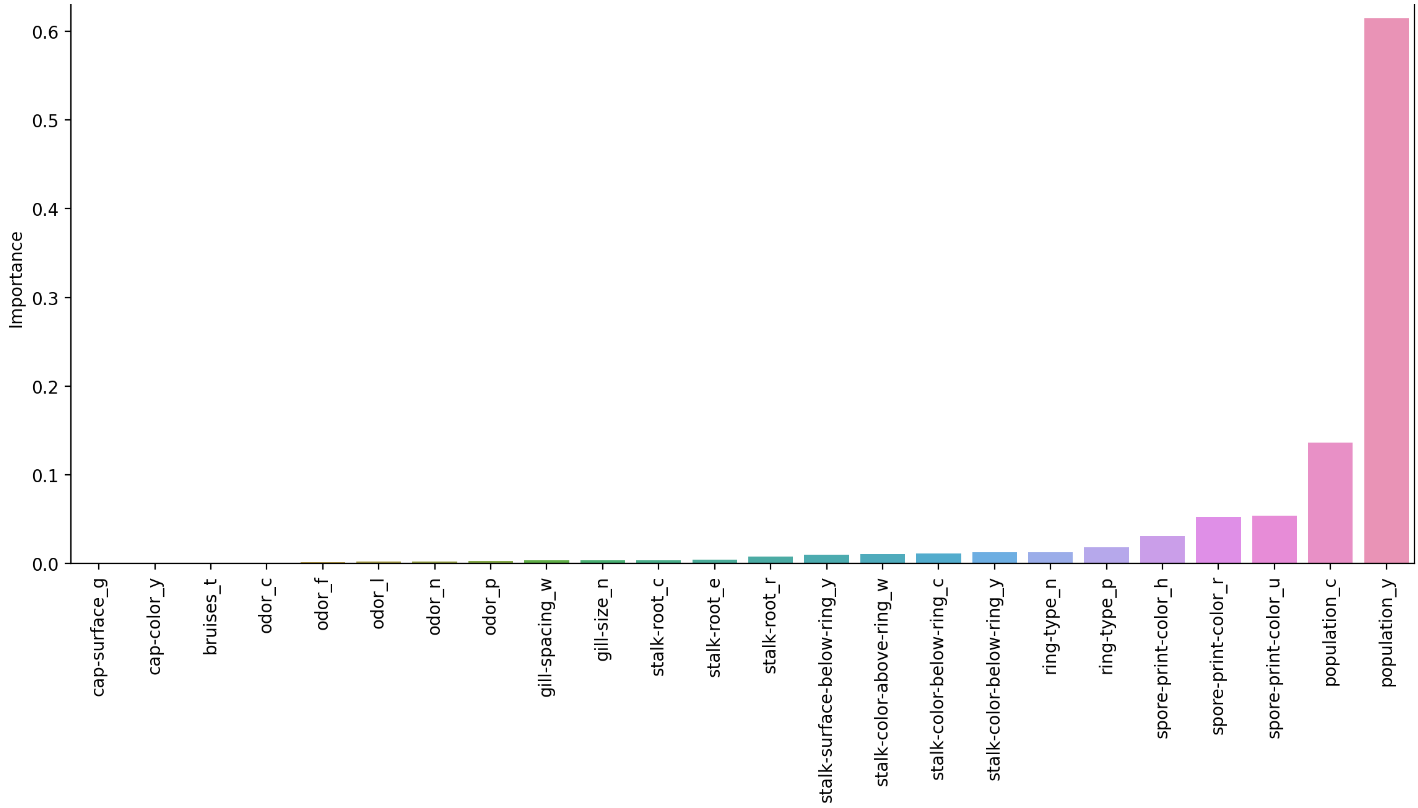
	count	mean	std	min	25%	50%	75%	max
Importance	95.0	0.010526	0.064707	0.0	0.0	2.351566e-16	0.000555	0.614744

In [149]:

```
imp_feats = imp_feats[imp_feats['Importance']>0.000587]
```

In [150]:

```
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);
```


Importance
0.6
0.5
0.4
0.3
0.2
0.1
0.0
cap-surface_g
cap-color_y
bruises_t
odor_c
odor_f
odor_l
odor_n
odor_p
gill-spacing_w
gill-size_n
stalk-root_c
stalk-root_e
stalk-root_r
stalk-surface-below-ring_y
stalk-color-above-ring_w
stalk-color-below-ring_c
stalk-color-below-ring_y
ring-type_n
ring-type_p
spore-print-color_h
spore-print-color_r
spore-print-color_u
population_c
population_y