

shroomies

December 16, 2022

```
[1]: # Used libraries
import numpy as np
import pandas as pd
import seaborn as sns
import missingno as msn
import matplotlib.pyplot as plt
import os
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import classification_report, confusion_matrix
from sklearn import tree

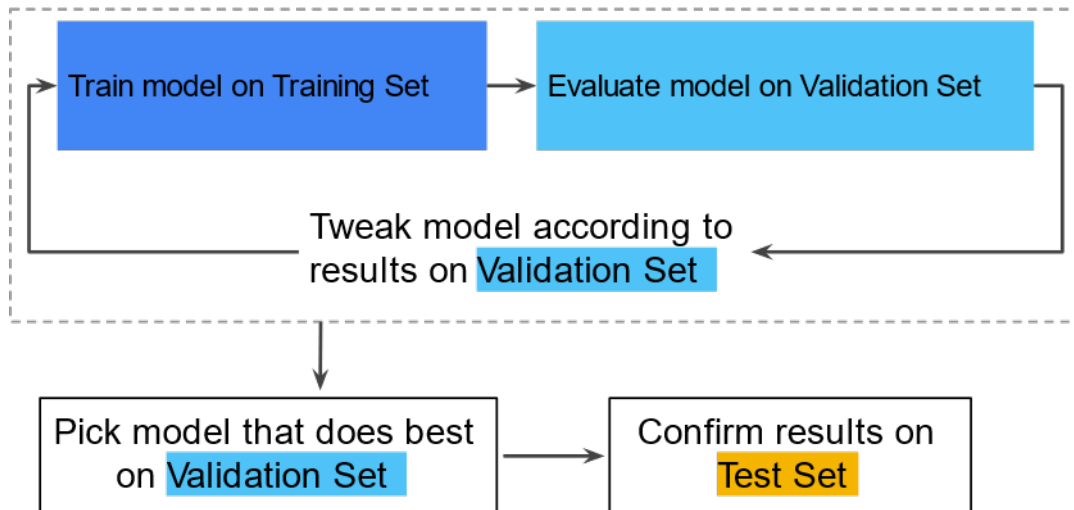
# Jupyter configs
%matplotlib inline
pd.set_option('display.max_columns', None)
import warnings
warnings.filterwarnings('ignore')
```

1 The Seen/Unseen split (aka the Test split)

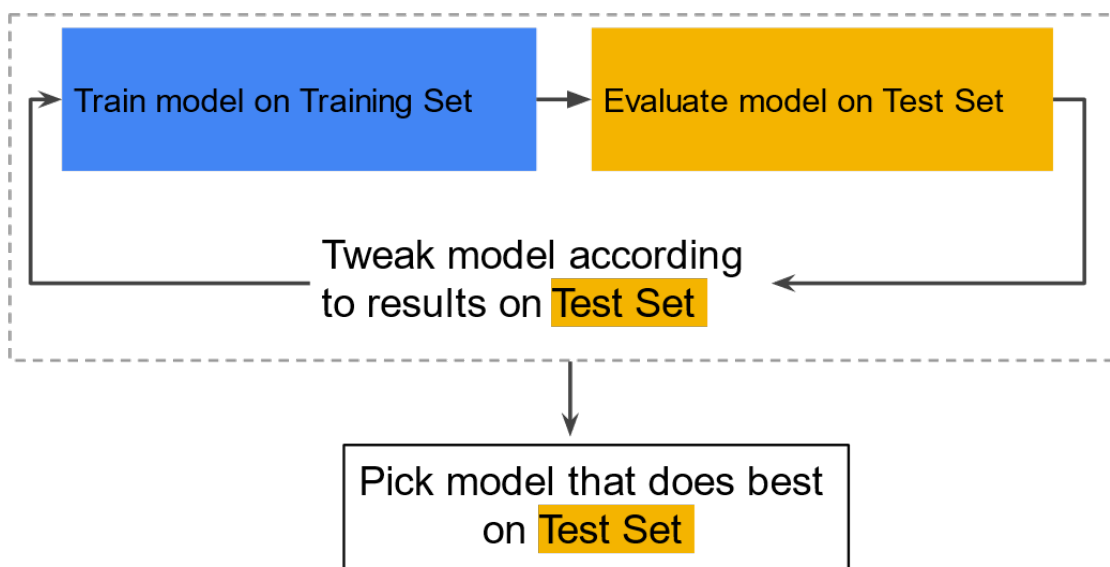
```
[2]: df = pd.read_csv('mushrooms.csv')
df_train, df_test = train_test_split(df, test_size=0.2, random_state=42)
print('Train size:', df_train.shape)
print('Test size:', df_test.shape)
```

Train size: (6499, 23)

Test size: (1625, 23)



2



```
[3]: df_test.to_csv('test_split.csv', index=False)
      df_train.to_csv('train_split.csv', index=False)
```

3 A first good glance at the data

```
[4]: df_train.head()
```

```
[4]:   class cap-shape cap-surface cap-color bruises odor gill-attachment \
7873    p      k          s      e    f    s          f
6515    p      x          s      n    f    f          f
6141    p      f          y      e    f    y          f
```

2764	e	f	f	n	t	n	f
438	e	b	y	y	t	l	f

	gill-spacing	gill-size	gill-color	stalk-shape	stalk-root	\
7873	c	n	b	t	?	
6515	c	n	b	t	?	
6141	c	n	b	t	?	
2764	c	b	u	t	b	
438	c	b	k	e	c	

	stalk-surface-above-ring	stalk-surface-below-ring	stalk-color-above-ring	\
7873		s	k	p
6515		k	s	w
6141		s	s	p
2764		s	s	g
438		s	s	w

	stalk-color-below-ring	veil-type	veil-color	ring-number	ring-type	\
7873		w	p	w	o	e
6515		w	p	w	o	e
6141		w	p	w	o	e
2764		p	p	w	o	p
438		w	p	w	o	p

	spore-print-color	population	habitat
7873	w	v	d
6515	w	v	p
6141	w	v	l
2764	n	v	d
438	n	n	m

```
[5]: df_train.tail()
```

```
[5]:
```

	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	\
5226	p	x	y	n	f	f	f	
5390	e	k	y	e	t	n	f	
860	e	f	y	n	t	l	f	
7603	p	k	s	e	f	f	f	
7270	e	k	f	g	f	n	f	

	gill-spacing	gill-size	gill-color	stalk-shape	stalk-root	\
5226	c	n	b	t	?	
5390	c	b	w	e	?	
860	c	b	w	e	r	
7603	c	n	b	t	?	
7270	w	b	g	e	?	

	stalk-surface-above-ring	stalk-surface-below-ring	stalk-color-above-ring	\
5226	k	s	p	
5390	s	s	w	
860	s	y	w	
7603	s	s	p	
7270	s	k	w	

	stalk-color-below-ring	veil-type	veil-color	ring-number	ring-type	\
5226	w	p	w	o	e	
5390	e	p	w	t	e	
860	w	p	w	o	p	
7603	p	p	w	o	e	
7270	w	p	w	t	p	

	spore-print-color	population	habitat
5226	w	v	p
5390	w	c	w
860	n	y	p
7603	w	v	p
7270	w	n	g

```
[6]: df_train.sample(5)
```

```
[6]:
```

	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	\
2045	e	x	y	y	t	a	f	
1258	e	f	s	w	f	n	f	
5134	e	k	s	n	t	n	f	
727	e	x	f	w	f	n	f	
5131	p	b	f	y	f	n	f	

	gill-spacing	gill-size	gill-color	stalk-shape	stalk-root	\
2045	c	b	p	e	r	
1258	w	b	h	t	e	
5134	c	b	w	e	?	
727	w	b	h	t	e	
5131	c	n	w	e	?	

	stalk-surface-above-ring	stalk-surface-below-ring	stalk-color-above-ring	\
2045	s	y	w	
1258	f	s	w	
5134	s	s	e	
727	f	s	w	
5131	k	y	w	

	stalk-color-below-ring	veil-type	veil-color	ring-number	ring-type	\
2045	w	p	w	o	p	
1258	w	p	w	o	e	

5134	w	p	w	t	e
727	w	p	w	o	e
5131	y	p	w	o	e

	spore-print-color	population	habitat
2045	n	s	p
1258	n	a	g
5134	w	c	w
727	n	s	g
5131	w	v	d

4

5

6 Exploratory Data Analysis (EDA)

7

7.1 Examining the Data

```
[7]: print('DataSet size:', df_train.shape)
      print()
      print(df_train.dtypes)
```

DataSet size: (6499, 23)

class	object
cap-shape	object
cap-surface	object
cap-color	object
bruises	object
odor	object
gill-attachment	object
gill-spacing	object
gill-size	object
gill-color	object
stalk-shape	object
stalk-root	object
stalk-surface-above-ring	object
stalk-surface-below-ring	object
stalk-color-above-ring	object
stalk-color-below-ring	object
veil-type	object
veil-color	object
ring-number	object
ring-type	object

```

spore-print-color      object
population             object
habitat               object
dtype: object

```

Data Types From A Machine Learning Perspective

```

[8]: for column in df_train.columns:
      print(column, '==>', df_train[column].unique())

```

```

class ==> ['p' 'e']
cap-shape ==> ['k' 'x' 'f' 'b' 's' 'c']
cap-surface ==> ['s' 'y' 'f' 'g']
cap-color ==> ['e' 'n' 'y' 'g' 'w' 'b' 'p' 'r' 'c' 'u']
bruises ==> ['f' 't']
odor ==> ['s' 'f' 'y' 'n' 'l' 'p' 'a' 'c' 'm']
gill-attachment ==> ['f' 'a']
gill-spacing ==> ['c' 'w']
gill-size ==> ['n' 'b']
gill-color ==> ['b' 'u' 'k' 'w' 'e' 'p' 'n' 'y' 'o' 'g' 'h' 'r']
stalk-shape ==> ['t' 'e']
stalk-root ==> ['?' 'b' 'c' 'e' 'r']
stalk-surface-above-ring ==> ['s' 'k' 'f' 'y']
stalk-surface-below-ring ==> ['k' 's' 'f' 'y']
stalk-color-above-ring ==> ['p' 'w' 'g' 'o' 'n' 'e' 'b' 'c' 'y']
stalk-color-below-ring ==> ['w' 'p' 'g' 'n' 'o' 'b' 'e' 'c' 'y']
veil-type ==> ['p']
veil-color ==> ['w' 'n' 'o' 'y']
ring-number ==> ['o' 't' 'n']
ring-type ==> ['e' 'p' 'l' 'n' 'f']
spore-print-color ==> ['w' 'n' 'h' 'k' 'b' 'y' 'u' 'r' 'o']
population ==> ['v' 'n' 'y' 'c' 's' 'a']
habitat ==> ['d' 'p' 'l' 'm' 'w' 'u' 'g']

```

```

[9]: df_train.describe()

```

```

[9]:      class cap-shape cap-surface cap-color bruises  odor gill-attachment \
count    6499      6499      6499      6499    6499  6499              6499
unique      2         6         4         10      2     9                2
top        e         x         y         n      f     n                f
freq     3365     2956     2602     1823    3802  2833              6331

      gill-spacing gill-size gill-color stalk-shape stalk-root \
count          6499      6499      6499      6499      6499
unique           2         2        12         2         5
top             c         b         b         t         b
freq          5451     4496     1398     3702     3007

```

	stalk-surface-above-ring	stalk-surface-below-ring		
count	6499	6499	\	
unique	4	4		
top	s	s		
freq	4119	3944		

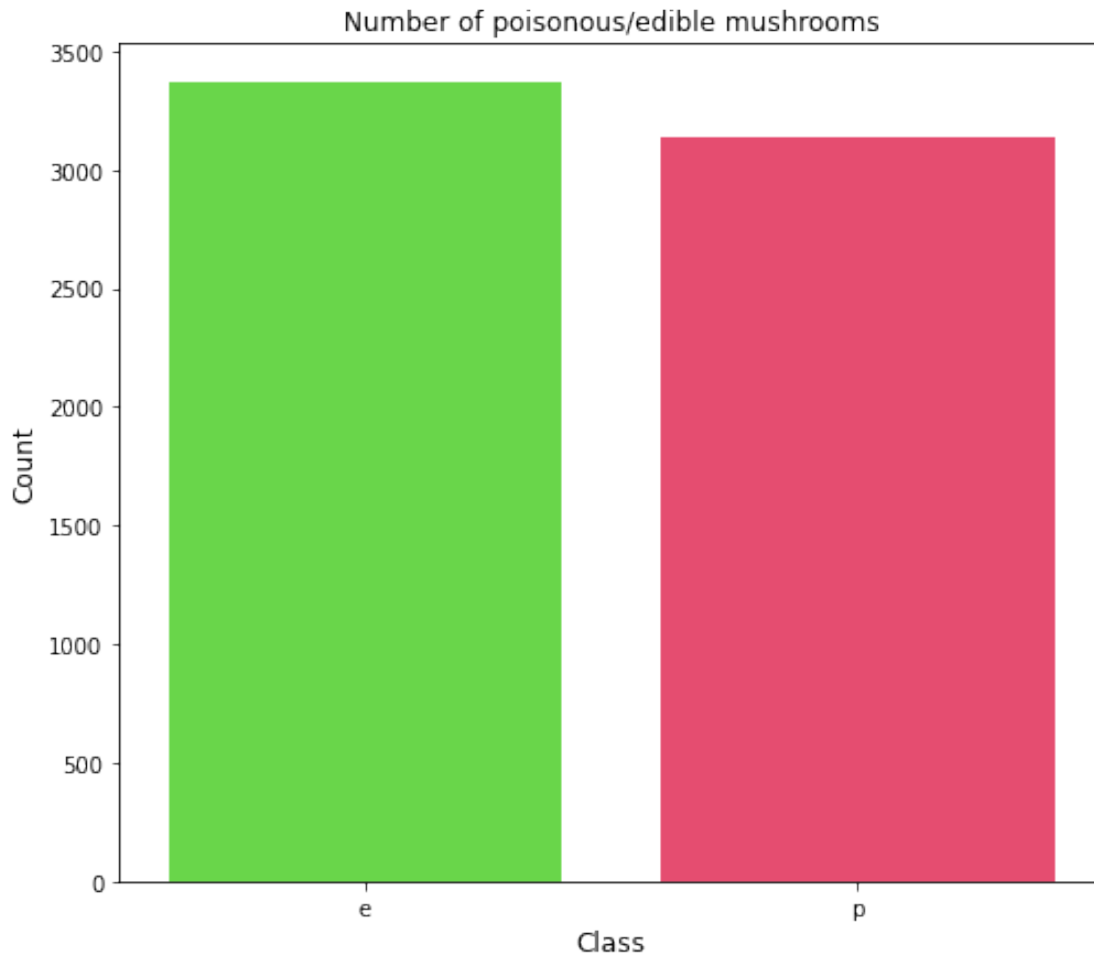
	stalk-color-above-ring	stalk-color-below-ring	veil-type	veil-color	\
count	6499	6499	6499	6499	
unique	9	9	1	4	
top	w	w	p	w	
freq	3573	3502	6499	6340	

	ring-number	ring-type	spore-print-color	population	habitat
count	6499	6499	6499	6499	6499
unique	3	5	9	6	7
top	o	p	w	v	d
freq	5976	3154	1936	3218	2513

7.2 Taking a look at the target feature/labe/classes

... their distribution/balance to be more specific

```
[10]: count = df_train['class'].value_counts()
plt.figure(figsize=(8,7))
sns.barplot(x=count.index, y=count.values, alpha=0.8, palette="prism")
plt.ylabel('Count', fontsize=12)
plt.xlabel('Class', fontsize=12)
plt.title('Number of poisonous/edible mushrooms')
#plt.savefig("mushrooms1.png", format='png', dpi=900)
plt.show()
```



7.3 Missing Values

NaN isn't the only missing value

```
[11]: print('DataSet size:', df_train.shape)
      print()
      print(df_train.info())
```

DataSet size: (6499, 23)

<class 'pandas.core.frame.DataFrame'>

Int64Index: 6499 entries, 7873 to 7270

Data columns (total 23 columns):

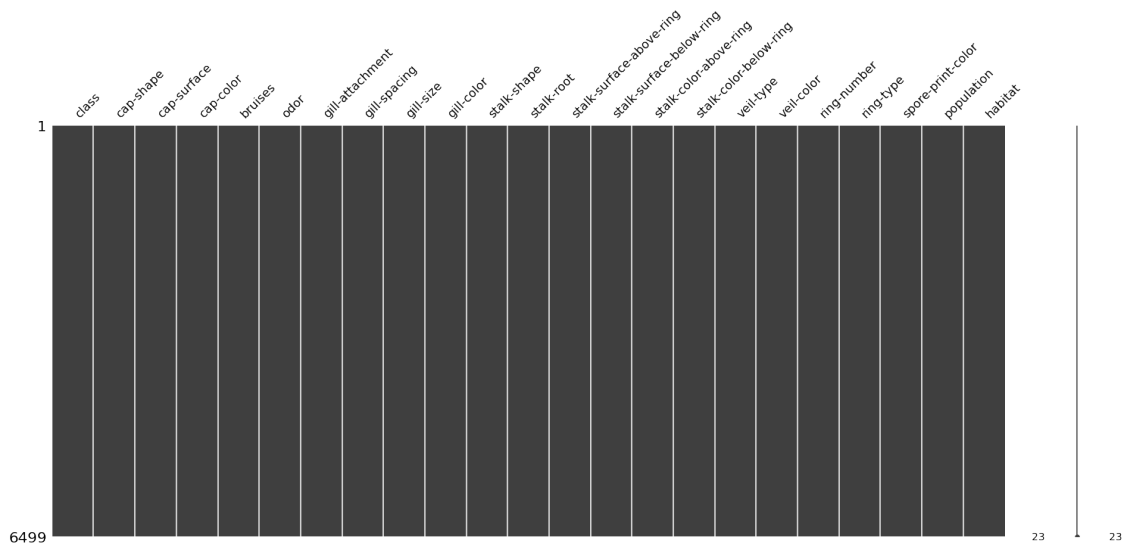
#	Column	Non-Null Count	Dtype
0	class	6499 non-null	object
1	cap-shape	6499 non-null	object
2	cap-surface	6499 non-null	object


```

3   cap-color          6499 non-null object
4   bruises            6499 non-null object
5   odor               6499 non-null object
6   gill-attachment    6499 non-null object
7   gill-spacing       6499 non-null object
8   gill-size          6499 non-null object
9   gill-color         6499 non-null object
10  stalk-shape        6499 non-null object
11  stalk-root         6499 non-null object
12  stalk-surface-above-ring 6499 non-null object
13  stalk-surface-below-ring 6499 non-null object
14  stalk-color-above-ring  6499 non-null object
15  stalk-color-below-ring  6499 non-null object
16  veil-type         6499 non-null object
17  veil-color        6499 non-null object
18  ring-number       6499 non-null object
19  ring-type         6499 non-null object
20  spore-print-color  6499 non-null object
21  population        6499 non-null object
22  habitat           6499 non-null object
dtypes: object(23)
memory usage: 1.2+ MB
None

```

```
[12]: msn.matrix(df_train);
```



```
[13]: print(df_train['stalk-root'].unique())

['?' 'b' 'c' 'e' 'r']

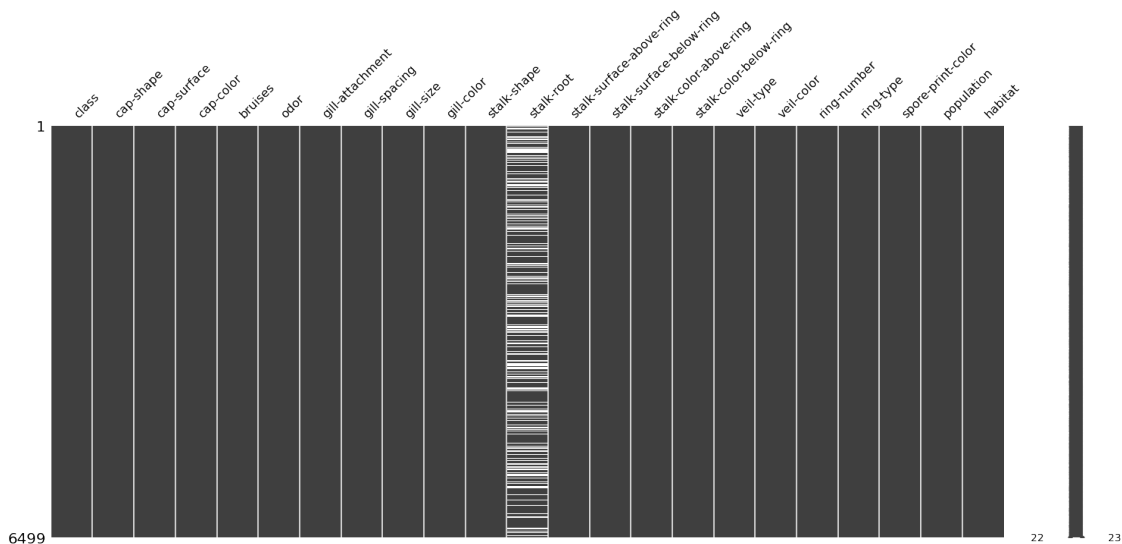
```

```
[14]: def replaceMissing(x):
        if(x=='?'):
            return np.NaN
        else:
            return x

        #df_train['stalk-root'] = df_train['stalk-root'].map(lambda x : np.NaN if x=='?'
        ↪ ' else x)
df_train['stalk-root'] = df_train['stalk-root'].map(replaceMissing)
print(df_train['stalk-root'].unique())
```

```
[nan 'b' 'c' 'e' 'r']
```

```
[15]: msn.matrix(df_train);
```



```
[16]: print("%.2f" % (df_train['stalk-root'].isna().sum()/df_train.shape[0]*100)),
        ↪ '%')
```

```
30.88 %
```

But what about the data we can't see? What do we do if we have missing values there?

7.4 Plotting the data for visualisation

For visualisation purposes ONLY, we encode for the data TEMPORARY using a very simple encoding scheme (ordinal encoding). The data must transformed in a format that allows us to visualise it.

Take the following example/metaphor: We have some text on a piece of paper. The text is written in reverse. We know how to read the text when it is not reversed, and we also know if we use

a mirror, and we reflect the text, we can see it in the correct orientation. So: “Text seems to be reversed” “Mirrors can be used to reverse text” Thus “Mirrors can reverse our reverse text to uncover the message”

The plot is a representation of the data (what we see) The mirror is the transformation you apply to it

Here’s another example of a such transformation.

```
[17]: # Change the dtypes of the data-frame to 'category'. Panda recognises this
      ↪data-type, and it improves compatibility within the data.
df_eval = df_train.astype('category')

# We run a default Label encoding over the categorical features (which for this
      ↪data, it's all the features)
labelencoder=LabelEncoder()
for column in df_eval.columns:
    df_eval[column] = labelencoder.fit_transform(df_eval[column])
df_eval.head()
```

```
[17]:
```

	class	cap-shape	cap-surface	cap-color	bruises	odor	\
7873	1	3	2	2	0	7	
6515	1	5	2	4	0	2	
6141	1	2	3	2	0	8	
2764	0	2	0	4	1	5	
438	0	0	3	9	1	3	

	gill-attachment	gill-spacing	gill-size	gill-color	stalk-shape	\
7873	1	0	1	0	1	
6515	1	0	1	0	1	
6141	1	0	1	0	1	
2764	1	0	0	9	1	
438	1	0	0	4	0	

	stalk-root	stalk-surface-above-ring	stalk-surface-below-ring	\
7873	4	2	1	
6515	4	1	2	
6141	4	2	2	
2764	0	2	2	
438	1	2	2	

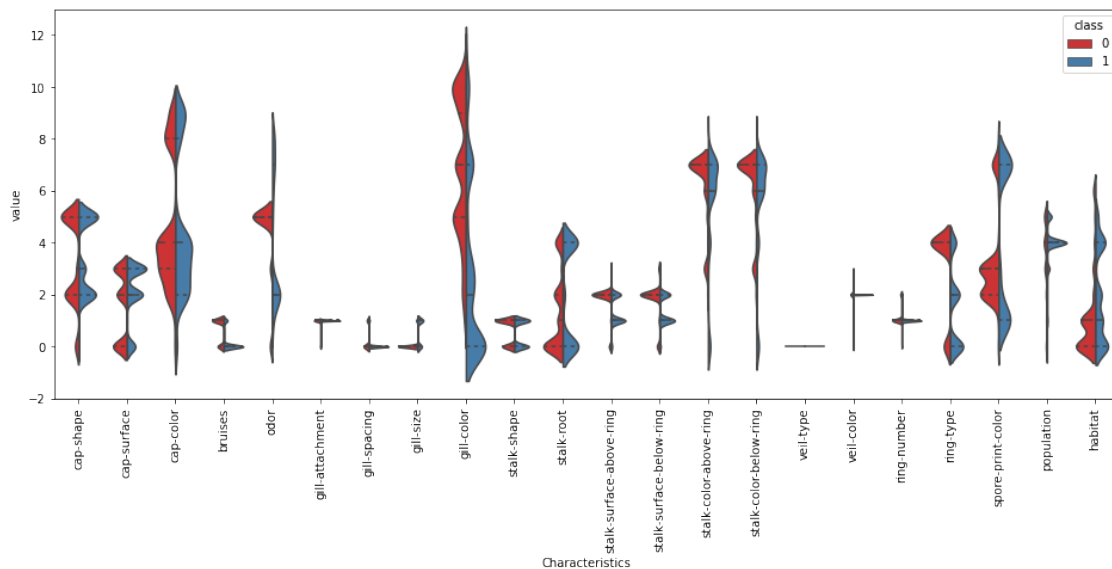
	stalk-color-above-ring	stalk-color-below-ring	veil-type	veil-color	\
7873	6	7	0	2	
6515	7	7	0	2	
6141	6	7	0	2	
2764	3	6	0	2	
438	7	7	0	2	

	ring-number	ring-type	spore-print-color	population	habitat
7873	1	0	7	4	0
6515	1	0	7	4	4
6141	1	0	7	4	2
2764	1	4	3	4	0
438	1	4	3	2	3

7.4.1 Violin Plot

A Violin Plot show the same information as a Box Plot, plus the entire distribution of the data.

```
[18]: df_div = pd.melt(df_eval, "class", var_name="Characteristics")
fig, ax = plt.subplots(figsize=(16,6))
p = sns.violinplot(ax = ax, x="Characteristics", y="value", hue="class", split=True,
    data=df_div, inner = 'quartile', palette = 'Set1')
df_features = df_eval.drop(["class"],axis = 1)
p.set_xticklabels(rotation = 90, labels = list(df_features.columns));
plt.savefig("IMG/violinplot.jpg", format='jpg', dpi=900, bbox_inches='tight')
#plt.savefig("IMG/violinplot.png", format='png', dpi=900, bbox_inches='tight')
```



The violin plot above represents the distribution of the classification characteristics. It allows us to see the distribution of properties per class:

For example, it is possible to see that “gill-color” property of the mushroom breaks to two parts, one below 3 and one above 3, that may contribute to the classification.

Also, is this deduction correlating to the real-life phenomena? What do we know about mushrooms? Are there any facts about mushrooms that can help us identify if it’s edible or not, without the need of a ML model?

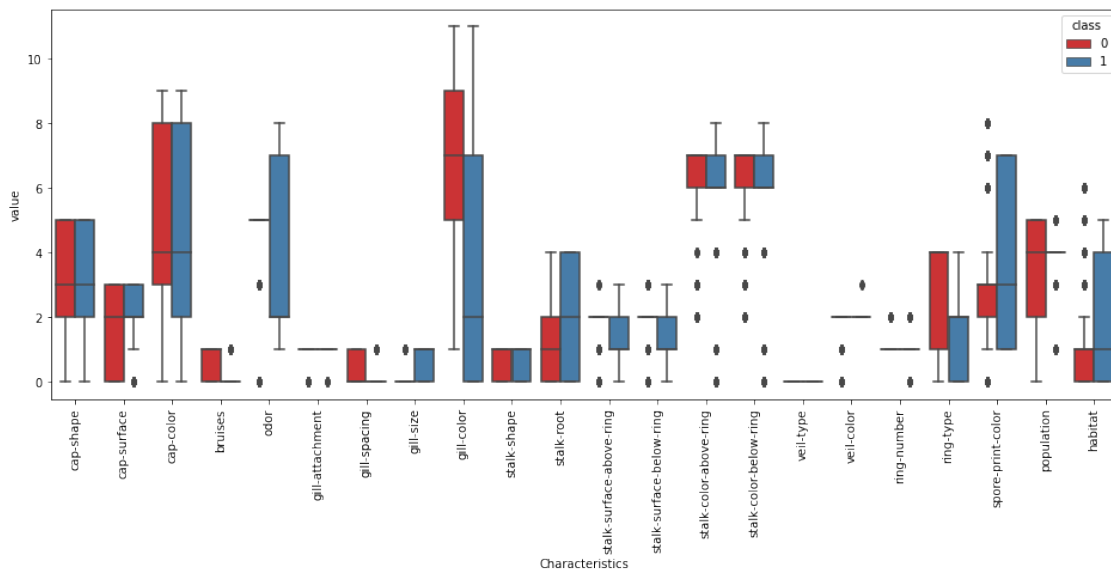
```
[19]: # Let's look at another property, like 'odor'. Does this have any tangent to
      ↪any real-life phenomena?
      pd.DataFrame(data=[df_train['odor'].unique(),df_eval['odor'].unique()])
```

```
[19]:    0  1  2  3  4  5  6  7  8
      0  s  f  y  n  l  p  a  c  m
      1  7  2  8  5  3  6  0  1  4
```

8

8.0.1 Box Plot

```
[20]: fig, ax = plt.subplots(figsize=(16,6))
      p = sns.boxplot(ax = ax, x="Characteristics", y="value", hue="class",
      ↪data=df_div, palette = 'Set1')
      p.set_xticklabels(rotation = 90, labels = list(df_features.columns));
      plt.savefig("IMG/boxplot.jpg", format='jpg', dpi=900, bbox_inches='tight')
      #plt.savefig("IMG/boxplot.png", format='png', dpi=900, bbox_inches='tight')
```



On the Box Plot above it is easier to spot outliers, looking at points that are furthest away from the mean.

9

9.0.1 Correlation matrix

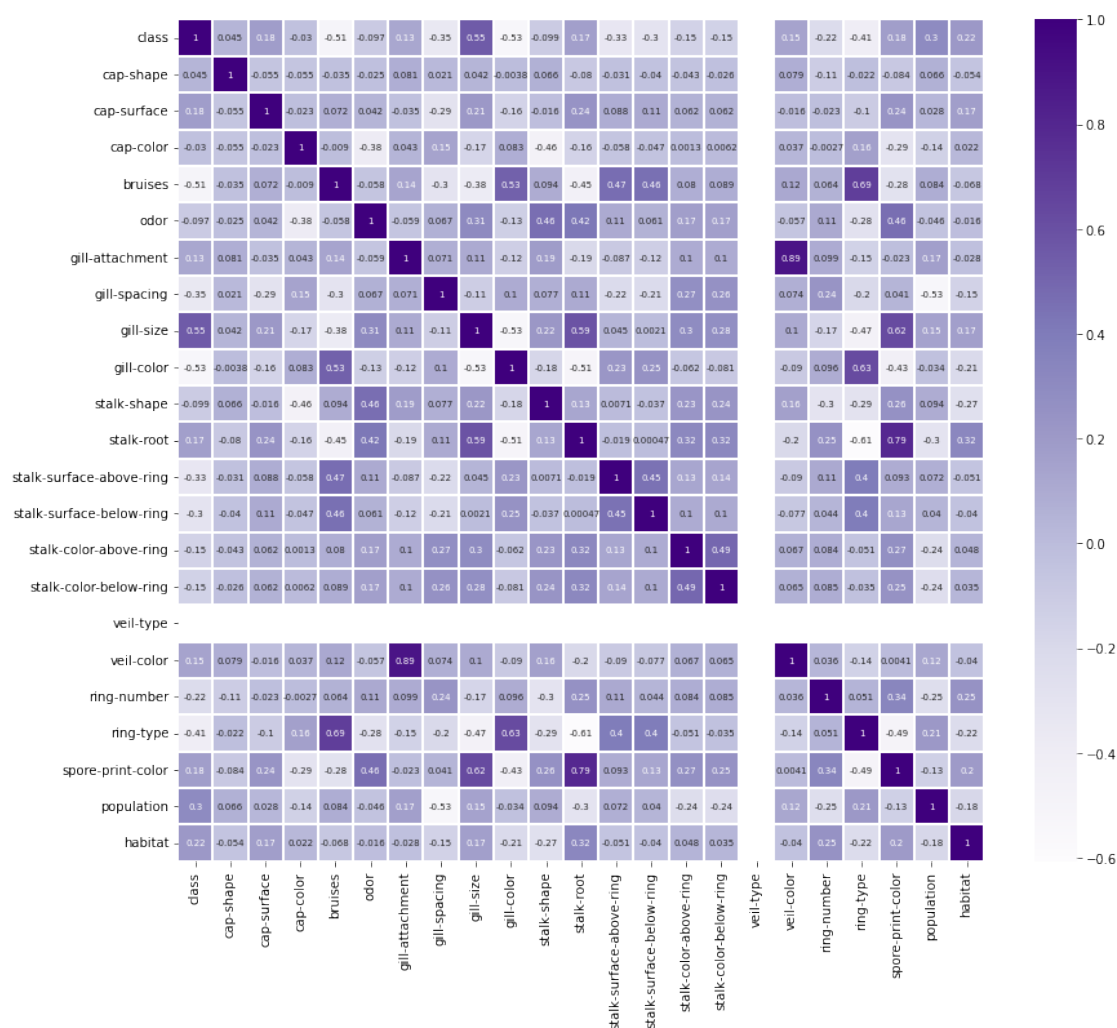
Correlation measures the strength of a relationship between two variables. The correlation coefficient expresses the degree of change in one variable as a function of the change in the other variable.

In other words, if two properties are strongly correlated, when one changes, we expect the other to change in the same manner.

The correlation between two variables can be positive or negative based on the value of the correlation coefficient.

It might be the case that out of these training features, some features are highly correlated. That may introduce redundancy (or noise) in your feature space, so it can indicate which features to drop and still achieve a good result.

```
[21]: plt.figure(figsize=(14,12))
sns.heatmap(df_eval.corr(),linewidths=.1,cmap="Purples", annot=True,
            annot_kws={"size": 7})
plt.xticks(rotation=0);
plt.savefig("IMG/corr.jpg", format='jpg', dpi=900, bbox_inches='tight')
#plt.savefig("IMG/corr.png", format='png', dpi=900, bbox_inches='tight')
```



We are seeing some really strong correlations between properties and some significant ones between features and the target label.

```
[22]: # For example, 'gill-attachment' and 'veil-color' are strongly correlated.  
print(df_train['veil-color'].unique())  
print(df_train['gill-attachment'].unique())  
df_train[['veil-color', 'gill-attachment']].sample(25)
```

```
['w' 'n' 'o' 'y']  
['f' 'a']
```

```
[22]:      veil-color gill-attachment  
1052          w                f  
1458          w                f  
5892          w                f  
7810          w                f  
3894          w                f  
6195          w                f  
6526          w                f  
3481          w                f  
300           w                f  
4242          w                f  
4948          w                f  
3462          w                f  
1722          w                f  
2197          w                f  
4746          w                f  
3971          w                f  
2967          w                f  
4829          w                f  
1958          w                f  
3744          w                f  
3690          w                f  
539           w                f  
6335          w                f  
5648          w                f  
275           w                f
```

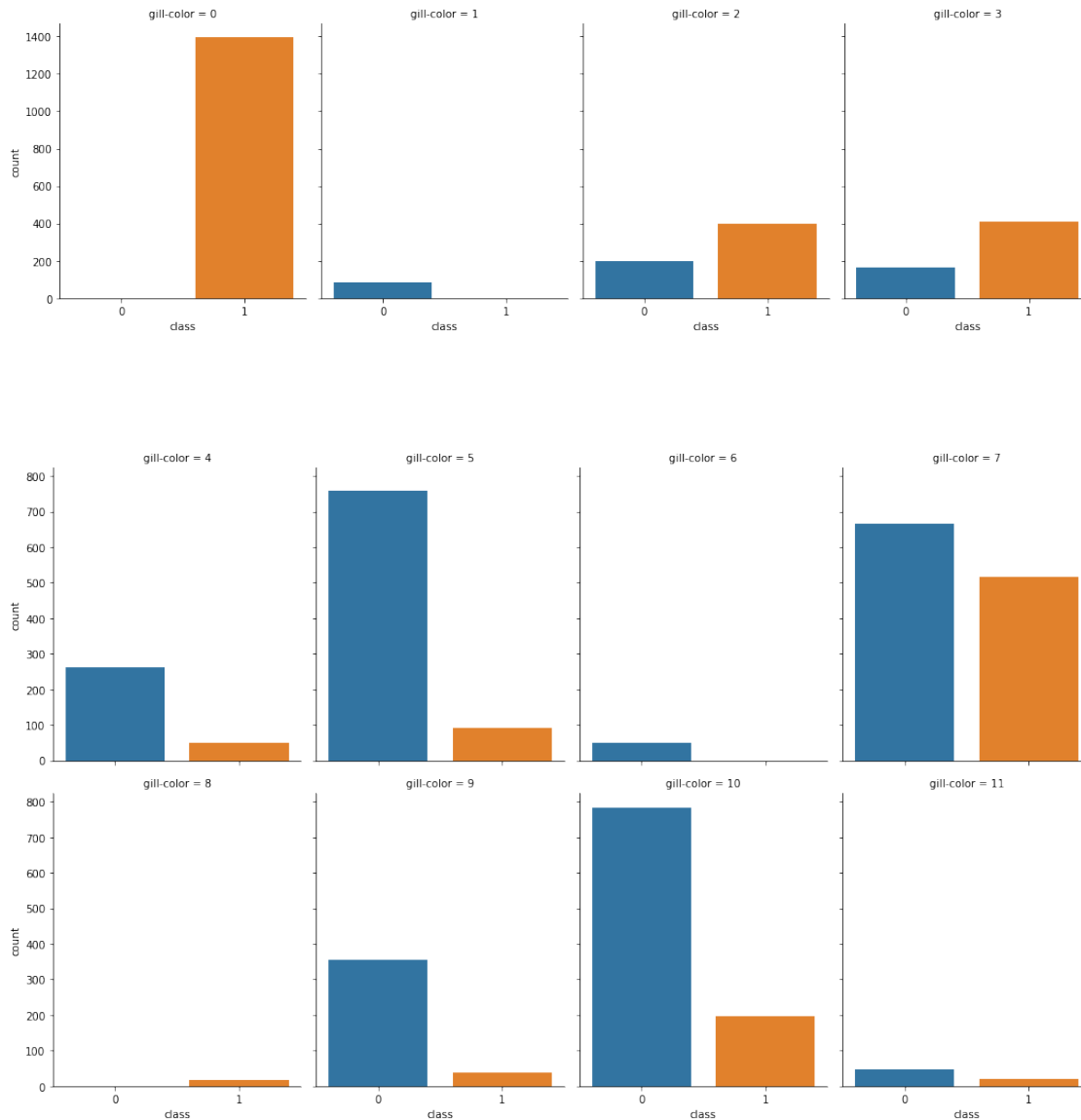
10

11

What about correlation between a feature and the target label? Let's take a closer look at 'gil-color'.

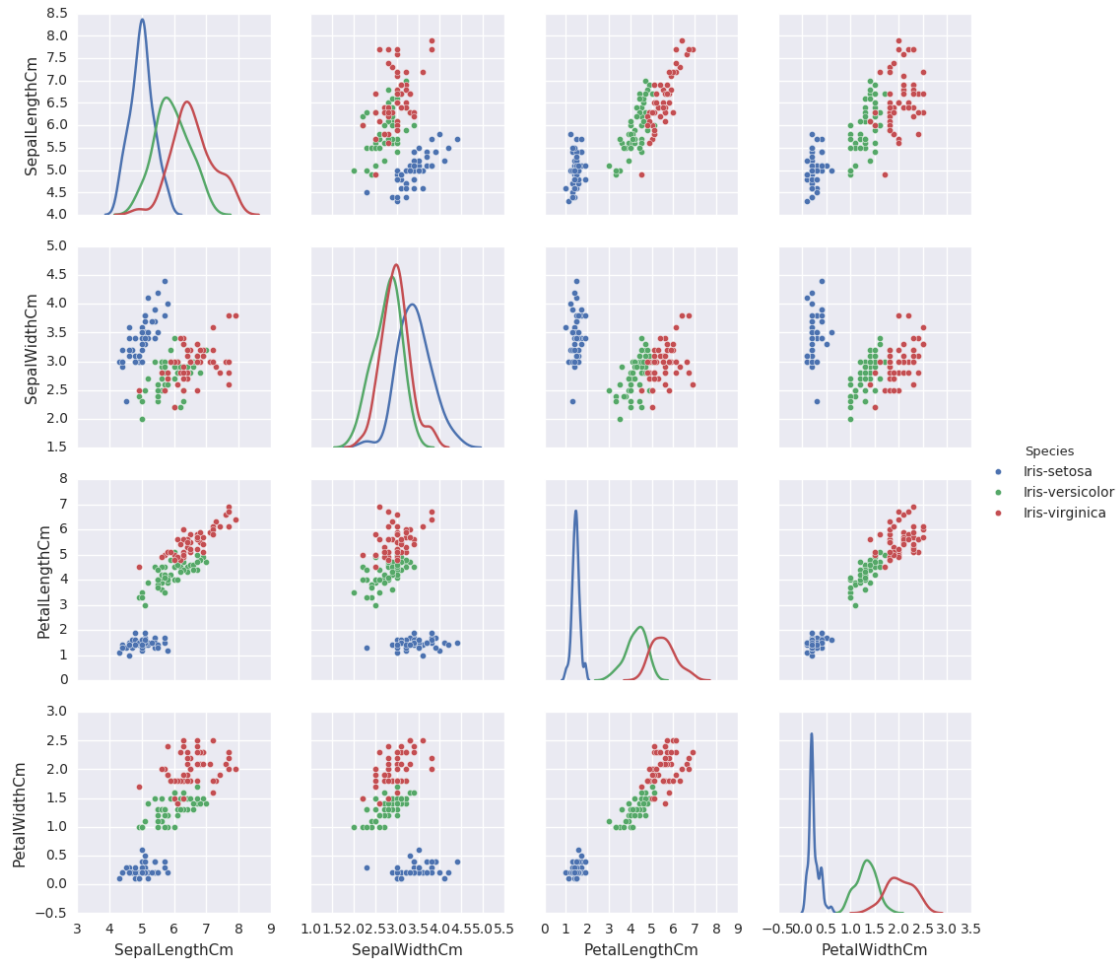
```
[23]: new_var = df_eval[['class', 'gill-color']]  
new_var = new_var[new_var['gill-color'] <= 3.5]  
sns.factorplot('class', col='gill-color', data=new_var, kind='count', size=4.5,   
               aspect=.8, col_wrap=4);
```

```
new_var=df_eval[['class', 'gill-color']]
new_var=new_var[new_var['gill-color']>3.5]
sns.factorplot('class', col='gill-color', data=new_var, kind='count', size=4.5,
↪aspect=.8, col_wrap=4);
```



Sometimes, through visualisation, we can extract meaningful information before we even reach the training stage.

Here is a similar example in the benchmark Iris data-set, where some class separation is more prominent.



12 Data Pre-Processing

Carrying out necessary transformations

```
[24]: df_train = df_train.astype('category')
      df_train.dtypes
```

```
[24]: class          category
      cap-shape      category
      cap-surface    category
      cap-color      category
      bruises        category
      odor           category
      gill-attachment category
      gill-spacing    category
      gill-size       category
      gill-color      category
      stalk-shape     category
      stalk-root      category
```

```
stalk-surface-above-ring    category
stalk-surface-below-ring   category
stalk-color-above-ring     category
stalk-color-below-ring     category
veil-type                  category
veil-color                 category
ring-number                category
ring-type                  category
spore-print-color          category
population                 category
habitat                    category
dtype: object
```

13

13.1 Data Cleaning

Getting rid of what we don't need: Missing Values, Redundant Values, Outliers

For missing values, let's look back at the Missingno Matrix. For redundant values, let's look back at the Correlation Matrix. For outliers, let's look back at the Box Plot

```
[25]: df_train_clean = df_train.drop(['stalk-root', 'gill-attachment', 'veil-type'],
    ↪axis=1)
df_train_clean.to_csv('df_train_clean.csv', index=False)
```

14

14.1 Data encoding

```
[26]: df_train_clean.sample(5)
```

```
[26]:      class cap-shape cap-surface cap-color bruises odor gill-spacing \
2316      e          x          y          e          t          n          c
5511      p          x          y          e          f          y          c
4718      p          x          f          y          f          f          c
2721      e          x          y          e          t          n          c
3450      e          f          y          e          t          n          c

      gill-size gill-color stalk-shape stalk-surface-above-ring \
2316          b          p          t          s
5511          n          b          t          k
4718          b          g          e          k
2721          b          n          t          s
3450          b          u          t          s

      stalk-surface-below-ring stalk-color-above-ring stalk-color-below-ring \
```

2316	s	w	w
5511	k	w	p
4718	k	b	b
2721	s	g	p
3450	s	w	w

	veil-color	ring-number	ring-type	spore-print-color	population	habitat
2316	w	o	p	k	v	d
5511	w	o	e	w	v	l
4718	w	o	l	h	y	g
2721	w	o	p	n	y	d
3450	w	o	p	k	y	d

14.2 One-Hot encoding

with trimming

```
[27]: df_train_oh_encoded = pd.get_dummies(df_train_clean)
```

```
[28]: df_train_oh_encoded
```

```
[28]:
```

	class_e	class_p	cap-shape_b	cap-shape_c	cap-shape_f	cap-shape_k	\
7873	0	1	0	0	0	1	
6515	0	1	0	0	0	0	
6141	0	1	0	0	1	0	
2764	1	0	0	0	1	0	
438	1	0	1	0	0	0	
...	
5226	0	1	0	0	0	0	
5390	1	0	0	0	0	1	
860	1	0	0	0	1	0	
7603	0	1	0	0	0	1	
7270	1	0	0	0	0	1	

	cap-shape_s	cap-shape_x	cap-surface_f	cap-surface_g	cap-surface_s	\
7873	0	0	0	0	1	
6515	0	1	0	0	1	
6141	0	0	0	0	0	
2764	0	0	1	0	0	
438	0	0	0	0	0	
...	
5226	0	1	0	0	0	
5390	0	0	0	0	0	
860	0	0	0	0	0	
7603	0	0	0	0	1	
7270	0	0	1	0	0	

	cap-surface_y	cap-color_b	cap-color_c	cap-color_e	cap-color_g	\
--	---------------	-------------	-------------	-------------	-------------	---

7873	0	0	0	1	0
6515	0	0	0	0	0
6141	1	0	0	1	0
2764	0	0	0	0	0
438	1	0	0	0	0
...
5226	1	0	0	0	0
5390	1	0	0	1	0
860	1	0	0	0	0
7603	0	0	0	1	0
7270	0	0	0	0	1

	cap-color_n	cap-color_p	cap-color_r	cap-color_u	cap-color_w	\
7873	0	0	0	0	0	
6515	1	0	0	0	0	
6141	0	0	0	0	0	
2764	1	0	0	0	0	
438	0	0	0	0	0	
...	
5226	1	0	0	0	0	
5390	0	0	0	0	0	
860	1	0	0	0	0	
7603	0	0	0	0	0	
7270	0	0	0	0	0	

	cap-color_y	bruises_f	bruises_t	odor_a	odor_c	odor_f	odor_l	\
7873	0	1	0	0	0	0	0	
6515	0	1	0	0	0	1	0	
6141	0	1	0	0	0	0	0	
2764	0	0	1	0	0	0	0	
438	1	0	1	0	0	0	1	
...	
5226	0	1	0	0	0	1	0	
5390	0	0	1	0	0	0	0	
860	0	0	1	0	0	0	1	
7603	0	1	0	0	0	1	0	
7270	0	1	0	0	0	0	0	

	odor_m	odor_n	odor_p	odor_s	odor_y	gill-spacing_c	gill-spacing_w	\
7873	0	0	0	1	0	1	0	
6515	0	0	0	0	0	1	0	
6141	0	0	0	0	1	1	0	
2764	0	1	0	0	0	1	0	
438	0	0	0	0	0	1	0	
...	
5226	0	0	0	0	0	1	0	
5390	0	1	0	0	0	1	0	

860	0	0	0	0	0	1	0
7603	0	0	0	0	0	1	0
7270	0	1	0	0	0	0	1

	gill-size_b	gill-size_n	gill-color_b	gill-color_e	gill-color_g	\
7873	0	1	1	0	0	
6515	0	1	1	0	0	
6141	0	1	1	0	0	
2764	1	0	0	0	0	
438	1	0	0	0	0	
...	
5226	0	1	1	0	0	
5390	1	0	0	0	0	
860	1	0	0	0	0	
7603	0	1	1	0	0	
7270	1	0	0	0	1	

	gill-color_h	gill-color_k	gill-color_n	gill-color_o	gill-color_p	\
7873	0	0	0	0	0	
6515	0	0	0	0	0	
6141	0	0	0	0	0	
2764	0	0	0	0	0	
438	0	1	0	0	0	
...	
5226	0	0	0	0	0	
5390	0	0	0	0	0	
860	0	0	0	0	0	
7603	0	0	0	0	0	
7270	0	0	0	0	0	

	gill-color_r	gill-color_u	gill-color_w	gill-color_y	stalk-shape_e	\
7873	0	0	0	0	0	
6515	0	0	0	0	0	
6141	0	0	0	0	0	
2764	0	1	0	0	0	
438	0	0	0	0	1	
...	
5226	0	0	0	0	0	
5390	0	0	1	0	1	
860	0	0	1	0	1	
7603	0	0	0	0	0	
7270	0	0	0	0	1	

	stalk-shape_t	stalk-surface-above-ring_f	stalk-surface-above-ring_k	\
7873	1	0	0	
6515	1	0	1	
6141	1	0	0	

2764	1	0	0
438	0	0	0
...
5226	1	0	1
5390	0	0	0
860	0	0	0
7603	1	0	0
7270	0	0	0

	stalk-surface-above-ring_s	stalk-surface-above-ring_y	\
7873	1	0	
6515	0	0	
6141	1	0	
2764	1	0	
438	1	0	
...	
5226	0	0	
5390	1	0	
860	1	0	
7603	1	0	
7270	1	0	

	stalk-surface-below-ring_f	stalk-surface-below-ring_k	\
7873	0	1	
6515	0	0	
6141	0	0	
2764	0	0	
438	0	0	
...	
5226	0	0	
5390	0	0	
860	0	0	
7603	0	0	
7270	0	1	

	stalk-surface-below-ring_s	stalk-surface-below-ring_y	\
7873	0	0	
6515	1	0	
6141	1	0	
2764	1	0	
438	1	0	
...	
5226	1	0	
5390	1	0	
860	0	1	
7603	1	0	
7270	0	0	

	stalk-color-above-ring_b	stalk-color-above-ring_c	\
7873	0	0	
6515	0	0	
6141	0	0	
2764	0	0	
438	0	0	
...	
5226	0	0	
5390	0	0	
860	0	0	
7603	0	0	
7270	0	0	

	stalk-color-above-ring_e	stalk-color-above-ring_g	\
7873	0	0	
6515	0	0	
6141	0	0	
2764	0	1	
438	0	0	
...	
5226	0	0	
5390	0	0	
860	0	0	
7603	0	0	
7270	0	0	

	stalk-color-above-ring_n	stalk-color-above-ring_o	\
7873	0	0	
6515	0	0	
6141	0	0	
2764	0	0	
438	0	0	
...	
5226	0	0	
5390	0	0	
860	0	0	
7603	0	0	
7270	0	0	

	stalk-color-above-ring_p	stalk-color-above-ring_w	\
7873	1	0	
6515	0	1	
6141	1	0	
2764	0	0	
438	0	1	
...	

5226	1	0
5390	0	1
860	0	1
7603	1	0
7270	0	1

	stalk-color-above-ring_y	stalk-color-below-ring_b	\
7873	0	0	
6515	0	0	
6141	0	0	
2764	0	0	
438	0	0	
...	
5226	0	0	
5390	0	0	
860	0	0	
7603	0	0	
7270	0	0	

	stalk-color-below-ring_c	stalk-color-below-ring_e	\
7873	0	0	
6515	0	0	
6141	0	0	
2764	0	0	
438	0	0	
...	
5226	0	0	
5390	0	1	
860	0	0	
7603	0	0	
7270	0	0	

	stalk-color-below-ring_g	stalk-color-below-ring_n	\
7873	0	0	
6515	0	0	
6141	0	0	
2764	0	0	
438	0	0	
...	
5226	0	0	
5390	0	0	
860	0	0	
7603	0	0	
7270	0	0	

	stalk-color-below-ring_o	stalk-color-below-ring_p	\
7873	0	0	

6515	0	0
6141	0	0
2764	0	1
438	0	0
...
5226	0	0
5390	0	0
860	0	0
7603	0	1
7270	0	0

	stalk-color-below-ring_w	stalk-color-below-ring_y	veil-color_n	\
7873	1	0	0	
6515	1	0	0	
6141	1	0	0	
2764	0	0	0	
438	1	0	0	
...	
5226	1	0	0	
5390	0	0	0	
860	1	0	0	
7603	0	0	0	
7270	1	0	0	

	veil-color_o	veil-color_w	veil-color_y	ring-number_n	ring-number_o	\
7873	0	1	0	0	1	
6515	0	1	0	0	1	
6141	0	1	0	0	1	
2764	0	1	0	0	1	
438	0	1	0	0	1	
...	
5226	0	1	0	0	1	
5390	0	1	0	0	0	
860	0	1	0	0	1	
7603	0	1	0	0	1	
7270	0	1	0	0	0	

	ring-number_t	ring-type_e	ring-type_f	ring-type_l	ring-type_n	\
7873	0	1	0	0	0	
6515	0	1	0	0	0	
6141	0	1	0	0	0	
2764	0	0	0	0	0	
438	0	0	0	0	0	
...	
5226	0	1	0	0	0	
5390	1	1	0	0	0	
860	0	0	0	0	0	

7603	0	1	0	0	0
7270	1	0	0	0	0

	ring-type_p	spore-print-color_b	spore-print-color_h	\
7873	0	0	0	
6515	0	0	0	
6141	0	0	0	
2764	1	0	0	
438	1	0	0	
...	
5226	0	0	0	
5390	0	0	0	
860	1	0	0	
7603	0	0	0	
7270	1	0	0	

	spore-print-color_k	spore-print-color_n	spore-print-color_o	\
7873	0	0	0	
6515	0	0	0	
6141	0	0	0	
2764	0	1	0	
438	0	1	0	
...	
5226	0	0	0	
5390	0	0	0	
860	0	1	0	
7603	0	0	0	
7270	0	0	0	

	spore-print-color_r	spore-print-color_u	spore-print-color_w	\
7873	0	0	1	
6515	0	0	1	
6141	0	0	1	
2764	0	0	0	
438	0	0	0	
...	
5226	0	0	1	
5390	0	0	1	
860	0	0	0	
7603	0	0	1	
7270	0	0	1	

	spore-print-color_y	population_a	population_c	population_n	\
7873	0	0	0	0	
6515	0	0	0	0	
6141	0	0	0	0	
2764	0	0	0	0	

438	0	0	0	1
...
5226	0	0	0	0
5390	0	0	1	0
860	0	0	0	0
7603	0	0	0	0
7270	0	0	0	1

	population_s	population_v	population_y	habitat_d	habitat_g \
7873	0	1	0	1	0
6515	0	1	0	0	0
6141	0	1	0	0	0
2764	0	1	0	1	0
438	0	0	0	0	0
...
5226	0	1	0	0	0
5390	0	0	0	0	0
860	0	0	1	0	0
7603	0	1	0	0	0
7270	0	0	0	0	1

	habitat_l	habitat_m	habitat_p	habitat_u	habitat_w
7873	0	0	0	0	0
6515	0	0	1	0	0
6141	1	0	0	0	0
2764	0	0	0	0	0
438	0	1	0	0	0
...
5226	0	0	1	0	0
5390	0	0	0	0	1
860	0	0	1	0	0
7603	0	0	1	0	0
7270	0	0	0	0	0

[6499 rows x 111 columns]

```
[29]: df_train_oh_encoded['class'] = df_train_oh_encoded['class_e']
df_train_oh_encoded.drop(['class_e', 'class_p', 'cap-shape_x', 'cap-surface_y',
↳ 'cap-color_y', 'bruises_t', 'odor_y', 'gill-spacing_w', 'gill-size_n',
↳ 'gill-color_y', 'stalk-shape_t', 'stalk-surface-above-ring_y',
↳ 'stalk-surface-below-ring_y', 'stalk-color-above-ring_y',
↳ 'stalk-color-below-ring_y', 'veil-color_y', 'ring-number_t', 'ring-type_p',
↳ 'spore-print-color_y', 'population_v', 'habitat_w'], axis=1, inplace=True)
```

```
[30]: print(df_train_oh_encoded.shape)
df_train_oh_encoded.to_csv('df_train_oh_encoded.csv', index=False)
```

(6499, 91)

15

15.1 Ordinal encoding

```
[31]: df_train_or_encoded = df_train_clean.copy()

labelencoder=LabelEncoder()
for column in df_train_clean.columns:
    df_train_or_encoded[column] = labelencoder.
    fit_transform(df_train_or_encoded[column])
df_train_or_encoded.to_csv('df_train_or_encoded.csv', index=False)
df_train_or_encoded.sample(5)
```

```
[31]:      class  cap-shape  cap-surface  cap-color  bruises  odor  gill-spacing  \
1678      0          2          2          4          0      5          1
988       0          5          2          3          0      5          1
4550      1          5          3          9          0      2          0
1798      1          2          3          8          1      6          0
7381      1          2          3          4          0      7          0
```

```
      gill-size  gill-color  stalk-shape  stalk-surface-above-ring  \
1678          0          5          1          2
988           0          4          1          2
4550          0          7          0          1
1798          1          4          0          2
7381          1          0          1          1
```

```
      stalk-surface-below-ring  stalk-color-above-ring  \
1678          2          7
988           0          7
4550          1          6
1798          2          7
7381          2          6
```

```
      stalk-color-below-ring  veil-color  ring-number  ring-type  \
1678          7          2          1          0
988           7          2          1          0
4550          4          2          1          2
1798          7          2          1          4
7381          6          2          1          0
```

```
      spore-print-color  population  habitat
1678          2          0          1
988           2          0          1
4550          1          5          4
1798          2          4          5
7381          7          4          2
```

16

17

18 Model Training

18.1 with Decision Trees Classifier

19

19.1 Train-Validation Split

```
[32]: # For each ML algorithm, we need to specify which part of the dataset contains
      ↪ the features ...
X = df_train_or_encoded.drop(['class'], axis=1)
# ... and which is the target
Y = df_train_or_encoded['class']

# Split dataset again, one big portion for training the model, the other to
↪ validate the model
X_train, X_validation, y_train, y_validation = train_test_split(X, Y,
      ↪ test_size=0.2, random_state=42)

print('X_train:', X_train.shape)
print('y_train:', y_train.shape)
print('X_validation:', X_validation.shape)
print('y_validation:', y_validation.shape)
```

```
X_train: (5199, 19)
y_train: (5199,)
X_validation: (1300, 19)
y_validation: (1300,)
```

19.2 Training the model

```
[33]: clf = DecisionTreeClassifier()
      clf.fit(X_train, y_train)
```

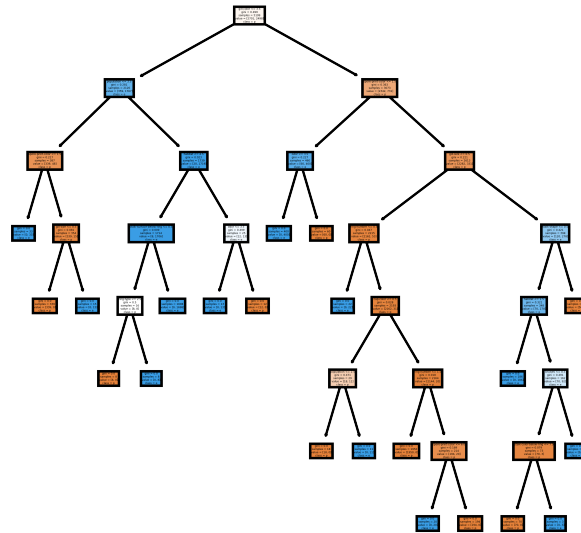
```
[33]: DecisionTreeClassifier()
```

19.2.1 Visualising the produced decision tree

```
[34]: fn = X_train.columns
      cn = df_train['class'].unique()

# Setting dpi = 900 to make image clearer than default
fig, axes = plt.subplots(nrows = 1,ncols = 1,figsize = (4,4), dpi=900)
```

```
tree.plot_tree(clf,
               feature_names = fn,
               class_names=cn,
               filled = True);
```



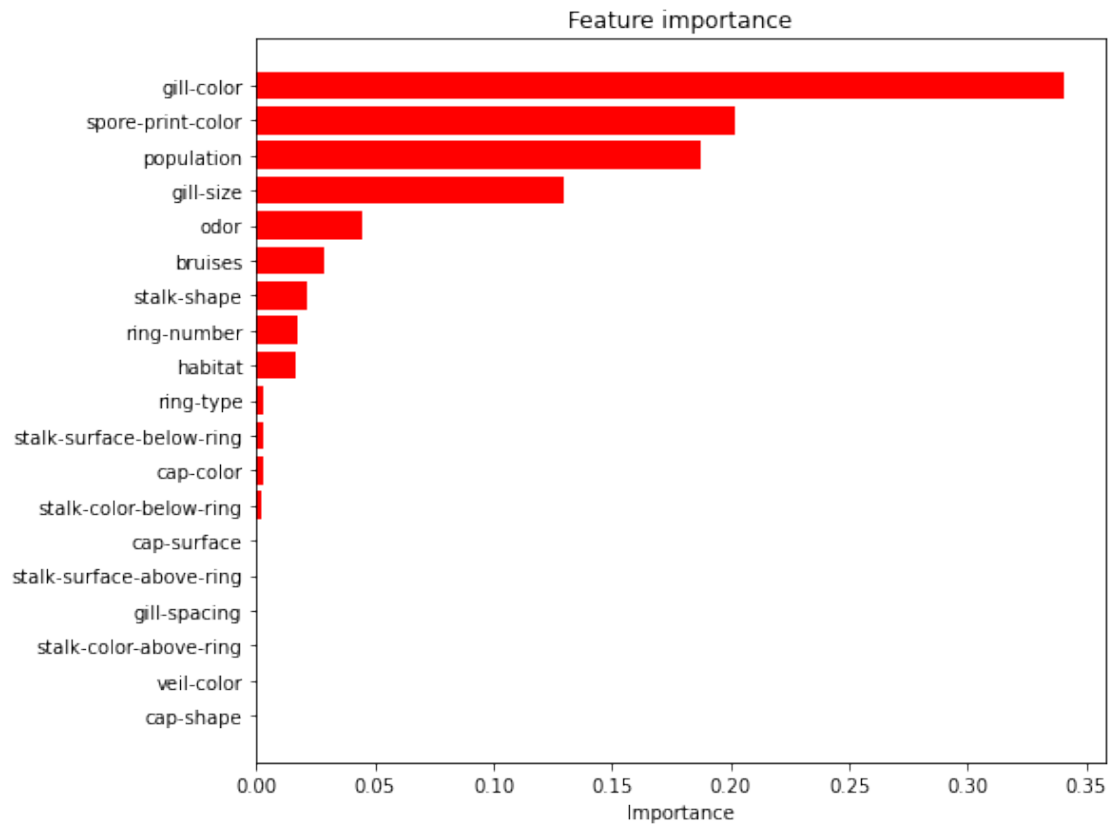
19.2.2 Feature importance

Drawing a graph showing the feature importance for the trained model. Looking both at the graph below and the three above, what relation can you see?

If you look back at the EDA stage, which assumption that we made about the data are reflected here?

```
[35]: features_list = X.columns.values
feature_importance = clf.feature_importances_
sorted_idx = np.argsort(feature_importance)

plt.figure(figsize=(8,7))
plt.barh(range(len(sorted_idx)), feature_importance[sorted_idx],
         align='center', color="red")
plt.yticks(range(len(sorted_idx)), features_list[sorted_idx])
plt.xlabel('Importance')
plt.title('Feature importance')
plt.draw()
#plt.savefig("IMG/featureimp.png", format='png', dpi=900, bbox_inches='tight')
plt.show()
```



20

21 Validation

Accuracy scores and Confusion Matrix

```
[36]: y_pred_validation = clf.predict(X_validation)
print("Decision Tree Classifier report: \n\n",
      ↪classification_report(y_validation, y_pred_validation))
print("Test Accuracy: {}%".format(round(clf.score(X_validation,
      ↪y_validation)*100, 2)))

# Confusion matrix
cm = confusion_matrix(y_validation, y_pred_validation)

x_axis_labels = ["Edible", "Poisonous"]
y_axis_labels = ["Edible", "Poisonous"]

f, ax = plt.subplots(figsize=(7,7))
```

```

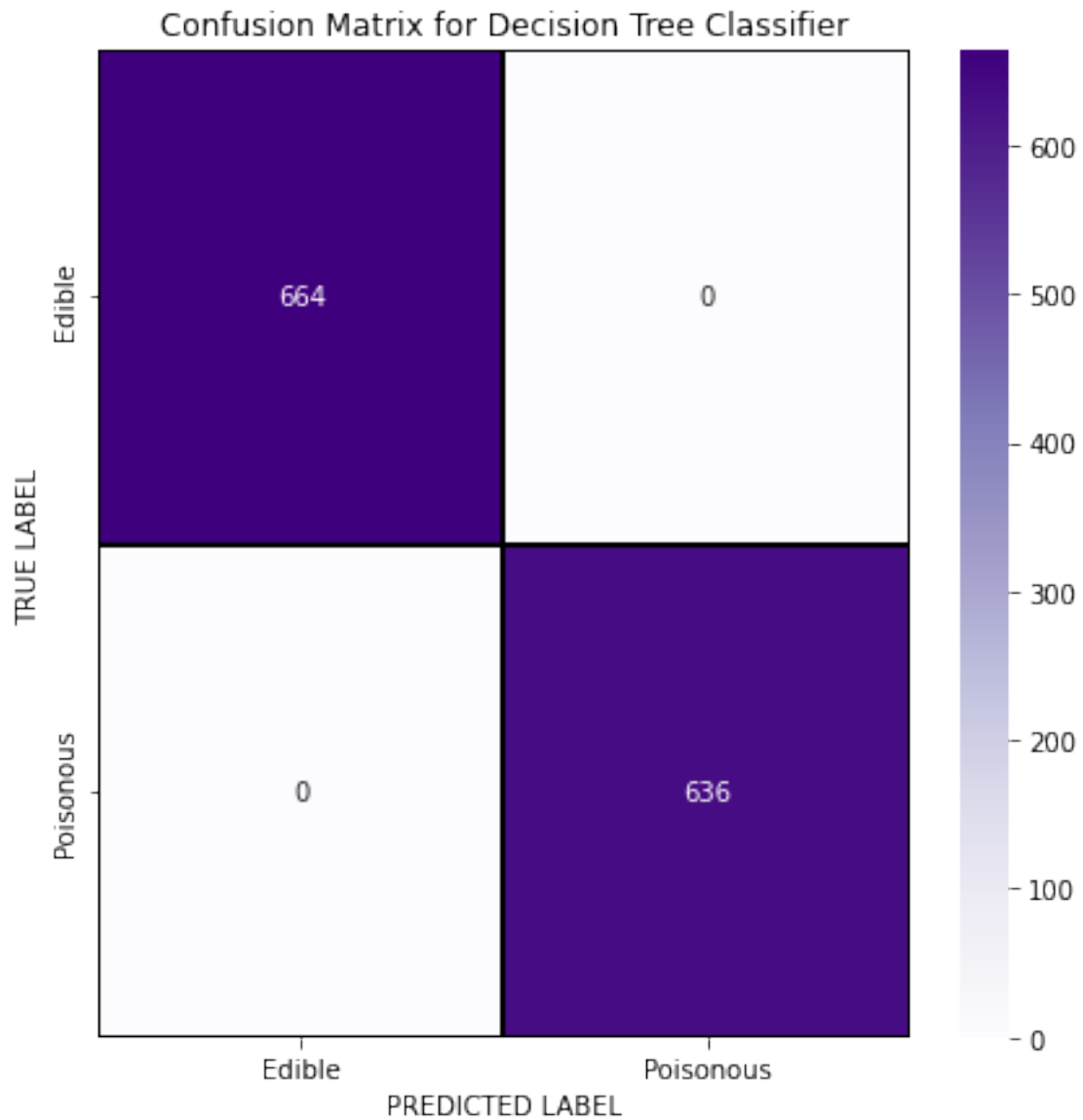
sns.heatmap(cm, annot = True, linewidths=0.2, linecolor="black", fmt = ".0f",
    ↪ax=ax, cmap="Purples", xticklabels=x_axis_labels, yticklabels=y_axis_labels)
plt.xlabel("PREDICTED LABEL")
plt.ylabel("TRUE LABEL")
plt.title('Confusion Matrix for Decision Tree Classifier')
#plt.savefig("IMG/dtcm_validation.png", format='png', dpi=900,
    ↪bbox_inches='tight')
plt.show()

```

Decision Tree Classifier report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	664
1	1.00	1.00	1.00	636
accuracy			1.00	1300
macro avg	1.00	1.00	1.00	1300
weighted avg	1.00	1.00	1.00	1300

Test Accuracy: 100.0%



22

23

24

25 Testing

With unseen data - Now we see how the model actually performs

26

26.1 Preparing the test data

First, to be able to fit the data into the model, we need to apply the EXACT SAME Pre-Processing steps as we did on the training data.

Think of it like this, you are carving a hole into a wall to mount a bar, and the bar must fit perfectly to not be too loose. The tool you use to cut the hole, is a CIRCLE bit of 35MM. Now, given that you have drilled then hole correctly, with the right bit, the you can fit a CIRCULAR bar in the hole with a diameter of 35MM.

Your model is the wall, your training data is the circle bit, training the model is cutting the hole with the bit, the test data is the bar and testing the model is to try and fit the bar in the cut hole. If your test data is not the same shape as your training data, it simply won't fit the algorithm. If your data is not encoded in the same way, then the algorithm will not be able to recognise the links it made out in the training data.

Finally, think as the test results as the error margin in how you've cut the hole, does the bar sit too loose, too tight or not at all?

```
[37]: # No visualisation of any sorts this time. Remember, you cannot see this data,
      ↪ it's like it wasn't produced yet.
df_test = df_test.astype('category')
df_test_clean = df_test.drop(['stalk-root', 'gill-attachment', 'veil-type'],
      ↪ axis=1)
df_test_or_encoded = df_test_clean.copy()

labelencoder=LabelEncoder()
for column in df_test_clean.columns:
    df_test_or_encoded[column] = labelencoder.
    ↪ fit_transform(df_test_or_encoded[column])
```

26.2 Predicting on test data

We predict on the test data using the SAME MODEL we trained earlier.

```
[38]: # features
X_test = df_test_or_encoded.drop(['class'], axis=1)
# target
Y_test = df_test_or_encoded['class']

y_pred_validation = clf.predict(X_test)
print("Decision Tree Classifier report: \n\n", classification_report(Y_test,
      ↪ y_pred_validation))
print("Test Accuracy: {}".format(round(clf.score(X_test, Y_test)*100, 2)))

# Confusion matrix
cm = confusion_matrix(Y_test, y_pred_validation)
```

```

x_axis_labels = ["Edible", "Poisonous"]
y_axis_labels = ["Edible", "Poisonous"]

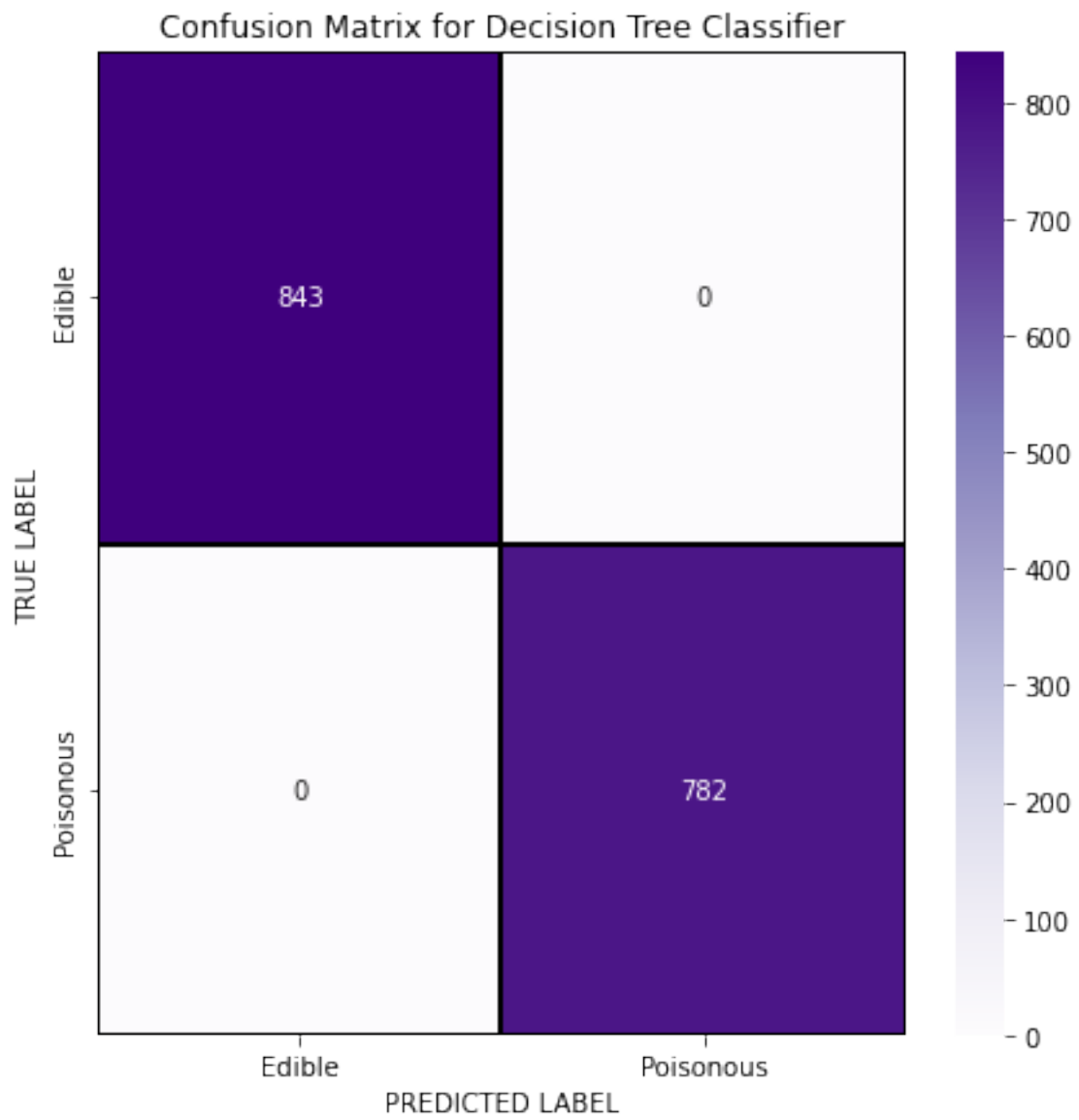
f, ax = plt.subplots(figsize=(7,7))
sns.heatmap(cm, annot = True, linewidths=0.2, linecolor="black", fmt = ".0f",
            ax=ax, cmap="Purples", xticklabels=x_axis_labels, yticklabels=y_axis_labels)
plt.xlabel("PREDICTED LABEL")
plt.ylabel("TRUE LABEL")
plt.title('Confusion Matrix for Decision Tree Classifier')
#plt.savefig("IMG/dtcm_test.png", format='png', dpi=900, bbox_inches='tight')
plt.show()

```

Decision Tree Classifier report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	843
1	1.00	1.00	1.00	782
accuracy			1.00	1625
macro avg	1.00	1.00	1.00	1625
weighted avg	1.00	1.00	1.00	1625

Test Accuracy: 100.0%



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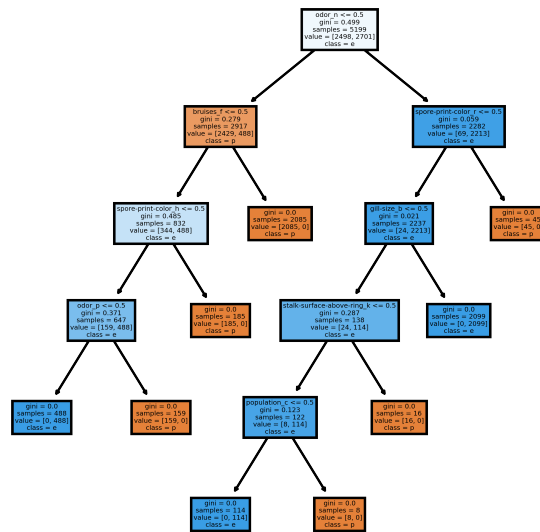
32 Appendix

I didn't forget about the one-hot encoded train set

```
[39]: # SPLITTING
X = df_train_oh_encoded.drop(['class'], axis=1)
Y = df_train_oh_encoded['class']
X_train, X_validation, y_train, y_validation = train_test_split(X, Y,
    ↪test_size=0.2, random_state=42)

# TRAINING
clf_oh = DecisionTreeClassifier() # New model this time btw
clf_oh.fit(X_train, y_train)

# Some visualisation
fn = X_train.columns
cn = df_train['class'].unique()
fig, axes = plt.subplots(nrows = 1,ncols = 1,figsize = (4,4), dpi=900)
tree.plot_tree(clf_oh,
    feature_names = fn,
    class_names=cn,
    filled = True);
```



```
[40]: # VALIDATION
y_pred_validation = clf_oh.predict(X_validation)
print("Decision Tree Classifier report: \n\n",
      ↪classification_report(y_validation, y_pred_validation))
print("Test Accuracy: {}%".format(round(clf_oh.score(X_validation,
      ↪y_validation)*100, 2)))

cm = confusion_matrix(y_validation, y_pred_validation)

x_axis_labels = ["Edible", "Poisonous"]
y_axis_labels = ["Edible", "Poisonous"]

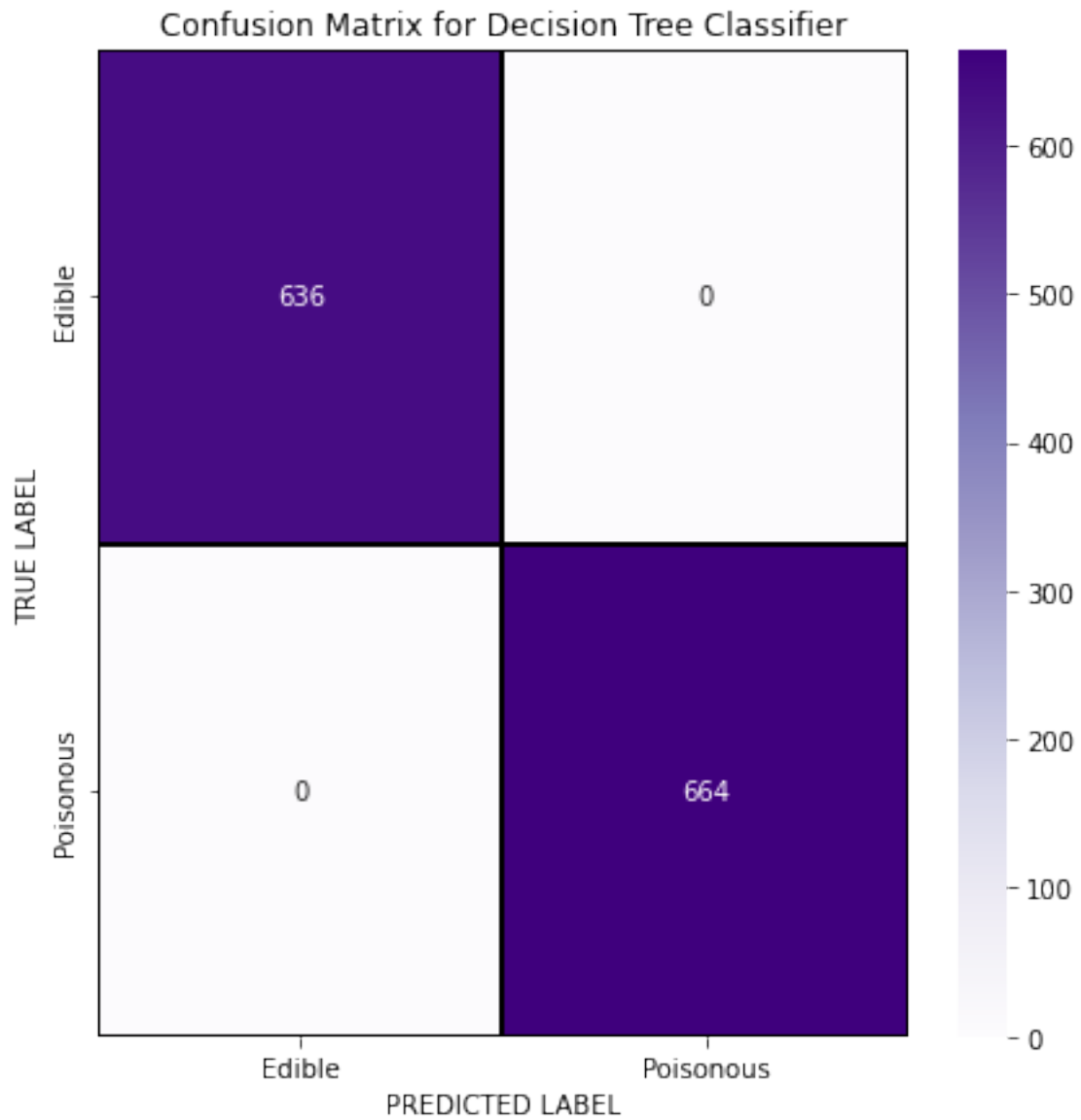
f, ax = plt.subplots(figsize=(7,7))
sns.heatmap(cm, annot = True, linewidths=0.2, linecolor="black", fmt = ".0f",
      ↪ax=ax, cmap="Purples", xticklabels=x_axis_labels, yticklabels=y_axis_labels)
plt.xlabel("PREDICTED LABEL")
plt.ylabel("TRUE LABEL")
plt.title('Confusion Matrix for Decision Tree Classifier')
plt.show()
```

Decision Tree Classifier report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	636
1	1.00	1.00	1.00	664

accuracy			1.00	1300
macro avg	1.00	1.00	1.00	1300
weighted avg	1.00	1.00	1.00	1300

Test Accuracy: 100.0%



[]: