Official Data Set Link: [https://www.kaggle.com/uciml/mushroom-classification (https://www.kaggle.com/uciml/mushroom-classification)](https://www.kaggle.com/uciml/mushroom-classification)

Data Set Columns:

Attribute Information: (classes: edible=e, poisonous=p)

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

Context
Although this dataset was originally contributed to the UCI Machine Learning repository nearly 30 years ago, mushroom hunting (otherwise known as "shrooming") is enjoying new peaks in popularity. Learn which features spell certain death and which are most palatable in this dataset of mushroom characteristics

####Resources:

- https://medium.com/@alex.ortner.1982/top-10-binary-classification-algorithms-a-beginners-guide-feeacbd7a3e2 (https://medium.com/@alex.ortner.1982/top-10-binary-classification-algorithms-a-beginners-guide-feeacbd7a3e2)
- https://machinelearningmastery.com/develop-first-xgboost-model-python-scikit-learn/ (https://machinelearningmastery.com/develop-first-xgboost-model-python-scikit-learn/)
- https://towardsdatascience.com/rip-correlation-introducing-the-predictive-power-score-3d90808b9598 (https://towardsdatascience.com/rip-correlation-introducing-the-predictive-power-score-3d90808b9598)
- https://scikit-learn.org/stable/modules/generated/sklearn.naive_bayes.MultinomialNB.html (https://scikit-learn.org/stable/modules/generated/sklearn.naive_bayes.MultinomialNB.html)
- https://medium.com/@dtuk81/confusion-matrix-visualization-fc31e3f30fea (https://medium.com/@dtuk81/confusion-matrix-visualization-fc31e3f30fea)
- https://www.machinecurve.com/index.php/2020/05/05/how-to-create-a-confusion-matrix-with-scikit-learn/ (https://www.machinecurve.com/index.php/2020/05/05/how-to-create-a-confusion-matrix-with-scikit-learn/)
- https://medium.com/python-in-plain-english/how-to-do-eda-with-one-line-of-code-db9a853409d (https://medium.com/python-in-plain-english/how-to-do-eda-with-one-line-of-code-db9a853409d)

In [2]:

```
import pandas as pd
import seaborn as sns
import pandas_profiling
from sklearn.model_selection import train_test_split
```

In [2]:

```
# Ignore competability warnings
import warnings
warnings.filterwarnings('ignore')

# Option to show all the DataFrame columns
pd.options.display.max_columns = None

data = pd.read_csv("mushrooms.csv")
print(data.shape)
```

```
(8124, 23)
```

Exploratory Data Analysis

In [3]:

```
data.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
```

In [4]:

```
data.describe()
```

Out[4]:

	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	gill-color	stalk-shape
count	8124	8124	8124	8124	8124	8124	8124	8124	8124	8124	8124
unique	2	6	4	10	2	9	2	2	2	12	2
top	e	x	y	n	f	n	f	c	b	b	t
freq	4208	3656	3244	2284	4748	3528	7914	6812	5612	1728	4608

In [5]:

```
data.head()
```

Out[5]:

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

In [6]:

```
data.tail()
```

Out[6]:

	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	gill-color	stalk-shape	st r
8119	e	k	s	n	f	n	a	c	b	y	e	
8120	e	x	s	n	f	n	a	c	b	y	e	
8121	e	f	s	n	f	n	a	c	b	n	e	
8122	p	k	y	n	f	y	f	c	n	b	t	
8123	e	x	s	n	f	n	a	c	b	y	e	

In [7]:

```
# Check for missing values in each column
data.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 [9]:

```
# performing EDA using pandas-profiling
profile = pandas_profiling.ProfileReport(data)

profile
```

```
HBox(children=(FloatProgress(value=0.0, description='Summarize datase
t', max=37.0, style=ProgressStyle(descrip…
```

```
HBox(children=(FloatProgress(value=0.0, description='Generate report s
tructure', max=1.0, style=ProgressStyle(…
```

```
HBox(children=(FloatProgress(value=0.0, description='Render HTML', max
=1.0, style=ProgressStyle(description_wi…
```

Out[9]:

In [8]:

```
# Check the unique target values
data['class'].unique()
```

Out[8]:

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

In [41]:

```
data.columns
```

Out[41]:

```
Index(['class', 'cap-shape', 'cap-surface', 'cap-color', 'bruises', 'o
dor',
       'gill-attachment', 'gill-spacing', 'gill-size', 'gill-color',
       'stalk-shape', 'stalk-root', 'stalk-surface-above-ring',
       'stalk-surface-below-ring', 'stalk-color-above-ring',
       'stalk-color-below-ring', 'veil-type', 'veil-color', 'ring-numb
er',
       'ring-type', 'spore-print-color', 'population', 'habitat'],
      dtype='object')
```

In [45]:

```
# Check sample count per class type
group_class = data.groupby('class')['cap-shape'].count()
print(group_class)
```

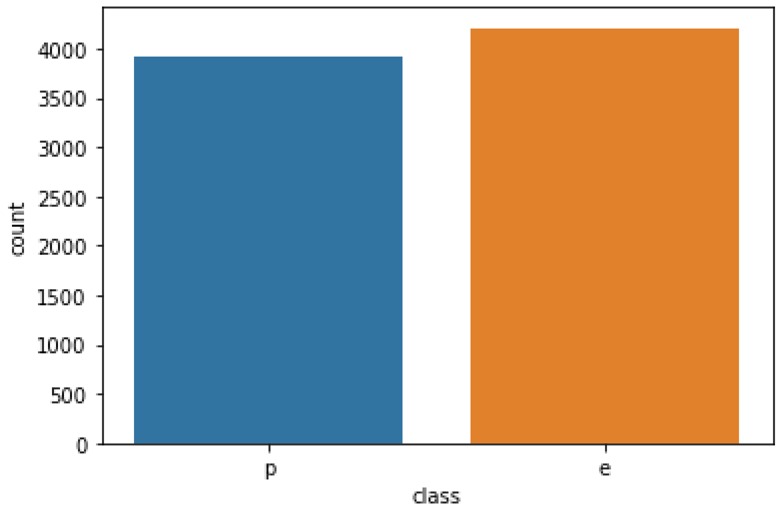
```
class
e    4208
p    3916
Name: cap-shape, dtype: int64
```

In [39]:

```
sns.countplot(data["class"])
```

Out[39]:

```
<AxesSubplot:xlabel='class', ylabel='count'>
```



In [33]:

```
# Not all relationships are symetrical, please read the following article
# https://towardsdatascience.com/rip-correlation-introducing-the-predictive-power-s
# The Predictive Power Score PPS may give us a better understanding
# of the categorical columns and their relationships

# If you dont have the lib - pip install ppscore
import ppscore as pps

# Create a matrix with all the results
pps_matrix = pps.matrix(data)
pps_matrix
```

Out[33]:

	class	cap-shape	cap-surface	cap-color	bruises	
class	1.000000e+00	0.000000e+00	1.160554e-01	1.611613e-01	4.791250e-01	9.70762
cap-shape	0.000000e+00	1.000000e+00	0.000000e+00	5.509413e-02	0.000000e+00	3.47662
cap-surface	0.000000e+00	1.811773e-03	1.000000e+00	2.051615e-01	0.000000e+00	1.55230
cap-color	0.000000e+00	3.411803e-02	3.382085e-02	1.000000e+00	0.000000e+00	2.09631
bruises	4.840616e-01	0.000000e+00	0.000000e+00	9.532663e-02	1.000000e+00	5.38717
odor	4.075156e-01	0.000000e+00	0.000000e+00	1.663641e-01	1.590353e-01	1.000000
gill-attachment	0.000000e+00	0.000000e+00	0.000000e+00	0.000000e+00	0.000000e+00	5.74460
gill-spacing	2.232028e-07	2.232028e-07	6.290731e-03	2.254455e-03	2.232028e-07	3.09824
gill-size	4.441454e-01	2.724207e-01	0.000000e+00	3.035336e-01	0.000000e+00	7.16691
gill-color	4.082435e-02	4.445877e-02	2.051044e-02	1.378161e-01	4.756018e-02	9.50485
stalk-shape	0.000000e+00	6.041573e-02	0.000000e+00	4.608734e-01	0.000000e+00	4.92750
stalk-root	0.000000e+00	2.866848e-01	2.331680e-01	3.374081e-01	2.283180e-01	4.87527
stalk-surface-above-ring	4.092593e-01	0.000000e+00	0.000000e+00	2.083670e-01	3.606962e-01	5.02312
stalk-surface-below-ring	3.559794e-01	0.000000e+00	1.069402e-07	2.374917e-01	3.053013e-01	4.72292
stalk-color-above-ring	1.057122e-07	1.057122e-07	1.057122e-07	1.057122e-07	1.057122e-07	2.03596
stalk-color-below-ring	0.000000e+00	0.000000e+00	0.000000e+00	5.372200e-03	0.000000e+00	1.67612
veil-type	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00	1.000000e+00	1.000000
veil-color	7.749480e-07	7.749480e-07	7.749480e-07	7.749480e-07	7.749480e-07	7.74948
ring-number	0.000000e+00	0.000000e+00	0.000000e+00	8.250109e-02	0.000000e+00	6.87380
ring-type	2.960125e-01	1.384185e-01	1.207734e-01	3.192065e-01	4.378510e-01	5.74256

class	cap-shape	cap-surface	cap-color	bruises

In [34]:

```
# Slice the data frame as we are interested only in the class column:
df_class_ppx = pps_matrix['class']
df_class_ppx
```

Out[34]:

```
class                       1.000000e+00
cap-shape                   0.000000e+00
cap-surface                 0.000000e+00
cap-color                   0.000000e+00
bruises                     4.840616e-01
odor                        4.075156e-01
gill-attachment             0.000000e+00
gill-spacing                2.232028e-07
gill-size                   4.441454e-01
gill-color                  4.082435e-02
stalk-shape                 0.000000e+00
stalk-root                  0.000000e+00
stalk-surface-above-ring    4.092593e-01
stalk-surface-below-ring    3.559794e-01
stalk-color-above-ring      1.057122e-07
stalk-color-below-ring      0.000000e+00
veil-type                   1.000000e+00
veil-color                  7.749480e-07
ring-number                 0.000000e+00
ring-type                   2.960125e-01
spore-print-color           8.515901e-02
population                  0.000000e+00
habitat                     0.000000e+00
Name: class, dtype: float64
```

In [36]:

```
# We are interested in only one column - class: pps.score(df, "feature_column", "ta
pps.score(data, 'odor', 'class')
```

Out[36]:

```
{'x': 'odor',
 'y': 'class',
 'task': 'classification',
 'ppscore': 0.9707622818773931,
 'metric': 'weighted F1',
 'baseline_score': 0.514,
 'model_score': 0.9857904689924131,
 'model': DecisionTreeClassifier()}
```

In [37]:

```
pps.score(data, 'habitat', 'class')
```

Out[37]:

```
{'x': 'habitat',
 'y': 'class',
 'task': 'classification',
 'ppscore': 0.3499142505367472,
 'metric': 'weighted F1',
 'baseline_score': 0.4972,
 'model_score': 0.6731368851698765,
 'model': DecisionTreeClassifier()}
```

Data Encoding and Preparation

In [56]:

```
data.columns
```

Out[56]:

```
Index(['class', 'cap-shape', 'cap-surface', 'cap-color', 'bruises', 'o
dor',
       'gill-attachment', 'gill-spacing', 'gill-size', 'gill-color',
       'stalk-shape', 'stalk-root', 'stalk-surface-above-ring',
       'stalk-surface-below-ring', 'stalk-color-above-ring',
       'stalk-color-below-ring', 'veil-type', 'veil-color', 'ring-numb
er',
       'ring-type', 'spore-print-color', 'population', 'habitat'],
      dtype='object')
```

In [59]:

```
data.shape
```

Out[59]:

```
(8124, 23)
```

In [58]:

```
# Encode all the categorical columns without the target class
df_encoded = pd.get_dummies(data=data, columns=['cap-shape', 'cap-surface', 'cap-co
       'gill-attachment', 'gill-spacing', 'gill-size', 'gill-color',
       'stalk-shape', 'stalk-root', 'stalk-surface-above-ring',
       'stalk-surface-below-ring', 'stalk-color-above-ring',
       'stalk-color-below-ring', 'veil-type', 'veil-color', 'ring-number',
       'ring-type', 'spore-print-color', 'population', 'habitat'])
```

In [60]:

```
df_encoded.shape
```

Out[60]:

```
(8124, 118)
```

In [61]:

```
df_encoded.head()
```

Out[61]:

	class	cap-shape_b	cap-shape_c	cap-shape_f	cap-shape_k	cap-shape_s	cap-shape_x	cap-surface_f	cap-surface_g	surfa
0	p	0	0	0	0	0	1	0	0	
1	e	0	0	0	0	0	1	0	0	
2	e	1	0	0	0	0	0	0	0	
3	p	0	0	0	0	0	1	0	0	
4	e	0	0	0	0	0	1	0	0	

In [62]:

```
# Split the data into train and test data frames
X = df_encoded.drop(columns=['class']).copy()
y = df_encoded['class'].copy()
print(X.shape)
print(y.shape)

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

```
(8124, 117)
(8124,)
```

In [63]:

```
X_train
```

Out[63]:

	cap-shape_b	cap-shape_c	cap-shape_f	cap-shape_k	cap-shape_s	cap-shape_x	cap-surface_f	cap-surface_g	cap-surface_s
6105	0	0	1	0	0	0	0	0	0
7073	0	0	1	0	0	0	0	0	1
1439	0	0	0	0	0	1	0	0	1
4749	0	0	0	0	0	1	1	0	0
2434	0	0	0	0	0	1	1	0	0
...	...	...	...	...	...	...	...	...	...
2581	0	0	0	0	0	1	0	0	0
7045	0	0	1	0	0	0	0	0	0
7257	0	0	0	1	0	0	0	0	0
3737	0	0	0	0	0	1	1	0	0
2878	0	0	1	0	0	0	1	0	0

6905 rows × 117 columns

In [64]:

```
len(y_train)
```

Out[64]:

6905

Machine Learning and Evaluation

In [114]:

```
import numpy as np
from sklearn.svm import LinearSVC
from sklearn.naive_bayes import MultinomialNB
from sklearn.ensemble import BaggingClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import confusion_matrix
from sklearn.metrics import plot_confusion_matrix
import matplotlib.pyplot as plt
```

Naive Bayes

In [115]:

```
mnb = MultinomialNB().fit(X_train, y_train)

print("score on test: " + str(mnb.score(X_test, y_test)))
print("score on train: "+ str(mnb.score(X_train, y_train)))
```

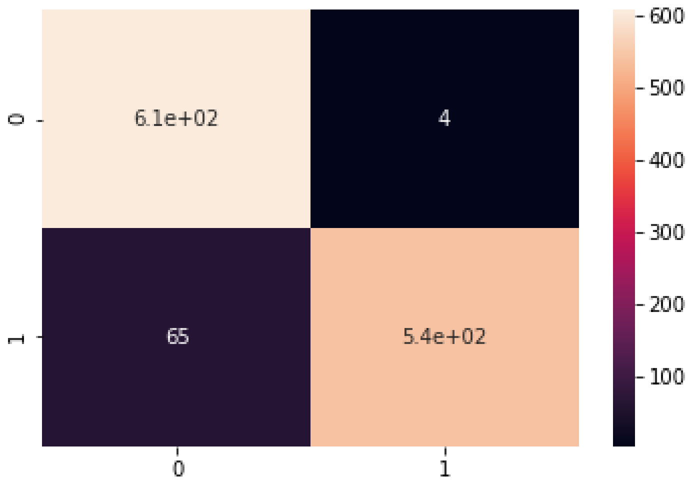
```
score on test: 0.9433962264150944
score on train: 0.9546705286024619
```

In [116]:

```
#Get the confusion matrix
y_pred = mnb.predict(X_test)
cf_matrix = confusion_matrix(y_test, y_pred)
sns.heatmap(cf_matrix, annot=True)
```

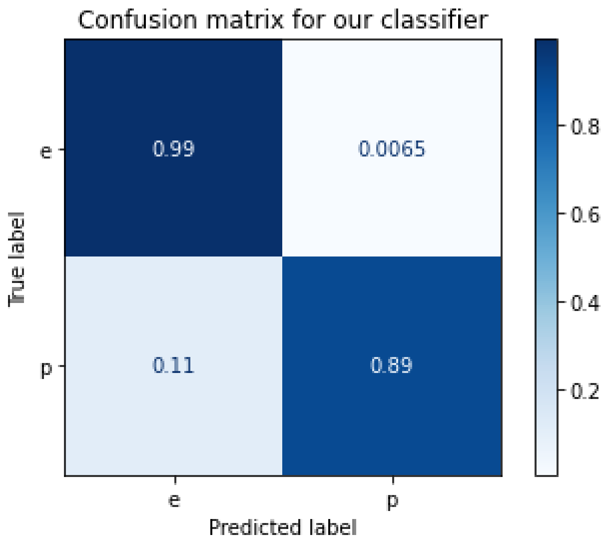
Out[116]:

```
<AxesSubplot:>
```



In [117]:

```
# Generate confusion matrix with labels
matrix = plot_confusion_matrix(mnb, X_test, y_test,
                                 cmap=plt.cm.Blues,
                                 normalize='true')
plt.title('Confusion matrix for our classifier')
plt.show(matrix)
plt.show()
```



Support Vector Machine SVM

In [118]:

```
svm=LinearSVC(C=0.0001)
svm.fit(X_train, y_train)

print("score on test: " + str(svm.score(X_test, y_test)))
print("score on train: "+ str(svm.score(X_train, y_train)))
```

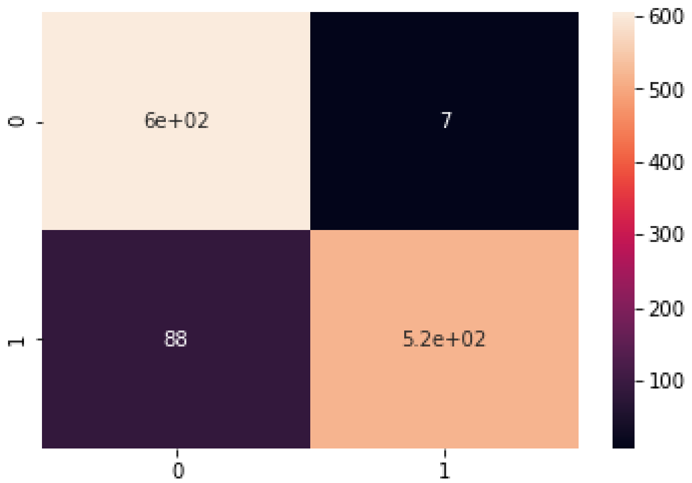
```
score on test: 0.9220672682526662
score on train: 0.9267197682838523
```

In [119]:

```
#Get the confusion matrix
y_pred = svm.predict(X_test)
cf_matrix = confusion_matrix(y_test, y_pred)
sns.heatmap(cf_matrix, annot=True)
```

Out[119]:

```
<AxesSubplot:>
```



Bagging Decision Tree

In [121]:

```
# max_samples: maximum size 0.5=50% of each sample taken from the full dataset
# max_features: maximum of features 1=100% taken here all 10K
# n_estimators: number of decision trees
bg=BaggingClassifier(DecisionTreeClassifier(),max_samples=0.5,max_features=1.0,n_es
bg.fit(X_train, y_train)
print("score on test: " + str(bg.score(X_test, y_test)))
print("score on train: "+ str(bg.score(X_train, y_train)))
```

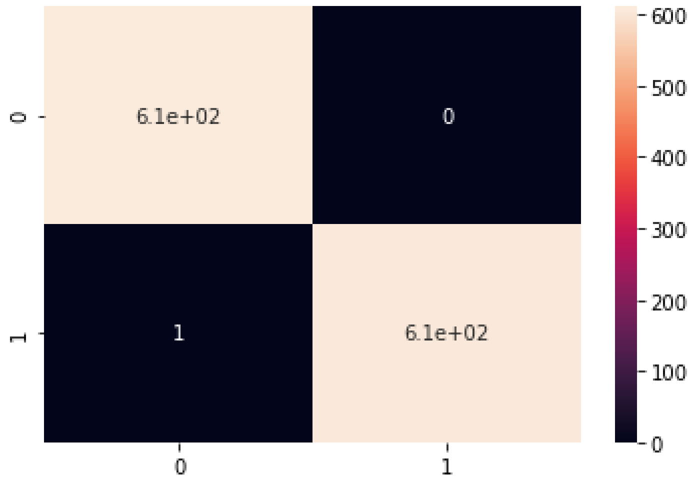
```
score on test: 0.9991796554552912
score on train: 0.9998551774076756
```

In [122]:

```
#Get the confusion matrix
y_pred = bg.predict(X_test)
cf_matrix = confusion_matrix(y_test, y_pred)
sns.heatmap(cf_matrix, annot=True)
```

Out[122]:

```
<AxesSubplot:>
```



ML Tests - Algorithms overfitting the data

Logistic Regression = OVERFITTING!

In [123]:

```
from sklearn.linear_model import LogisticRegression

lr=LogisticRegression(max_iter=1000)
lr.fit(X_train, y_train)

print("score on test: " + str(lr.score(X_test, y_test)))
print("score on train: "+ str(lr.score(X_train, y_train)))
```

```
score on test: 1.0
score on train: 1.0
```

Decision Tree = OVERFITTING!

In [124]:

```
clf = DecisionTreeClassifier()
clf.fit(X_train, y_train)

print("score on test: "  + str(clf.score(X_test, y_test)))
print("score on train: " + str(clf.score(X_train, y_train)))
```

```
score on test: 1.0
score on train: 1.0
```

XGBoost = OVERFITTING!

In [125]:

```
from xgboost import XGBClassifier
from sklearn.metrics import accuracy_score
```

In [126]:

```
# fit model to training data
model = XGBClassifier()
model.fit(X_train, y_train)
```

Out[126]:

```
XGBClassifier()
```

In [127]:

```
# make predictions for test data
y_pred = model.predict(X_test)
```

In [128]:

```
# evaluate predictions
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy: %.2f%%" % (accuracy * 100.0))
```

```
Accuracy: 100.00%
```

AdaBoost = OVERFITTING!

In [129]:

```
from sklearn.ensemble import AdaBoostClassifier
from sklearn.tree import DecisionTreeClassifier

adb = AdaBoostClassifier(DecisionTreeClassifier(min_samples_split=10,max_depth=4),n
adb.fit(X_train, y_train)

print("score on test: " + str(adb.score(X_test, y_test)))
print("score on train: "+ str(adb.score(X_train, y_train)))
```

```
score on test: 1.0
score on train: 1.0
```

Random Forest = OVERFITTING!

In [130]:

```
from sklearn.ensemble import RandomForestClassifier
# n_estimators = number of decision trees
rf = RandomForestClassifier(n_estimators=30, max_depth=9)
rf.fit(X_train, y_train)
print("score on test: " + str(rf.score(X_test, y_test)))
print("score on train: "+ str(rf.score(X_train, y_train)))
```

```
score on test: 1.0
score on train: 1.0
```

Final ML choice

In [110]:

```
from sklearn.ensemble import VotingClassifier
# 1) naive bias = mnb
# 2) logistic regression =lr
# 3) random forest =rf
# 4) support vector machine = svm
evc=VotingClassifier(estimators=[('mnb',mnb),('lr',lr),('rf',rf),('svm',svm)],votin
evc.fit(X_train, y_train)
print("score on test: " + str(evc.score(X_test, y_test)))
print("score on train: "+ str(evc.score(X_train, y_train)))
```

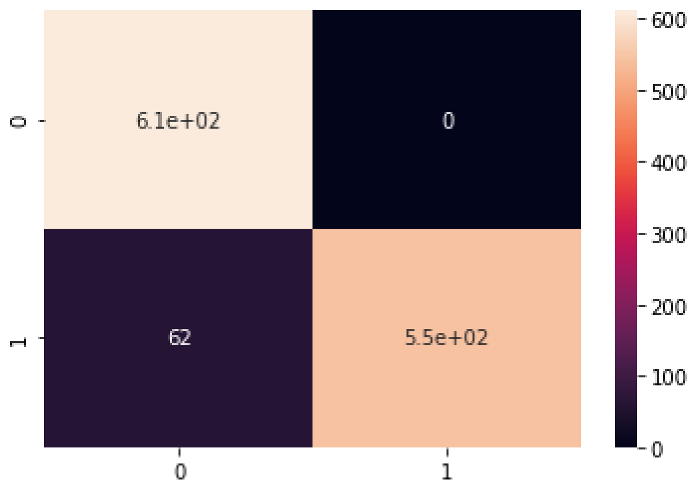
```
score on test: 0.9491386382280558
score on train: 0.9590152063721941
```

In [111]:

```
#Get the confusion matrix
y_pred = evc.predict(X_test)
cf_matrix = confusion_matrix(y_test, y_pred)
sns.heatmap(cf_matrix, annot=True)
```

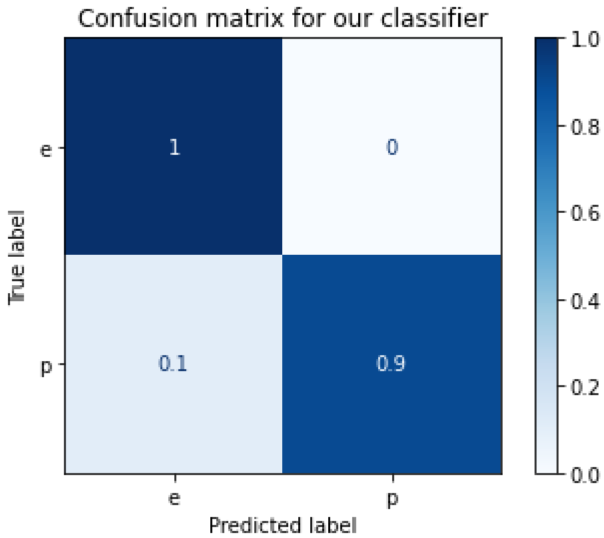
Out[111]:

```
<AxesSubplot:>
```



In [112]:

```
# Generate confusion matrix with labels
matrix = plot_confusion_matrix(evc, X_test, y_test,
                               cmap=plt.cm.Blues,
                               normalize='true')
plt.title('Confusion matrix for our classifier')
plt.show(matrix)
plt.show()
```



NOTE: Possible descrease of the False Negative predictions with NN

Test Env

In [3]:

```
# Naive Bayes
# Bagging Decision Tree
# Voting Classifier

# Fill in the mushroom data
test_data = {
        'cap-shape': ['b']
    }
df_test = pd.DataFrame(test_data)
print(df_test)
```

```
  cap-shape
0         b
```

In [ ]:

```
df_test_encoded = pd.get_dummies(data=df_test, columns=['cap-shape', 'cap-surface',
            'gill-attachment', 'gill-spacing', 'gill-size', 'gill-color',
            'stalk-shape', 'stalk-root', 'stalk-surface-above-ring',
            'stalk-surface-below-ring', 'stalk-color-above-ring',
            'stalk-color-below-ring', 'veil-type', 'veil-color', 'ring-number',
            'ring-type', 'spore-print-color', 'population', 'habitat'])
```

In [ ]:

```
y_pred = svm.predict(df_test_encodedt)
print(y_pred)
```