Machine Learning in Mushroomia

Computer Science M148

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https://github.com/toba717/DataScience/tree/main/Project3

I. Introduction

Mushroomia is a land filled with diverse fauna and flora, but it's particularly well-known for its vast variety of mushrooms. Unfortunately, not all of the mushrooms in Mushroomia are edible, and it can be challenging to differentiate between the ones that are and the ones that aren't. To solve this problem, I have employed Shroomster Pro Max, an advanced data collection device that allows us to gather various data points on any mushroom found in the wild, and The National Archives on Mushrooms, a dataset collected by the Mushroomia government over the years.

Our goal is to construct and train machine learning models on The National Archives on Mushrooms dataset to determine which mushrooms I encounter on our journey are poisonous. I have done so through a systematic process of data loading and exploration, data pre-processing, data augmentation, statistical hypothesis testing, constructing models through non-ensemble and ensemble methods, and tuning the hyperparameters.

II. Methodology

A. Data Loading, Splitting, Exploration, and Visualization

The training dataset and testing dataset was loaded into Google Colab from Google Drive. First, the dataset was split into features and labels, where the "class" column represented the label or the variable in which the machine learning model aims to predict. The rest of the columns were used as tentative predictor variables. The testing data was also split into features and labels as well. Furthermore, the label or the "class" column was transformed from categorical variables ('p' and 'e') to numeric variables (1 and 0) using the map function. Additionally, I ensured that there was no skewness to the label values as this can potentially introduce bias to the model. Next, when scoping each of the predictors, the majority of them were categorical and only three of them were numerical. I visualized the numerical predictors through bar graphs and categorical variables as pie charts. Overall, I ensured that the predictors and the labels did not have any major flaws by first visually inspecting the shape and distribution.

B. Data Pre-Processing

The data must be processed prior to analysis. First, the missing values were identified by checking the number of missing values in the dataset for training and testing separately. The 'veil-type' predictor was identified to have 100% missing values in the testing dataset, and thus it was removed from both the training and testing datasets as it did not provide valuable information.

Overall, to process the data into the best way possible for the model to be used, I constructed a transformation pipeline. First, to handle the missing values or NaN values, an imputation strategy was used where missing values were replaced by the mode of the corresponding column. This strategy was chosen as it is a simple and effective way to handle missing values in categorical data.

Next, a numeric pipeline was built using the StandardScaler method to scale the numerical features in the dataset. This way, the numeric value's difference in magnitude will not create bias within the model. Finally, the OneHotEncoder method was used to convert categorical data into numerical data suitable for machine learning algorithms. Many of the predictor variables consisted of more than two distinct values. It will be dangerous to assign numeric values with difference in magnitude to these characters as these numbers will possess meanings. The prepared data was then transformed using the built pipeline. Similarly, the testing data was run through this pipeline as well. Overall, I pre-processed my data this way so that the machine learning model can better capture the fed data and further will not run into errors from missing values.

C. Data Augmentation

I aimed to aid the machine learning model through data augmentation or increasing the size and dimension of the dataset. The first new feature we are creating is called "stem_vol". This feature is constructed by multiplying the "stem-height" and "stem-width" columns of the dataset. This new feature represents the volume of the stem of the plant. This can be useful as certain mushrooms can have a very long stem, but can be skinny and vice versa. Overall, we would like to consider the overall volume so that we are not leaning towards one aspect of the dimension.

The second new feature we are creating is called "diam_stem_ratio". We obtain this new feature through dividing the "cap-diameter" column by the "stem-width" column. This new feature represents the ratio of the diameter of the cap to the overall width of the stem. This predictor illustrates the overall shape of the mushroom while simultaneously considering the cap as well as the stem. All in all, I expect that these two features that involve distinct viewpoints of the mushroom can present invaluable insights regarding the class of the mushroom.

D. Statistical Hypothesis Testing

I utilized a subset of the original dataset to perform statistical hypothesis testing. The chosen subset was the numerical predictors: "cap-diameter", "stem-height", and "stem-width". The results of the logistic regression model showed that all three numerical variables had a statistically significant relationship with the class variable. Two of the variables had p-values less than 0.05 and "stem-height" had a p-value that was very close to 0.05. I should therefore include all of these variables when constructing a model.

Furthermore, I noticed that the pseudo R-squared value is 0.02134 which shows that the model was able to explain a very small amount of variance. This indicates that there may be other factors that contribute to the classification that assess if a mushroom is poisonous or not that is not captured by these three variables. Other categorical variables that I have excluded when performing the hypothesis testing should be included when constructing the machine learning models. This is intuitive as there are definitely more components that we must consider to assess the class of a mushroom than its physical dimension.

E. Models of your choice

I considered multiple models including logistic regression, decision tree, and naive bayes. Logistic Regression was initially used to transform the linear combination of the predictor variables into probability estimates of the binary outcome. Next Decision Trees were considered because they can handle both categorical and continuous data and are simple to understand and interpret. The pruning technique was used to reduce the depth of the tree and make the model less complex. However, pruning the tree led to a drop in accuracy score, highlighting the trade-off between computational cost and performance.
The last non-ensemble method I considered was Naive Bayes because it assumes that the features are independent of each other and that each feature contributes equally to the probability of the class. The Gaussian Naive Bayes model did not yield a high accuracy rate because the normality assumption likely does not hold in these given features. The Bernoulli Naive Bayes model provided a higher accuracy rate because it is most appropriate when working with binary or boolean data, and the data frame had more features involving binary values. Overall, the two distinct Naive Bayes models did not perform very well due to the data having both binary and continuous values, and the overall model assumption that the predictors are independent could have been violated. From the three models that were considered, the decision tree without pruning has performed the best.

F. Ensemble Method

The ensemble method I chose was Random Forest Classifier. The model involves constructing a large number of decision trees on different subsets of the input data and then aggregating their predictions to come up with a prediction. It is an ensemble method because it combines multiple decision trees to generate a more robust and less sensitive model. Random forest showed that it is a great fit for this dataset as it can handle a large number of features and can detect complex relationships between them.Furthermore, by the nature of random forest models, it reduces the risk of overfitting which inevitably implies an increase in testing accuracy. Overall, the random forest classification model has outperformed all of the models that we have constructed thus far.

G. Hyper-parameter Tuning

I aimed to identify the best model through hyper-parameter tuning and finding the best set of hyperparameters. The grid search method is used to explore all possible combinations of hyperparameters by defining a grid of parameter values to search over.
For each model, the corresponding hyperparameters were specified as a list of values to explore using the grid search method. The models were then fitted on the training data, and the function chose the best hyperparameters based on the cross-validation results. The best model was then determined based on the best accuracy score achieved by the model during the cross-validation.
The best hyperparameters found through the evaluations are the following:

- ☐ **Decision Tree Classifier**: max_depth=30, splitter='random'
- ☐ **Naive Bayes Classifier**: alpha=0.5, force_alpha=True
- ☐ **Random Forest Classifier**: max_depth=30, n_estimators=10

III. Results

Implementing the best hyper-parameters that was achieved previously, the following was achieved:

- ☐ **Decision Tree Classifier**:
  - ☐ Accuracy: 0.432019
  - ☐ Precision: 0.792294
  - ☐ Recall Score: 0.414434
  - ☐ F1 Score: 0.544205
- ☐ **Naive Bayes Classifier**:
  - ☐ Accuracy: 0.498066
  - ☐ Precision: 1
  - ☐ Recall Score: 0.460228
  - ☐ F1 SCore: 0.63051
- ☐ **Random Forest Classifier**:
  - ☐ Accuracy: 0.459285
  - ☐ Precision: 0.956522
  - ☐ Recall Score: 0.4394778
  - ☐ F1 Score: 0.602250

Note that above values can fluctuate for random forest classifier based on the specific seed value that is used.
The Naive Bayes Classifier has yielded the best result at classifying whether a mushroom is poisonous or not. It had yielded the highest value for all four of the evaluation metrics. Overall, the three models tend to have a higher precision score compared to the accuracy score, meaning that the model is correctly classifying positive instances more accurately compared to the negative cases.

These values were obtained through utilizing cross validation with K fold splits of 10. This strategy was chosen as it can provide a good trade off in terms of bias and variance. Furthermore, this method is computationally efficient compared to other strategies.

IV. Conclusion

I look forward to using the Naive Bayes Classifier (with hyperparameters alpha - 0.5 and for_alpha = True) during my adventure through Mushroomia. This is because the overall accuracy metrics was the highest amongst the model indicating that it can capture the true class of the mushroom more accurately so that I can identify which mushroom is poisonous and which one is not.

However, we must consider the limitations of this project. The dataset from the National Archives on Mushrooms which may not necessarily capture the entire picture of the current notion as it may be out of date or in reality may involve more predictors than given in the dataset. For example, if there are more predators or mushroom eaters in a specific region, there is a high chance that the mushrooms are not poisonous. Moreover, it is difficult to truly identify if a mushroom is poisonous or not and thus when recording and collecting the data, there could have been misclassification which can heavily impact the machine learning model. Furthermore, the results of our visualization were limited by the quality of the available data. There were a limited number of numerical and categorical variables to accurately visualize the data.

Regarding next steps, numerical variables can be assessed amongst each other through considering multicollinearity and further considering association for categorical variables. Additionally, locations can be addressed as well so that the machine learning model can be used in other contexts of mushroom classification as well.

You are exploring the wilderness of *Mushroomia*, a land populated by a plethora of diverse fauna and flora. In particular, *Mushroomia* is known for its unparalleled variety in mushrooms. However, not all the mushrooms in *Mushroomia* are edible. As you make your way through *Mushroomia*, you would like to know which mushrooms are edible, in order to forage for supplies for your daily mushroom soup.

You have access to:

- *Shroomster Pro Max* ^{TM} - a state of the art data collection device, developed by *Mushroomia*, that allows you to collect various data points about any mushroom you encounter in the wild
- *The National Archives on Mushrooms* - a dataset collected over the years by the government of *Mushroomia*

To address this problem, you decide to use the skills you learnt in CSM148 and train machine learning models on the *The National Archives on Mushrooms* in order to use your *Shroomster Pro Max* ^{TM} to determine whether the mushrooms you encounter on your adventure can be added to your daily mushroom soup.

This project will be more unstructured than the previous two projects in order to allow you to experience how data science problems are solved in practice. There are two parts to this project: a Jupyter Notebook with your code (where you explore, visualize, process your data and train machine learning models) and a report (where you explain the various choices you make in your implementation and analyze the final performance of your models).

1. Loading and Viewing Data

```
[10] # mount to google drive and retrieve files
     from google.colab import drive
     drive.mount('/content/drive')
```

```
Mounted at /content/drive
```

```
[11] # importing neccesary modules
     import numpy as np
     import pandas as pd

     %matplotlib inline
     import matplotlib.pyplot as plt
```

```
[12] # download the necessary files that is stored in the google drive
     train = pd.read_csv("/content/drive/MyDrive/CS148_data/project3/mushroom_train.csv", sep = ";")
     test = pd.read_csv("/content/drive/MyDrive/CS148_data/project3/mushroom_test.csv", sep = ";")
```

```
[13] # viewing the training data
     train.head()
```

	class	cap-diameter	cap-shape	cap-surface	cap-color	does-bruise-or-bleed	gill-attachment	gill-spacing	gill-color	stem-height	...	stem-root	stem-surface	stem-color	veil-type	veil-color	has-ring	ring-type	spore-print-color	habitat	season
0	p	15.26	x	g	o	f	e	NaN	w	16.95	...	s	y	w	u	w	t	g	NaN	d	w
1	p	16.60	x	g	o	f	e	NaN	w	17.99	...	s	y	w	u	w	t	g	NaN	d	u
2	p	14.07	x	g	o	f	e	NaN	w	17.80	...	s	y	w	u	w	t	g	NaN	d	w
3	p	14.17	f	h	e	f	e	NaN	w	15.77	...	s	y	w	u	w	t	p	NaN	d	w
4	p	14.64	x	h	o	f	e	NaN	w	16.53	...	s	y	w	u	w	t	p	NaN	d	w

5 rows × 21 columns

```
[14] # viewing the testing data
     test.head()
```

	class	cap-diameter	cap-shape	cap-surface	cap-color	does-bruise-or-bleed	gill-attachment	gill-spacing	gill-color	stem-height	...	stem-root	stem-surface	stem-color	veil-type	veil-color	has-ring	ring-type	spore-print-color	habitat	season
0	p	2.50	b	NaN	k	f	a	NaN	k	8.42	...	NaN	NaN	g	NaN	w	f	f	k	g	u
1	p	3.07	b	NaN	k	f	a	NaN	n	7.24	...	NaN	NaN	n	NaN	w	f	f	k	g	a
2	p	3.30	b	NaN	n	f	a	NaN	n	10.22	...	NaN	NaN	n	NaN	w	f	f	k	g	u
3	p	3.49	b	NaN	k	f	a	NaN	k	11.00	...	NaN	NaN	n	NaN	w	f	f	k	g	a
4	p	2.79	b	NaN	n	f	a	NaN	n	6.97	...	NaN	NaN	g	NaN	w	f	f	k	g	u

5 rows × 21 columns

2. Splitting Data into Features and Labels

```
[15] # This will be the label that the model aims to predict
     label = train['class']
     label
```

```
0        p
1        p
2        p
3        p
4        p
        ..
50208    p
50209    p
50210    p
50211    p
50212    p
Name: class, Length: 50213, dtype: object
```

```
[16] # This will be the tentative predictor variables
     train_dropped = train.drop(['class'], axis = 1)
     train_dropped
```

	cap-diameter	cap-shape	cap-surface	cap-color	does-bruise-or-bleed	gill-attachment	gill-spacing	gill-color	stem-height	stem-width	stem-root	stem-surface	stem-color	veil-type	veil-color	has-ring	ring-type	spore-print-color	habitat	season
0	15.26	x	g	o	f	e	NaN	w	16.95	17.09	s	y	w	u	w	t	g	NaN	d	w
1	16.60	x	g	o	f	e	NaN	w	17.99	18.19	s	y	w	u	w	t	g	NaN	d	u
2	14.07	x	g	o	f	e	NaN	w	17.80	17.74	s	y	w	u	w	t	g	NaN	d	w
3	14.17	f	h	e	f	e	NaN	w	15.77	15.98	s	y	w	u	w	t	p	NaN	d	w
4	14.64	x	h	o	f	e	NaN	w	16.53	17.20	s	y	w	u	w	t	p	NaN	d	w
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
50208	1.18	s	s	y	f	f	f	f	3.93	6.22	NaN	NaN	y	NaN	NaN	f	f	NaN	d	a
50209	1.27	f	s	y	f	f	f	f	3.18	5.43	NaN	NaN	y	NaN	NaN	f	f	NaN	d	a
50210	1.27	s	s	y	f	f	f	f	3.86	6.37	NaN	NaN	y	NaN	NaN	f	f	NaN	d	u
50211	1.24	f	s	y	f	f	f	f	3.56	5.44	NaN	NaN	y	NaN	NaN	f	f	NaN	d	u
50212	1.17	s	s	y	f	f	f	f	3.25	5.45	NaN	NaN	y	NaN	NaN	f	f	NaN	d	u

50213 rows × 20 columns

```
# predictors for the testing dataset
test_dropped = test.drop(['class'], axis = 1)
test_dropped
```

	cap-diameter	cap-shape	cap-surface	cap-color	does-bruise-or-bleed	gill-attachment	gill-spacing	gill-color	stem-height	stem-width	stem-root	stem-surface	stem-color	veil-type	veil-color	has-ring	ring-type	spore-print-color	habitat	season
0	2.50	b	NaN	k	f	a	NaN	k	8.42	2.46	NaN	NaN	g	NaN	w	f	f	k	g	u
1	3.07	b	NaN	k	f	a	NaN	n	7.24	2.41	NaN	NaN	n	NaN	w	f	f	k	g	a
2	3.30	b	NaN	n	f	a	NaN	n	10.22	2.53	NaN	NaN	n	NaN	w	f	f	k	g	u
3	3.49	b	NaN	k	f	a	NaN	k	11.00	2.81	NaN	NaN	n	NaN	w	f	f	k	g	a
4	2.79	b	NaN	n	f	a	NaN	n	6.97	2.37	NaN	NaN	g	NaN	w	f	f	k	g	u
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
10851	52.41	o	y	y	f	p	NaN	y	5.47	25.02	NaN	k	k	NaN	NaN	f	f	NaN	d	u
10852	54.81	o	y	y	f	p	NaN	y	6.67	22.15	NaN	k	k	NaN	NaN	f	f	NaN	d	s
10853	49.95	o	y	y	f	p	NaN	y	6.43	26.35	NaN	k	n	NaN	NaN	f	f	NaN	d	u
10854	53.16	o	y	y	f	p	NaN	y	6.99	40.29	NaN	k	k	NaN	NaN	f	f	NaN	d	s
10855	49.78	o	y	y	f	p	NaN	y	5.77	18.26	NaN	k	k	NaN	NaN	f	f	NaN	d	u

10856 rows × 20 columns

```
[18] # the target variable for the testing data
     label_test = test["class"]
     print(label_test)
```

```
0        p
1        p
2        p
3        p
4        p
        ..
10851    e
10852    e
10853    e
10854    e
10855    e
Name: class, Length: 10856, dtype: object
```

```
[19] # changing the labels to numeric values
     label = label.map({"p":1, "e":0})
     label_test = label_test.map({"p":1, "e":0})
```

3. Data Exploration, Visualization, and Data Processing

```
[20] # view the dimensions of the training and testing data
     print(train.shape)
     print(test.shape)
     print(train_dropped.shape)
     print(test_dropped.shape)
```

```
(50213, 21)
(10856, 21)
(50213, 20)
(10856, 20)
```

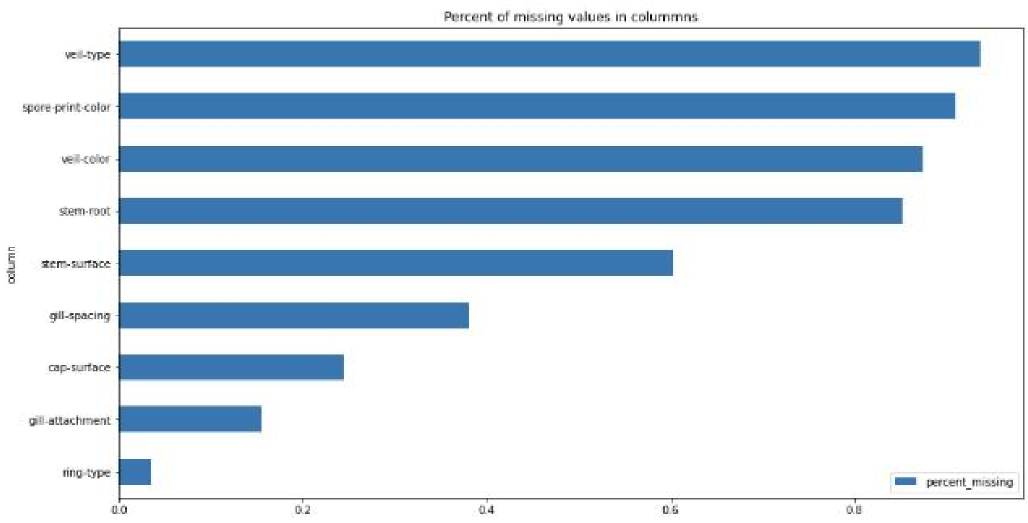
```
[21] # look at the type of each predictors
     train.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 50213 entries, 0 to 50212
Data columns (total 21 columns):
 #   Column                Non-Null Count  Dtype  
---  ------                --------------  -----  
 0   class                 50213 non-null  object 
 1   cap-diameter          50213 non-null  float64
 2   cap-shape             50213 non-null  object 
 3   cap-surface           37915 non-null  object 
 4   cap-color             50213 non-null  object 
 5   does-bruise-or-bleed  50213 non-null  object 
 6   gill-attachment       42447 non-null  object 
 7   gill-spacing          31064 non-null  object 
 8   gill-color            50213 non-null  object 
 9   stem-height           50213 non-null  float64
 10  stem-width            50213 non-null  float64
 11  stem-root             7413 non-null   object 
 12  stem-surface          19912 non-null  object 
 13  stem-color            50213 non-null  object 
 14  veil-type             3177 non-null   object 
 15  veil-color            6297 non-null   object 
 16  has-ring              50213 non-null  object 
 17  ring-type             48448 non-null  object 
 18  spore-print-color     4532 non-null   object 
 19  habitat               50213 non-null  object 
 20  season                50213 non-null  object 
dtypes: float64(3), object(18)
memory usage: 8.0+ MB
```

```
# view the amount of NA values in this dataset for training
train.isnull().sum()
```

```
class                       0
cap-diameter                0
cap-shape                   0
cap-surface             12298
cap-color                   0
does-bruise-or-bleed        0
gill-attachment          7766
gill-spacing            19149
gill-color                  0
stem-height                 0
stem-width                  0
stem-root               42800
stem-surface            30301
stem-color                  0
veil-type               47036
veil-color              43916
has-ring                    0
ring-type                1765
spore-print-color       45681
habitat                     0
season                      0
dtype: int64
```

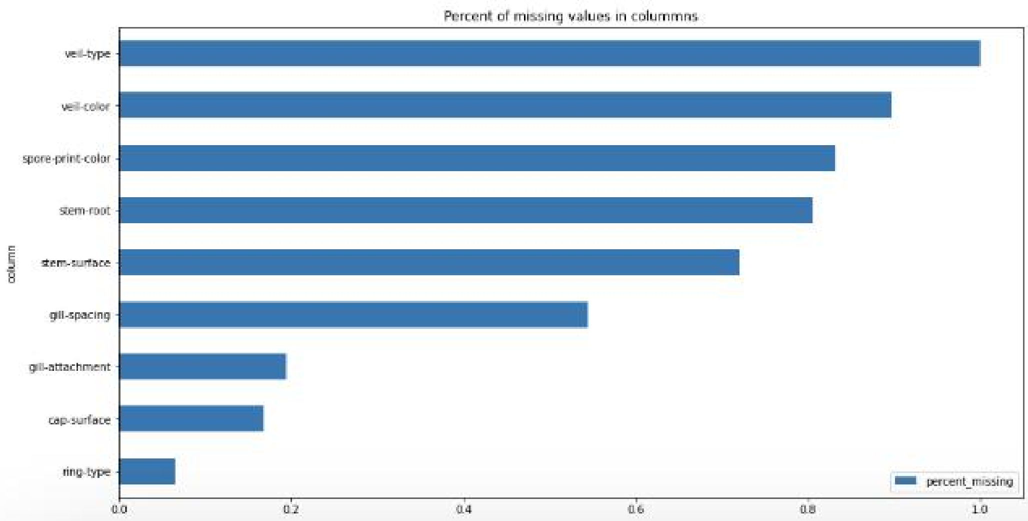
```
# Visualize the amount of missing values for each column

import pylab

def plot_missing_values(df):
    data = [(col, df[col].isnull().sum() / len(df))
            for col in df.columns if df[col].isnull().sum() > 0]
    col_names = ['column', 'percent_missing']
    missing_df = pd.DataFrame(data, columns=col_names).sort_values('percent_missing')
    pylab.rcParams['figure.figsize'] = (15, 8)
    missing_df.plot(kind='barh', x='column', y='percent_missing');
    plt.title('Percent of missing values in colummns');


plot_missing_values(train)
```



```
# view the amount of missing values for testing
test.isnull().sum()

# columns with missing values are the following
# missing_vals = ["cap-surface", "gill-attachment", "gill-spacing", "stem-root", "stem-surface", "veil-type", "veil-color", "ring-type", "spore-print-color"]
```

```
class                       0
cap-diameter                0
cap-shape                   0
cap-surface              1822
cap-color                   0
does-bruise-or-bleed        0
gill-attachment          2118
gill-spacing             5914
gill-color                  0
stem-height                 0
stem-width                  0
stem-root                8738
stem-surface             7823
stem-color                  0
veil-type               10856
veil-color               9740
has-ring                    0
ring-type                 706
spore-print-color        9034
habitat                     0
season                      0
dtype: int64
```

```
[25] # Visualize the amount of missing values for each column
     plot_missing_values(test)
```



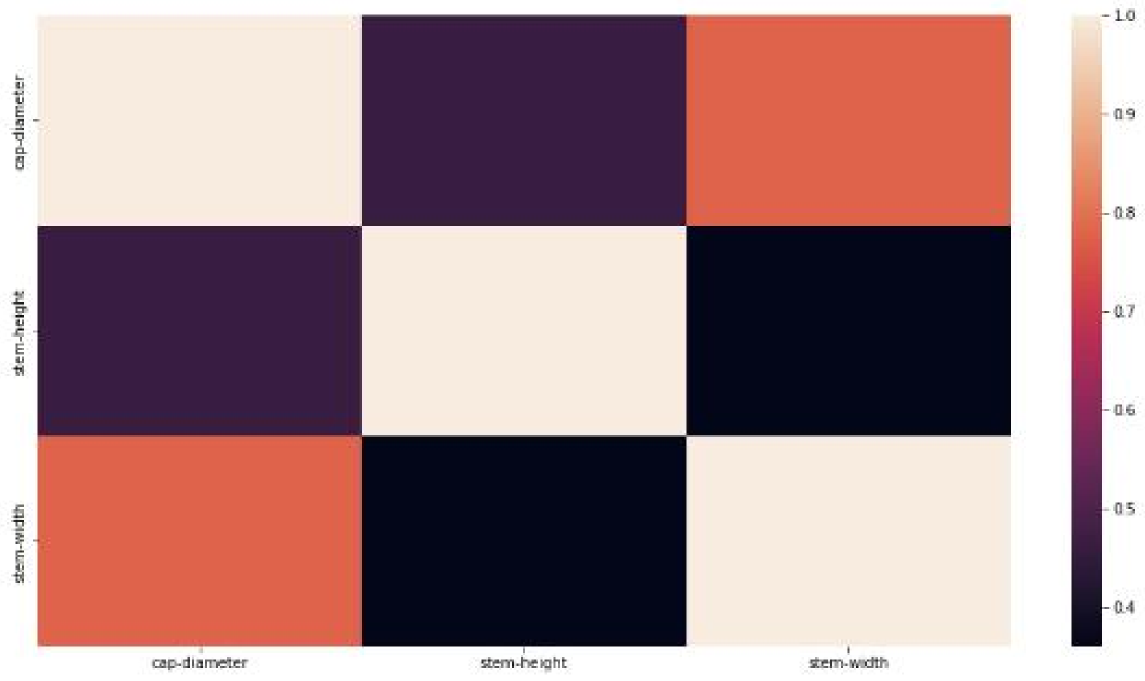
Note that 100% of the values in the "veil-type" column is missing (there are 10856 observations in the testing data set and 10856 of them are missing values for this specific column). Thus, we have that this column does not provide us with valuable information, and can be removed from both the training and testing dataset.

```
[26] # drop "veil-type"
     train_dropped = train_dropped.drop(["veil-type"], axis = 1)
     test_dropped = test_dropped.drop(["veil-type"], axis = 1)
```

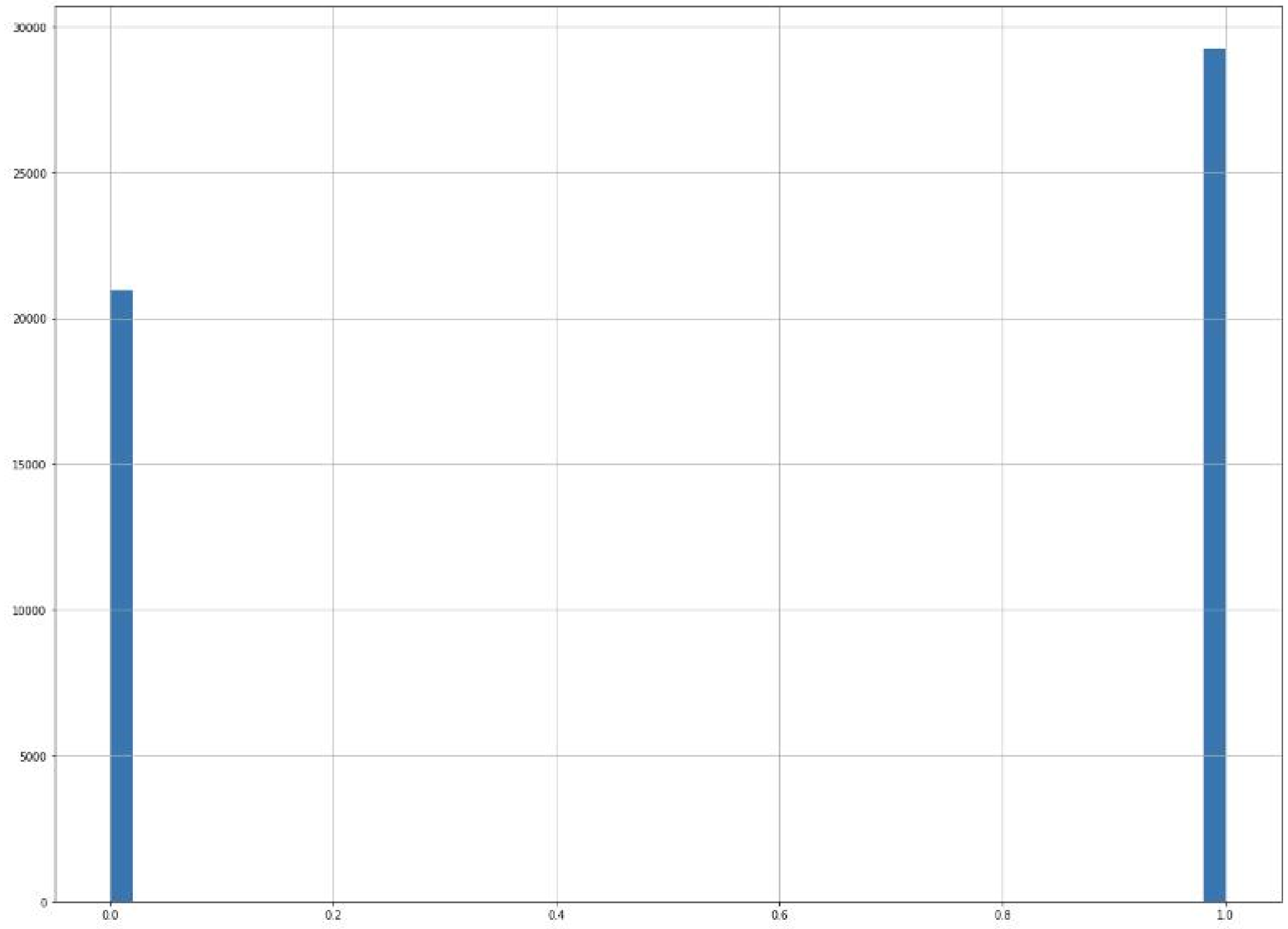
```
[27] # find the specifics for each of the numerical predictors
     train_dropped.describe()
```

	cap-diameter	stem-height	stem-width
count	50213.000000	50213.000000	50213.000000
mean	6.245186	6.600561	10.763191
std	4.542552	3.221714	7.744992
min	0.380000	1.200000	0.520000
25%	3.290000	4.680000	4.720000
50%	5.540000	5.900000	9.130000
75%	8.100000	7.600000	15.210000
max	58.890000	33.920000	58.950000

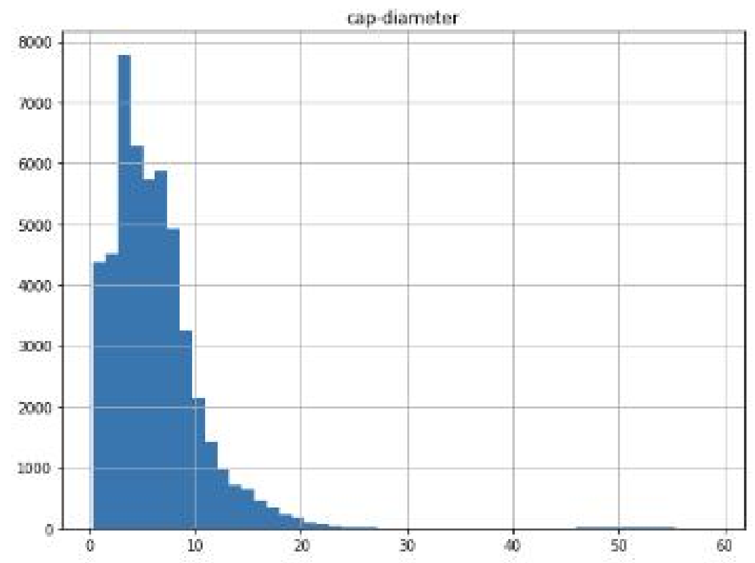
```
[28] # find correlation of the numeric predictors
     train_dropped.corr()
     import seaborn as sns
     sns.heatmap(train_dropped.corr())
     plt.show()
```

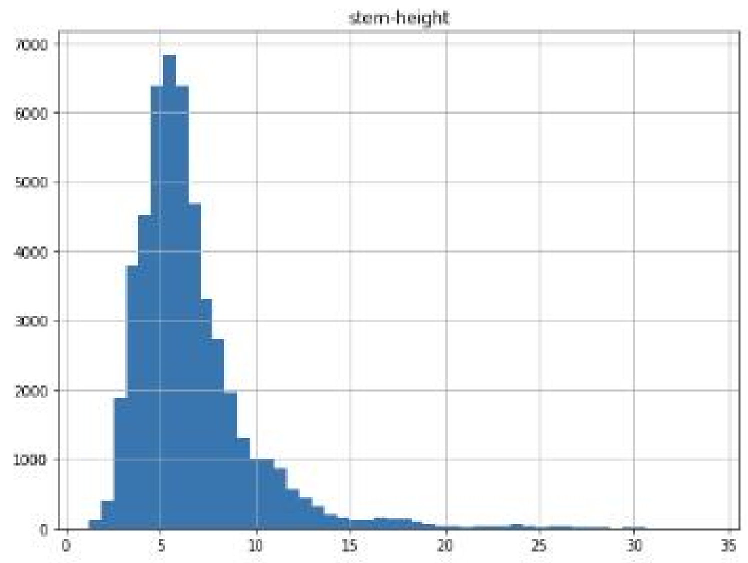


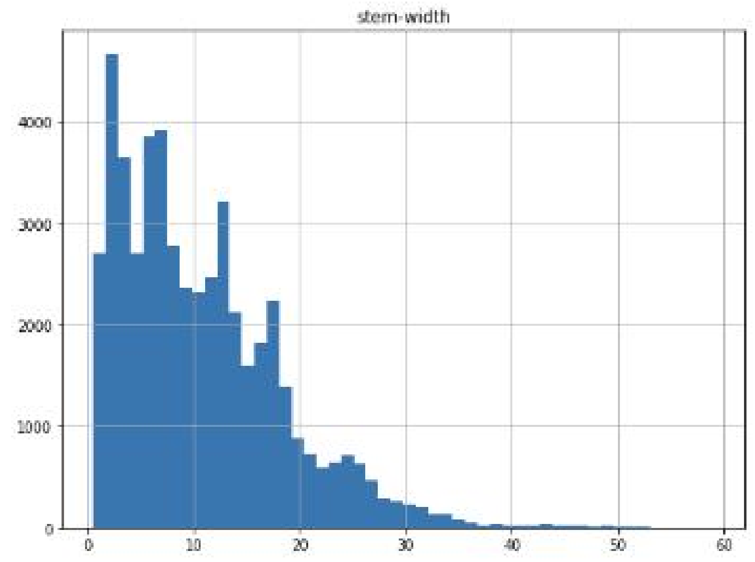
```
# visualization for the target variable
label.hist(bins = 50, figsize = (20,15))
plt.show()
```



```python
# visualization for numeric, predictor variables
train_dropped.hist(bins = 50, figsize = (20,15))
plt.show()
```

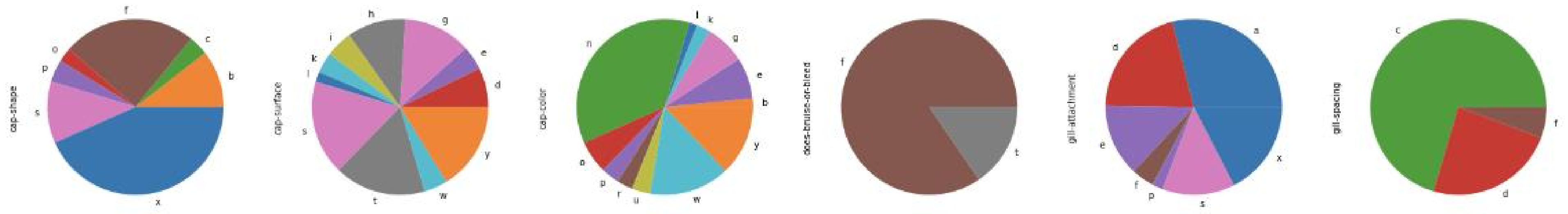




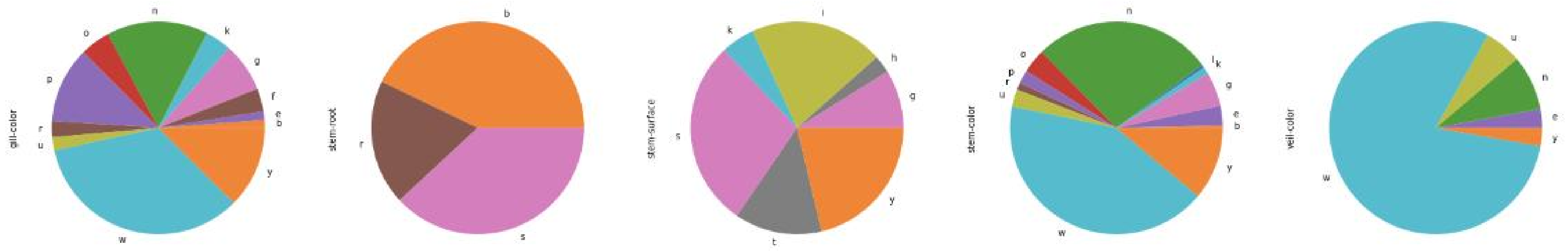


From above, we can see that there is a great amount of samples that are both poisonous and not poisonous. We can conclude that our classifier will have a sufficiently balanced dataset to adequately classify the two (i.e. there is no high skew in the two values as this can be problematic when considering accuracy rates).

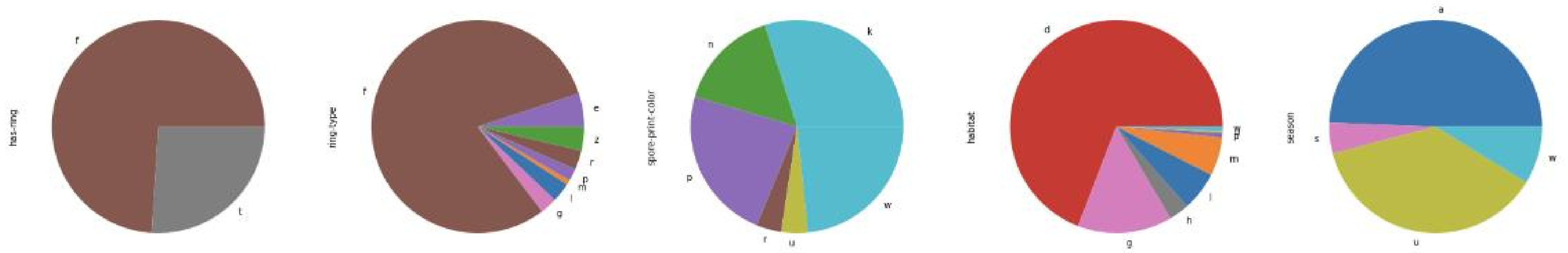
```
# visualization of the categorical variables
temp = (train_dropped.drop(["cap-diameter","stem-height","stem-width"], axis = 1)).apply(pd.value_counts).fillna(0)
temp1 = temp.iloc[:,0:6]
fig = temp1.plot(kind = 'pie',subplots = True, figsize = (30,30), legend = None)

plt.show()
```



```
[32] # next 5 predictors
     temp2 = temp.iloc[:, 6:11]
     fig = temp2.plot(kind = 'pie',subplots = True, figsize = (30,30), legend = None)

     plt.show()
```



```
[33] # next 5 predictors
     temp3 = temp.iloc[:,11:]
     fig = temp3.plot(kind = 'pie',subplots = True, figsize = (30,30), legend = None)

     plt.show()
```



[34]

```python
# below shows whether we should scale or encode any of the variables
for col in train_dropped:
  print(col)
  print(train_dropped[col].unique())
```

```
cap-diameter
[15.26 16.6  14.07 ... 21.8  20.42 22.71]
cap-shape
['x' 'f' 'p' 'b' 'c' 's' 'o']
cap-surface
['g' 'h' nan 't' 'y' 'e' 's' 'l' 'd' 'w' 'i' 'k']
cap-color
['o' 'e' 'n' 'g' 'r' 'w' 'y' 'p' 'u' 'b' 'l' 'k']
does-bruise-or-bleed
['f' 't']
gill-attachment
['e' nan 'a' 'd' 's' 'x' 'p' 'f']
gill-spacing
[nan 'c' 'd' 'f']
gill-color
['w' 'n' 'p' 'u' 'b' 'g' 'y' 'r' 'e' 'o' 'k' 'f']
stem-height
[16.95 17.99 17.8  ... 17.7  14.62 15.15]
stem-width
[17.09 18.19 17.74 ... 21.78 21.56 22.53]
stem-root
['s' nan 'b' 'r']
stem-surface
['y' nan 's' 'k' 'i' 'h' 't' 'g']
stem-color
['w' 'y' 'n' 'u' 'b' 'l' 'r' 'p' 'e' 'k' 'g' 'o']
veil-color
['w' 'y' nan 'n' 'e' 'u']
has-ring
['t' 'f']
ring-type
['g' 'p' 'e' 'l' 'f' 'm' nan 'r' 'z']
spore-print-color
[nan 'w' 'p' 'k' 'r' 'u' 'n']
habitat
['d' 'm' 'g' 'h' 'l' 'p' 'w' 'u']
season
['w' 'u' 'a' 's']
```

```python
# since "stem-width" is in mm and "stem-height", "cap-diameter" are in cm, we aim to convert "stem-height" and "cap-diameter"
# if we aim to convert "stem-width", since it is a small value, we may lose precision


# for training data
train_dropped['cap-diameter'] = train_dropped['cap-diameter']*100
train_dropped['stem-height'] = train_dropped['stem-height']*100

# for testing data
test_dropped['cap-diameter'] = test_dropped['cap-diameter']*100
test_dropped['stem-height'] = test_dropped['stem-height']*100
```

[36]

```python
# build numeric pipeline
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.impute import SimpleImputer
from sklearn.compose import ColumnTransformer, make_column_transformer

train_num = train_dropped[["cap-diameter","stem-height","stem-width"]]

num_pipeline = Pipeline([
    ('std_scalar', StandardScaler())
])

numerical_features = list(train_num)
```

[37]

```python
# generate variable that will capture features that are used for one hot encoding
OHE = list(train_dropped.drop(["cap-diameter","stem-height","stem-width"], axis = 1))
```

[38]
```python
# for training data
#  use to impute missing values with mode

# first store column names in variable
column_names = train_dropped.columns

# simple imputation using mode
imp = SimpleImputer(missing_values = np.nan, strategy = 'most_frequent')

# fit the simple imputation strategy
imputed_train_dropped = imp.fit_transform(train_dropped)

# revert back to data frame
imputed_train_dropped = pd.DataFrame(imputed_train_dropped, columns = column_names).reset_index(drop = 'index')
imputed_train_dropped
```

	cap-diameter	cap-shape	cap-surface	cap-color	does-bruise-or-bleed	gill-attachment	gill-spacing	gill-color	stem-height	stem-width	stem-root	stem-surface	stem-color	veil-color	has-ring	ring-type	spore-print-color	habitat	season
0	1526.0	x	g	o	f	e	c	w	1695.0	17.09	s	y	w	w	t	g	k	d	w
1	1660.0	x	g	o	f	e	c	w	1799.0	18.19	s	y	w	w	t	g	k	d	u
2	1407.0	x	g	o	f	e	c	w	1780.0	17.74	s	y	w	w	t	g	k	d	w
3	1417.0	f	h	e	f	e	c	w	1577.0	15.98	s	y	w	w	t	p	k	d	w
4	1464.0	x	h	o	f	e	c	w	1653.0	17.2	s	y	w	w	t	p	k	d	w
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
50208	118.0	s	s	y	f	f	f	f	393.0	6.22	b	s	y	w	f	f	k	d	a
50209	127.0	f	s	y	f	f	f	f	318.0	5.43	b	s	y	w	f	f	k	d	a
50210	127.0	s	s	y	f	f	f	f	386.0	6.37	b	s	y	w	f	f	k	d	u
50211	124.0	f	s	y	f	f	f	f	356.0	5.44	b	s	y	w	f	f	k	d	u
50212	117.0	s	s	y	f	f	f	f	325.0	5.45	b	s	y	w	f	f	k	d	u

50213 rows × 19 columns

```python
# for testing data
#  use to impute missing values with mode

# first store column names in variable
column_names = test_dropped.columns

# simple imputation using mode
imp = SimpleImputer(missing_values = np.nan, strategy = 'most_frequent')

# fit the simple imputation strategy
imputed_test_dropped = imp.fit_transform(test_dropped)

# revert back to data frame
imputed_test_dropped = pd.DataFrame(imputed_test_dropped, columns = column_names).reset_index(drop = 'index')
imputed_test_dropped
```

	cap-diameter	cap-shape	cap-surface	cap-color	does-bruise-or-bleed	gill-attachment	gill-spacing	gill-color	stem-height	stem-width	stem-root	stem-surface	stem-color	veil-color	has-ring	ring-type	spore-print-color	habitat	season
0	250.0	b	t	k	f	a	c	k	842.0	2.46	f	f	g	w	f	f	k	g	u
1	307.0	b	t	k	f	a	c	n	724.0	2.41	f	f	n	w	f	f	k	g	a
2	330.0	b	t	n	f	a	c	n	1022.0	2.53	f	f	n	w	f	f	k	g	u
3	349.0	b	t	k	f	a	c	k	1100.0	2.81	f	f	n	w	f	f	k	g	a
4	279.0	b	t	n	f	a	c	n	697.0	2.37	f	f	g	w	f	f	k	g	u
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
10851	5241.0	o	y	y	f	p	c	y	547.0	25.02	f	k	k	w	f	f	k	d	u
10852	5481.0	o	y	y	f	p	c	y	667.0	22.15	f	k	k	w	f	f	k	d	s
10853	4995.0	o	y	y	f	p	c	y	643.0	26.35	f	k	n	w	f	f	k	d	u
10854	5316.0	o	y	y	f	p	c	y	699.0	40.29	f	k	k	w	f	f	k	d	s
10855	4978.0	o	y	y	f	p	c	y	577.0	18.26	f	k	k	w	f	f	k	d	u

10856 rows × 19 columns

```
[40] # build fill pipeline
     full_pipeline = ColumnTransformer([
         ("num", num_pipeline, numerical_features),
         ("cat", OneHotEncoder(categories = "auto", handle_unknown = "ignore", sparse_output = False), OHE),
     ])
```

```
[41] # transform training data
     train_prepared = full_pipeline.fit_transform(imputed_train_dropped)
     print(train_prepared.shape)
```

```
(50213, 112)
```

```
[42] # transform testing data
     test_prepared = full_pipeline.fit_transform(imputed_test_dropped)
     print(test_prepared.shape)
```

```
(10856, 87)
```

```
# as fit_transform outputs an np.array, we aim to convert to a df

# for training data

# we aim to retrieve column names
ohe_encoder = OneHotEncoder(categories = "auto", handle_unknown = "ignore", sparse_output = False)
X_object = (imputed_train_dropped.drop(["cap-diameter","stem-height","stem-width"], axis = 1))
ohe_encoder.fit(X_object)

# features that will be introduced through One Hot Encoding
feature_names_ohe = ohe_encoder.get_feature_names_out(OHE)
feature_names_ohe

# convert the np.array to df (this df will not have column names)
train_prepared_df = pd.DataFrame(train_prepared)

# combine numerical features and features that were OHE
features_df = numerical_features + list(feature_names_ohe)
features_df

# rename df
train_prepared_df.set_axis(features_df, axis = 1, inplace = True)

train_prepared_df.head()
```

	cap-diameter	stem-height	stem-width	cap-shape_b	cap-shape_c	cap-shape_f	cap-shape_o	cap-shape_p	cap-shape_s	cap-shape_x	...	habitat_h	habitat_l	habitat_m	habitat_p	habitat_u	habitat_w	season_a	season_s	season_u	season_w
0	1.984546	3.212433	0.816899	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	1.0
1	2.279537	3.535246	0.958927	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	1.0	0.0
2	1.722576	3.476271	0.900825	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	1.0
3	1.744590	2.846165	0.673579	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	1.0
4	1.848058	3.082067	0.831101	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	1.0

5 rows × 112 columns

```
[44] # for testing data

     # we aim to retrieve column names
     ohe_encoder = OneHotEncoder(categories = "auto", handle_unknown = "ignore", sparse_output = False)
     X_object = (imputed_test_dropped.drop(["cap-diameter","stem-height","stem-width"], axis = 1))
     ohe_encoder.fit(X_object)

     # features that will be introduced through One Hot Encoding
     feature_names_ohe = ohe_encoder.get_feature_names_out(OHE)
     feature_names_ohe

     # convert the np.array to df (this df will not have column names)
     test_prepared_df = pd.DataFrame(test_prepared)

     # combine numerical features and features that were OHE
     features_df = numerical_features + list(feature_names_ohe)
     features_df

     # rename df
     test_prepared_df.set_axis(features_df, axis = 1, inplace = True)

     test_prepared_df.head()
```

	cap-diameter	stem-height	stem-width	cap-shape_b	cap-shape_f	cap-shape_o	cap-shape_p	cap-shape_s	cap-shape_x	cap-surface_d	...	spore-print-color_p	spore-print-color_w	habitat_d	habitat_g	habitat_h	habitat_l	season_a	season_s	season_u	season_w
0	-0.881539	0.483594	-1.041207	1.0	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	1.0	0.0
1	-0.804165	0.187381	-1.044440	1.0	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	1.0	0.0	0.0	1.0	0.0	0.0	0.0
2	-0.772944	0.935446	-1.036680	1.0	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	1.0	0.0
3	-0.747152	1.131248	-1.018573	1.0	0.0	0.0	0.0	0.0	0.0	0.0	...	0.0	0.0	0.0	1.0	0.0	0.0	1.0	0.0	0.0	0.0
4	-0.842173	0.119603	-1.047027	1.0	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	1.0	0.0

5 rows × 87 columns

5. Data Augmentation (Creating at least 2 New Features)

"stem_vol" Predictor

```
[45] # use volume of stem as a new predictor
     stem_vol_train = train_prepared_df["stem-height"]*train_prepared_df["stem-width"] # training data
     stem_vol_train
```

```
0        2.624232
1        3.390044
2        3.131510
3        1.917116
4        2.561510
           ...
50208    0.486255
50209    0.731114
50210    0.482526
50211    0.648674
50212    0.713467
Length: 50213, dtype: float64
```

```
[46] # adding feature to the prepared training dataframe
     train_prepared_df["stem_vol"] = stem_vol_train
```

```
[47] # do the same for testing data
     stem_vol_test = test_prepared_df["stem-height"]*test_prepared_df["stem-width"]
     stem_vol_test
```

```
0       -0.503522
1       -0.195708
2       -0.969758
3       -1.152259
4       -0.125227
           ...
10851   -0.107316
10852    0.010280
10853   -0.008035
10854    0.175111
10855    0.003538
Length: 10856, dtype: float64
```

```
[48] # adding feature to the prepared testing dataframe
     test_prepared_df["stem_vol"] = stem_vol_test
```

"diam_stem_ratio" Predictor

```
# ratio between cap-diameter and stem-width

diam_stem_ratio_train = train_prepared_df["cap-diameter"]/train_prepared_df["stem-width"] # training data
diam_stem_ratio_train
```

```
0        2.429367
1        2.377175
2        1.912222
3        2.590032
4        2.223625
           ...
50208    1.900883
50209    1.590535
50210    1.930858
50211    1.603132
50212    1.628612
Length: 50213, dtype: float64
```

```
[50] # adding feature to the prepared training dataframe
     train_prepared_df["diam_stem_ratio"] = diam_stem_ratio_train
```

```
[51] # do the same for testing data

     diam_stem_ratio_test = test_prepared_df["cap-diameter"]/test_prepared_df["stem-width"]
     diam_stem_ratio_test
```

```
0          0.846651
1          0.769948
2          0.745595
3          0.733528
4          0.804348
            ...
10851     14.110339
10852     26.798266
10853     11.037903
10854      4.266704
10855   -284.261085
Length: 10856, dtype: float64
```

```
[52] # adding feature to the prepared testing dataframe
     test_prepared_df["diam_stem_ratio"] = diam_stem_ratio_test
```

6. Logistic Regression & Statistical Hypothesis Testing

Logistic Regression

[53]
```python
# splitting training data to have a validation set
from sklearn.model_selection import train_test_split, cross_val_score, GridSearchCV
X_train, X_test, Y_train, Y_test = train_test_split(train_prepared_df, label, test_size = 0.2)
```

[54]
```python
# fit logistic regression model
from sklearn.linear_model import LogisticRegression
log_model = LogisticRegression(random_state = 0, max_iter = 3000)
log_model_fit = log_model.fit(X_train, Y_train)
log_pred = log_model.predict(X_test)
```

[55]
```python
# accuracy metrics of logistic regression model
from sklearn import metrics

# the accuracy of the model
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(log_pred, Y_test)))

# the precision of the model
print("%-12s %f" % ('Precision:', metrics.precision_score(log_pred, Y_test)))

# the recall score of the model
print("%-12s %f" % ('Recall Score:', metrics.recall_score(log_pred, Y_test)))

# the F1 score of the model
print("%-12s %f" % ('F1 Score:', metrics.f1_score(log_pred, Y_test)))
```

```
Accuracy:    0.859803
Precision:   0.875297
Recall Score: 0.884892
F1 Score:    0.880068
```

Statistical Hypothesis Testing

```python
# the subset with 3 or more features
# define the subset to be the first three columns or the numerical features
train_prepared_df.iloc[:,0:3]
```

	cap-diameter	stem-height	stem-width
0	1.984546	3.212433	0.816899
1	2.279537	3.535246	0.958927
2	1.722576	3.476271	0.900825
3	1.744590	2.846165	0.673579
4	1.848058	3.082067	0.831101
...	...	...	...
50208	-1.115064	-0.828934	-0.586603
50209	-1.095251	-1.061732	-0.688605
50210	-1.095251	-0.850662	-0.567236
50211	-1.101855	-0.943781	-0.687314
50212	-1.117265	-1.040004	-0.686023

50213 rows × 3 columns

[57]
```python
import statsmodels.api as sm

# run to add_constant to add a constant feature to df that will serve as Y intercept
sm_x = sm.add_constant(train_prepared_df.iloc[:,0:3])

shroom_stats = sm.Logit(label, sm_x)

results_stats = shroom_stats.fit()

print(results_stats.summary())
```

```
Optimization terminated successfully.
         Current function value: 0.665016
         Iterations 5
                           Logit Regression Results
==============================================================================
Dep. Variable:                  class   No. Observations:                50213
Model:                          Logit   Df Residuals:                    50209
Method:                           MLE   Df Model:                            3
Date:                Sun, 05 Mar 2023   Pseudo R-squ.:                 0.02134
Time:                        11:11:00   Log-Likelihood:                -33392.
converged:                       True   LL-Null:                       -34121.
Covariance Type:            nonrobust   LLR p-value:                     0.000
================================================================================
                   coef    std err          z      P>|z|      [0.025      0.975]
--------------------------------------------------------------------------------
const            0.3326      0.009     36.200      0.000       0.315       0.351
cap-diameter    -0.4377      0.020    -21.460      0.000      -0.478      -0.398
stem-height      0.0210      0.011      1.918      0.055      -0.000       0.042
stem-width       0.0512      0.016      3.162      0.002       0.019       0.083
================================================================================
```

7. Dimensionality Reduction using PCA

```
[58] # PCA: https://scikit-learn.org/stable/modules/generated/sklearn.decomposition.PCA.html
```

```
[59] # import necessary packages
     from sklearn import decomposition
```

```
[60] # notice the shape of the current training set
     X_train.shape
```

```
(40170, 114)
```

```
[61] # we aim to decompose this through pca
     # first, we decompose through singular value decomposition
     # asign a value to number of components that will be utilized
     pca = decomposition.PCA(n_components = 10)

     pca_train = pca.fit_transform(X_train)
```

```
# notice that this aligns with the number of components
pca_train.shape
```

```
(40170, 10)
```

```
[63] # perform logistic regression on these components
     log_reg = LogisticRegression(solver = 'liblinear')
     log_reg.fit(pca_train, Y_train)
```

```
▾          LogisticRegression
LogisticRegression(solver='liblinear')
```

```
[64] # now that we have our model from these components, we assess accuracy on validation data
     pca_val = pca.transform(X_test)
     predicted = log_reg.predict(pca_val)

     print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(Y_test, predicted)))
```

```
Accuracy:    0.652096
```

```
[65] # tells us the proportion of the total variance in the data that is explained by each PC.
     print(pca.explained_variance_ratio_)

     # represent the amount of variance in the data that is accounted for by each principal component
     print(pca.singular_values_)
```

```
[9.77369313e-01 4.54321975e-03 2.41092619e-03 1.15340704e-03
 9.21429073e-04 8.27259717e-04 8.02206587e-04 7.76805854e-04
 6.50134638e-04 6.16988100e-04]
[4505.17409913  307.15960544  223.75574069  154.76527682  138.32898318
  131.06996021  129.07000919  127.01016319  116.19404789  113.19327435]
```

The accuracy has gone down when utilizing principal component analysis.

```
[66] # Now we do the same for the testing data
     pca = decomposition.PCA(n_components = 10)

     pca_test = pca.fit_transform(test_prepared_df)

     pca_test.shape
```

```
(10856, 10)
```

8. Experiment with any 2 other models (Non-Ensemble)

```
[67] # Models: https://scikit-learn.org/stable/supervised_learning.html
```

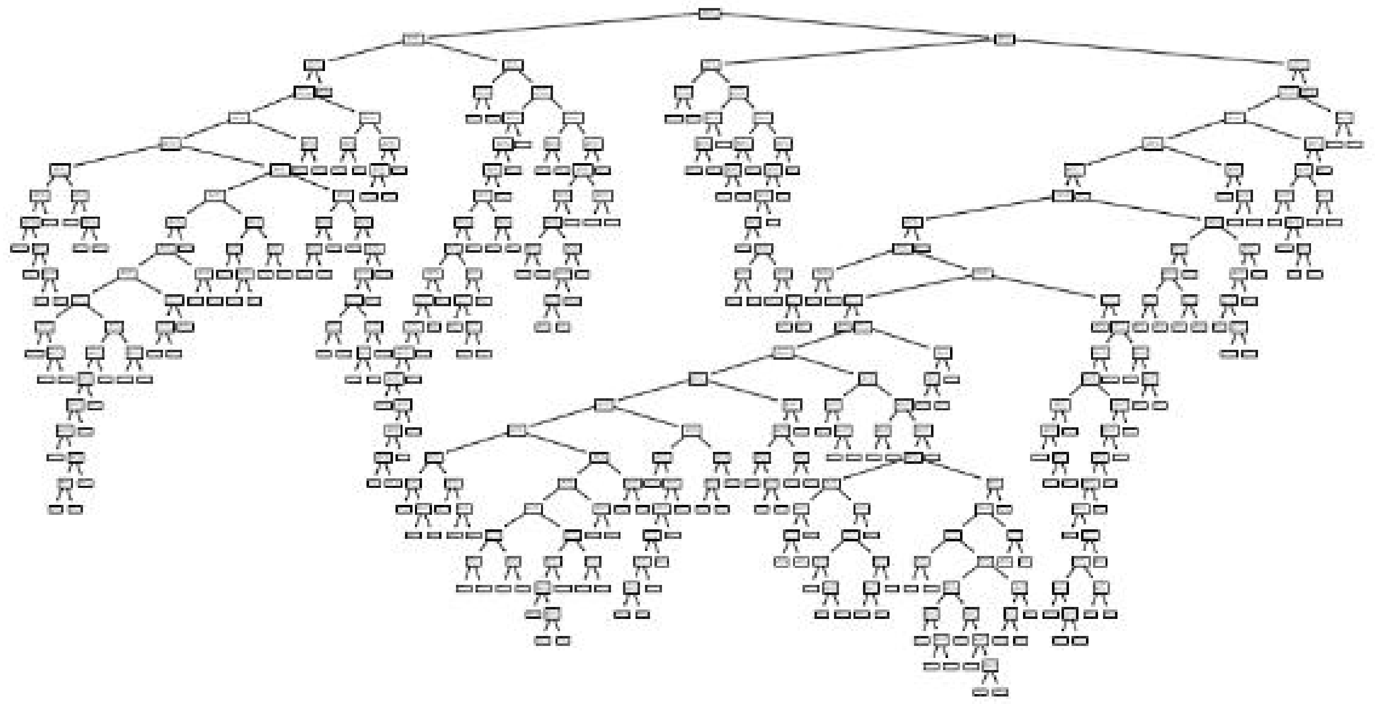
Model 1: Decision Trees

```
# Decision Trees

from sklearn import tree

# call the model
tree_model = tree.DecisionTreeClassifier()

# fit the model with our data
tree_fit = tree_model.fit(X_train, Y_train)

# predict using our model
tree_pred = tree_fit.predict(X_test)

# accuracy score
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(tree_pred, Y_test)))
```

```
Accuracy:    0.998208
```

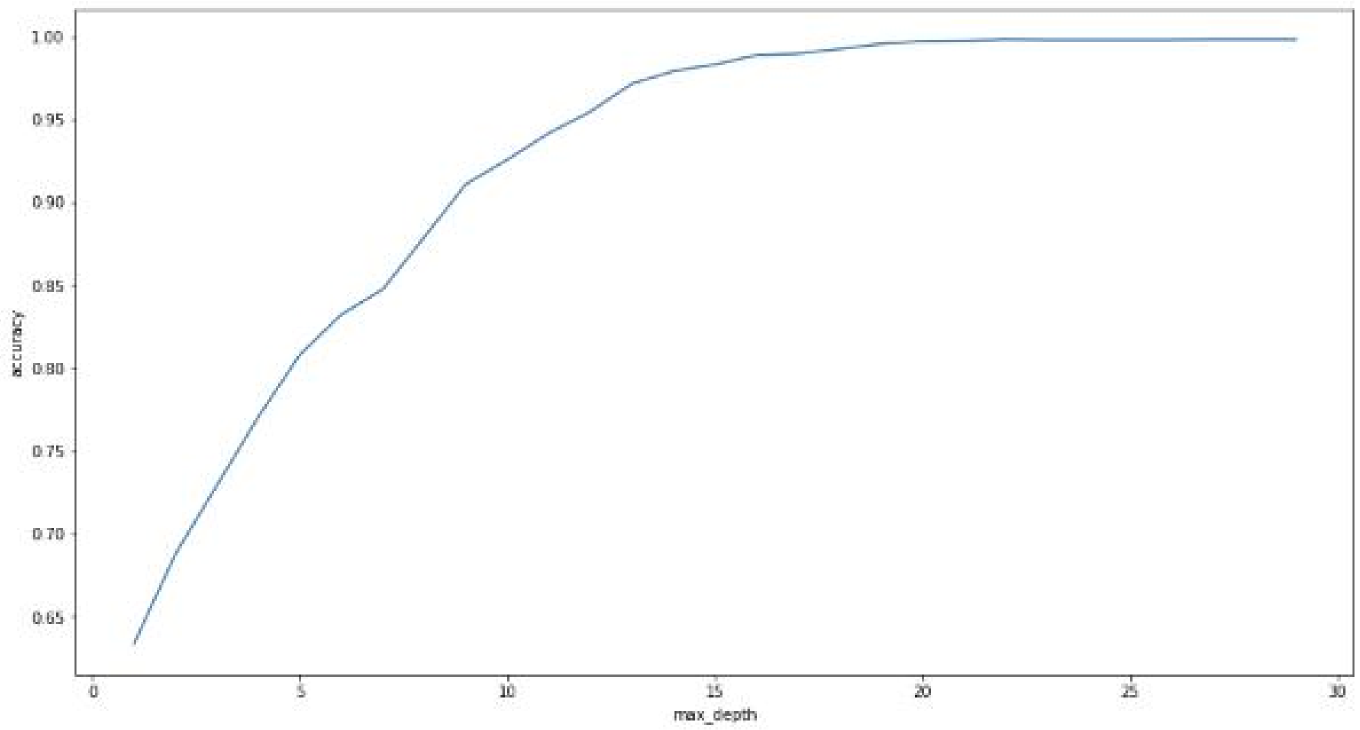
```
[69] # overall image of decision tree
     print(tree.plot_tree(tree_model))
```

```
[Text(0.5163931005141315, 0.9814814814814815, 'x[77] <= 0.5\ngini = 0.487\nsamples = 40170\nvalue = [168
```



```
### pruning decision tree

# find the best max_length to use without negatively affecting the decision tree
max_depth = []
acc_gini = []
acc_entropy = []
for i in range(1,30):
 dtree = tree.DecisionTreeClassifier(criterion='gini', max_depth=i)
 dtree.fit(X_train, Y_train)
 pred = dtree.predict(X_test)
 acc_gini.append(metrics.accuracy_score(Y_test, pred))
 ####
 max_depth.append(i)
d = pd.DataFrame({'acc_gini':pd.Series(acc_gini),
 'max_depth':pd.Series(max_depth)})

# plot to find the max_depth value when elbow occurs
plt.plot('max_depth','acc_gini', data=d, label='gini')
plt.xlabel('max_depth')
plt.ylabel('accuracy')

# we should use max_depth = 15
```

```
Text(0, 0.5, 'accuracy')
```

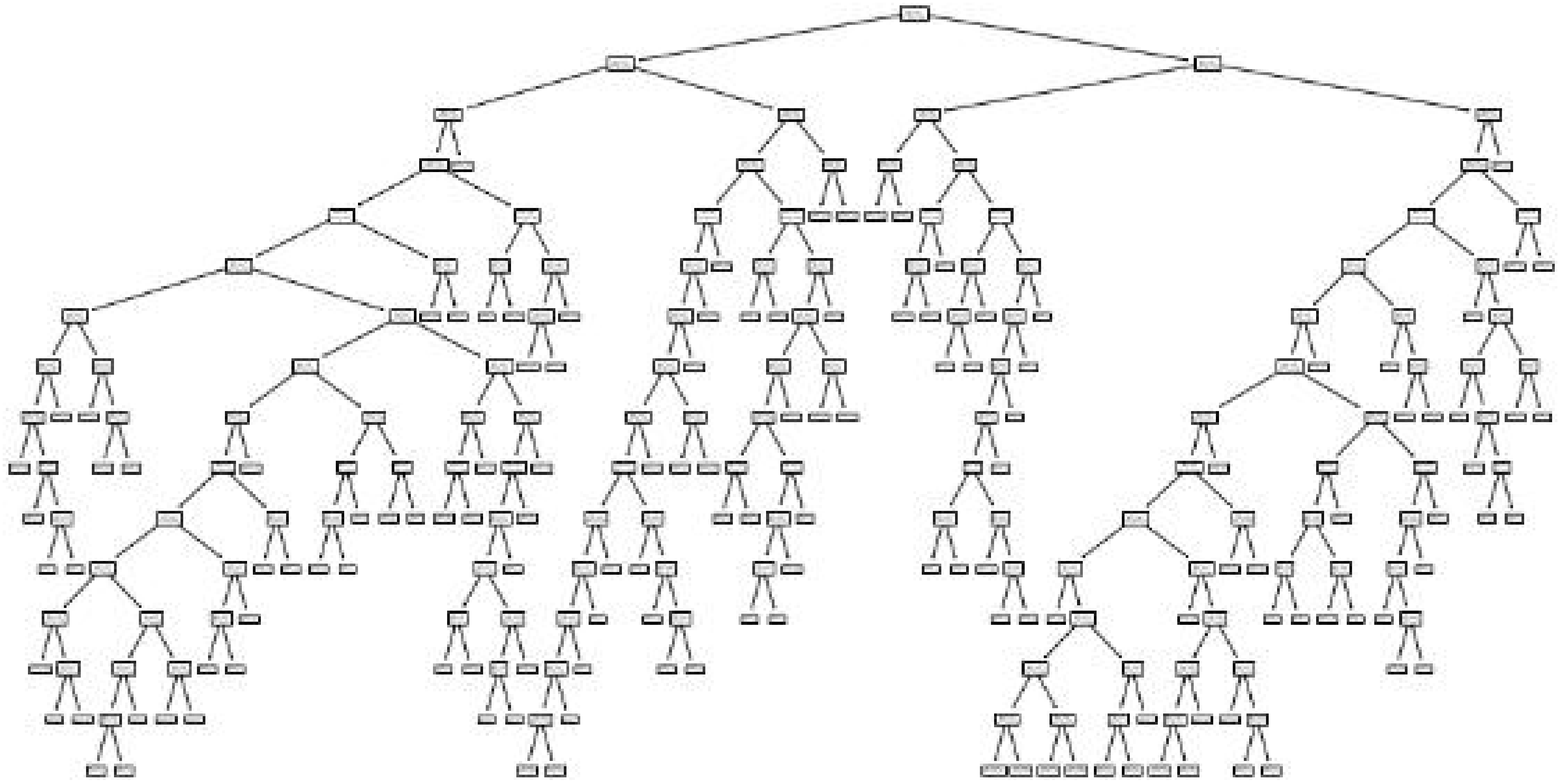


```
[71] # prune the decision tree by using max_depth = 15

# call the pruned model
tree_model_prune = tree.DecisionTreeClassifier(max_depth = 15)

# fit the model with our data
tree_fit_prune = tree_model_prune.fit(X_train, Y_train)

# predict using our model
tree_pred_prune = tree_fit_prune.predict(X_test)

# accuracy score of pruned model
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(tree_pred_prune, Y_test)))
```

```
Accuracy:    0.983172
```

```
# overall image of the pruned decision tree
print(tree.plot_tree(tree_model_prune))
```

```
[Text(0.5856309557174888, 0.96875, 'x[77] <= 0.5\ngini = 0.487\nsamples = 40170\nvalue = [16830, 23340]'), Text(0.396
```



From above, we can see that the decision tree clearly became less deep. This made the model less complex. However, we noticed a drop in accuracy score after pruning the tree so there is a tradeoff between computational cost and performance.

Model 2: Naive Bayes

Naive Bayes is a probabilistic machine learning model used for classification tasks. It is based on Bayes' theorem, which is a fundamental principle in probability theory that describes how to update probabilities based on new evidence. The Naive Bayes model makes some simplifying assumptions about the data, including that the features are independent of each other and that each feature contributes equally to the probability of the class.

```
# Gaussian Naive Bayes

from sklearn.naive_bayes import GaussianNB

G_bayes_model = GaussianNB()
G_bayes_model.fit(X_train,Y_train)

G_bayes_pred = G_bayes_model.predict(X_test)

print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(G_bayes_pred, Y_test)))
```

```
Accuracy:    0.626904
```

```
[74] # Bernoulli Naive Bayes

from sklearn.naive_bayes import BernoulliNB

B_bayes_model = BernoulliNB()

B_bayes_model.fit(X_train, Y_train)

B_bayes_pred = B_bayes_model.predict(X_test)

print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(B_bayes_pred, Y_test)))
```

```
Accuracy:    0.785024
```

Since the normality assumption likely does not hold in these given features, the Gaussian Naive Bayes model did not yield a very high accuracy rate. In contrary, the Bernoulli Naive Bayes model had provided us with a higher accuracy rate. This is because the Bernoulli Naive Bayes mdoel is most appropriate when working with binary or boolean data and in our prepared data frame, there were more features that involved binary values. Overall, since the data had both binary and continuous values, the Naive Bayes Model did not perform very well. Additionally, the overall model assumption that the predictors are independent could have been violated as well.

9. Experiment with 1 Ensemble Method

```
[75] # Ensemble Methods: https://scikit-learn.org/stable/modules/ensemble.html
```

Random Forest

```
# import necessary packages
from sklearn.ensemble import RandomForestClassifier

# call the random forest model
forest_model = RandomForestClassifier(n_estimators = 5)

# fit the model with data
forest_model_fit = forest_model.fit(X_train, Y_train)

# predict using our model
forest_model_pred = forest_model_fit.predict(X_test)

# accuracy score
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(forest_model_pred, Y_test)))
```

```
Accuracy:    0.999502
```

```
[77] # now try with n_estimators = 10

# call the random forest model
forest_model = RandomForestClassifier(n_estimators = 10)

# fit the model with data
forest_model_fit = forest_model.fit(X_train, Y_train)

# predict using our model
forest_model_pred = forest_model_fit.predict(X_test)

# accuracy score
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(forest_model_pred, Y_test)))
```

```
Accuracy:    0.999801
```

The accuracy has slightly gone up after tuning the number of estimators.

```
[78] # now we experiment with the max depth

# call the random forest model
forest_model = RandomForestClassifier(n_estimators = 10, max_depth = 15)

# fit the model with data
forest_model_fit = forest_model.fit(X_train, Y_train)

# predict using our model
forest_model_pred = forest_model_fit.predict(X_test)

# accuracy score
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(forest_model_pred, Y_test)))
```

```
Accuracy:    0.994324
```

The accuracy has slightly gone down after manipulating the max_depth

10. Cross-Validation & Hyperparameter Tuning for All 3 Models

```
[79] # Cross-Validation: https://scikit-learn.org/stable/modules/cross_validation.html
     # Hyperparameter Tuning: https://scikit-learn.org/stable/modules/grid_search.html
```

Cross-Validation

```
[80] from sklearn import model_selection
     from sklearn.model_selection import KFold

     # define number of splits, seed, and let data be shuffled
     kfold = model_selection.KFold(n_splits = 10, random_state = 42, shuffle = True)

     # call cross_val_score with argument cv = kfold to get accuracy performance score
     # of our modelon the 10 fold validation data
     # other arguments: model, training_data, training labels
     results = model_selection.cross_val_score(log_model, train_prepared_df, label, cv = kfold)

     # print the average score for your model on the 10 folds
     print("Cross Validation Accuracy: %.2f%%" % (results.mean()*100.0))
```

```
Cross Validation Accuracy: 85.68%
```

```
     # for tree model
     results = model_selection.cross_val_score(tree_model, train_prepared_df, label, cv = kfold)

     # print the average score for your model on the 10 folds
     print("Cross Validation Accuracy: %.2f%%" % (results.mean()*100.0))
```

```
Cross Validation Accuracy: 99.84%
```

```
[82] # for pruned tree model
     results = model_selection.cross_val_score(tree_model_prune, train_prepared_df, label, cv = kfold)

     # print the average score for your model on the 10 folds
     print("Cross Validation Accuracy: %.2f%%" % (results.mean()*100.0))
```

```
Cross Validation Accuracy: 98.31%
```

```
[83] # for bayes classifier
     results = model_selection.cross_val_score(B_bayes_model, train_prepared_df, label, cv = kfold)

     # print the average score for your model on the 10 folds
     print("Cross Validation Accuracy: %.2f%%" % (results.mean()*100.0))
```

```
Cross Validation Accuracy: 77.93%
```

```
[84] # for random forest
     results = model_selection.cross_val_score(forest_model, train_prepared_df, label, cv = kfold)

     # print the average score for your model on the 10 folds
     print("Cross Validation Accuracy: %.2f%%" % (results.mean()*100.0))
```

```
Cross Validation Accuracy: 99.43%
```

Hyperparameter Tuning

```
[85] from sklearn.model_selection import GridSearchCV
```

Decision Tree Model

```
[86] params = [{
         'criterion' : ['gini', 'entropy', 'log_loss'],
         'splitter' : ["best", 'random'],
         'max_depth' : [5, 10, 20, 30]
     }]

     # define grid search cross validation
     clf2 = model_selection.GridSearchCV(estimator = tree_model, param_grid = params, scoring = "accuracy", cv = kfold, verbose = True)

     # call on the data
     clf2_fit = clf2.fit(train_prepared_df, label)

     # retrieve estimator which gave highest score on cross validation
     best_model = clf2_fit.best_estimator_
     print(best_model)

     # get the mean score for your best model
     print(clf2_fit.best_score_)
```

```
     Fitting 10 folds for each of 24 candidates, totalling 240 fits
     DecisionTreeClassifier(max_depth=30, splitter='random')
     0.9995220273973169
```

Bayes Classifier

```
[87] params = [{
         'alpha' : [0.5, 0.8, 1],
         'force_alpha' : [True, False]
     }]

     # define grid search cross validation
     clf3 = model_selection.GridSearchCV(estimator = B_bayes_model, param_grid = params, scoring = "accuracy", cv = kfold, verbose = True)

     # call on the data
     clf3_fit = clf3.fit(train_prepared_df, label)

     # retrieve estimator which gave highest score on cross validation
     best_model = clf3_fit.best_estimator_
     print(best_model)

     # get the mean score for your best model
     print(clf3_fit.best_score_)
```

```
     Fitting 10 folds for each of 6 candidates, totalling 60 fits
     BernoulliNB(alpha=0.5, force_alpha=True)
     0.7793800526042316
```

Random Forest

```
[94] params = [{
         'n_estimators' : [10, 50, 100],
         'criterion' : ["gini", "entropy", "log_loss"],
         'max_depth' : [10, 20, 30],
         'min_samples_leaf': [1, 2, 3]
     }]

     # define grid search cross validation
     clf4 = model_selection.GridSearchCV(estimator = forest_model, param_grid = params, scoring = "accuracy", cv = kfold, verbose = True)

     # call on the data
     clf4_fit = clf4.fit(train_prepared_df, label)

     # retrieve estimator which gave highest score on cross validation
     best_model = clf4_fit.best_estimator_
     print(best_model)

     # get the mean score for your best model
     print(clf4_fit.best_score_)
```

```
     Fitting 10 folds for each of 81 candidates, totalling 810 fits
     RandomForestClassifier(max_depth=30, n_estimators=50)
     0.9999203425263434
```

11. Report Final Results

```
[108] # Temporarily combining the training and testing, so that necessary OHE can be made
      train_test_comb = imputed_train_dropped.append(imputed_test_dropped)


      # as fit_transform outputs an np.array, we aim to convert to a df

      # we aim to retrieve column names
      ohe_encoder = OneHotEncoder(categories = "auto", handle_unknown = "ignore", sparse_output = False)
      X_object = (train_test_comb.drop(["cap-diameter","stem-height","stem-width"], axis = 1))
      ohe_encoder.fit(X_object)

      # fit the full pipeline
      train_test_comb_prepared = full_pipeline.fit_transform(train_test_comb)

      # features that will be introduced through One Hot Encoding
      feature_names_ohe = ohe_encoder.get_feature_names_out(OHE)

      # convert the np.array to df (this df will not have column names)
      train_test_comb_prepared_df = pd.DataFrame(train_test_comb_prepared)

      # combine numerical features and features that were OHE
      features_df = numerical_features + list(feature_names_ohe)

      # rename df
      train_test_comb_prepared_df.set_axis(features_df, axis = 1, inplace = True)

      train_test_comb_prepared_df.head()
```

	cap-diameter	stem-height	stem-width	cap-shape_b	cap-shape_c	cap-shape_f	cap-shape_o	cap-shape_p	cap-shape_s	cap-shape_x	...	habitat_h	habitat_l	habitat_m	habitat_p	habitat_u	habitat_w	season_a	season_s	season_u	season_w
0	1.619462	3.076705	0.492293	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	1.0
1	1.873982	3.385311	0.601900	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	1.0	0.0
2	1.393432	3.328931	0.557061	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	1.0
3	1.412426	2.726555	0.381690	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	1.0
4	1.501699	2.952075	0.503254	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	1.0

5 rows × 118 columns

```
[109] # resplit back to training and testing
      train_final = train_test_comb_prepared_df.iloc[:50213, :]
      test_final = train_test_comb_prepared_df.iloc[50213:, :]
```

Decision Tree

```
[116] # model with best hyperparameter

      # call the model
      tree_model_best = tree.DecisionTreeClassifier(max_depth=30, splitter='random')

      # fit the model with our data
      tree_best_fit = tree_model_best.fit(train_final, label)

      # predict using our model
      tree_best_pred = tree_best_fit.predict(test_final)
```

```
[117] # the accuracy of the model
      print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(tree_best_pred, label_test)))

      # the precision of the model
      print("%-12s %f" % ('Precision:', metrics.precision_score(tree_best_pred, label_test)))

      # the recall score of the model
      print("%-12s %f" % ('Recall Score:', metrics.recall_score(tree_best_pred, label_test)))

      # the F1 score of the model
      print("%-12s %f" % ('F1 Score:', metrics.f1_score(tree_best_pred, label_test)))
```

```
Accuracy:    0.432019
Precision:   0.792294
Recall Score: 0.414434
F1 Score:    0.544205
```

Bayes Classifier

[118]
```
# model with best hyperparameter

# call the bayes model
B_bayes_model_best = BernoulliNB(alpha=0.5, force_alpha=True)

# fit the best model
B_bayes_best_fit = B_bayes_model_best.fit(train_final, label)

# predict using our model
B_bayes_best_pred = B_bayes_best_fit.predict(test_final)
```

[119]
```
# the accuracy of the model
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(B_bayes_best_pred, label_test)))

# the precision of the model
print("%-12s %f" % ('Precision:', metrics.precision_score(B_bayes_best_pred, label_test)))

# the recall score of the model
print("%-12s %f" % ('Recall Score:', metrics.recall_score(B_bayes_best_pred, label_test)))

# the F1 score of the model
print("%-12s %f" % ('F1 Score:', metrics.f1_score(B_bayes_best_pred, label_test)))
```

```
Accuracy:    0.498066
Precision:   1.000000
Recall Score: 0.460228
F1 Score:    0.630351
```

Random Forest Classification

[120]
```
# model with best hyperparameter

# call the random forest model
forest_model_best = RandomForestClassifier(max_depth=30, n_estimators=50)

# fit the model with data
forest_model_best_fit = forest_model_best.fit(train_final, label)

# predict using our model
forest_model_best_pred = forest_model_best_fit.predict(test_final)
```

[121]
```
# the accuracy of the model
print("%-12s %f" % ('Accuracy:', metrics.accuracy_score(forest_model_best_pred, label_test)))

# the precision of the model
print("%-12s %f" % ('Precision:', metrics.precision_score(forest_model_best_pred, label_test)))
-
# the recall score of the model
print("%-12s %f" % ('Recall Score:', metrics.recall_score(forest_model_best_pred, label_test)))

# the F1 score of the model
print("%-12s %f" % ('F1 Score:', metrics.f1_score(forest_model_best_pred, label_test)))
```

```
Accuracy:    0.459285
Precision:   0.956522
Recall Score: 0.439478
F1 Score:    0.602250
```