

Mushroom Identifier 3000

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Why Mushrooms?



Personal motivation

Super Mario!



Social impact

- 1) Yun Nan Mushroom Situation
- 2) 100 over deaths a year around the world



Commercial Impact

- 1) Shroomers
- 2) Small Businesses

Problem Definition:

To investigate the identifiable characteristics of a poisonous mushroom and use ML models to predict whether they are edible.



Exploratory Data Analysis and Visualization

Data cleaning -> Visualization -> Analysis

02

Data Cleaning

1) Through analysis, all the variables are categorical variables with no empty slot

class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	gill-color	...	stalk-surface-below-ring	stalk-color-above-ring	stalk-color-below-ring	veil-type	veil-color	ring-number	ring-type	spore-print-color	popu
0	p	x	s	n	t	p	f	c	n	k	s	w	w	p	w	o	p	k	
1	e	x	s	y	t	a	f	c	b	k	s	w	w	p	w	o	p	n	
2	e	b	s	w	t	i	f	c	b	n	s	w	w	p	w	o	p	n	
3	p	x	y	w	t	p	f	c	n	n	s	w	w	p	w	o	p	k	
4	e	x	s	g	f	n	f	w	b	k	s	w	w	p	w	o	e	n	
...	
8119	e	k	s	n	f	n	a	c	b	y	s	o	o	p	o	o	p	b	
8120	e	x	s	n	f	n	a	c	b	y	s	o	o	p	n	o	p	b	
8121	e	f	s	n	f	n	a	c	b	n	s	o	o	p	o	o	p	b	
8122	p	k	y	n	f	y	f	c	n	b	k	w	w	p	w	o	e	w	
8123	e	x	s	n	f	n	a	c	b	y	s	o	o	p	o	o	p	o	

Data Cleaning

2) Using their readme, we converted all the variables to make them readable.

	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	gill-color	...	stalk-surface-below-ring	stalk-color-above-ring	stalk-color-below-ring	veil-type	veil-color	ring-number	ring-type	?
0	p	convex	smooth	brown	have bruises	pungent	free	close	narrow	black	...	smooth	white	white	partial	white	one	pendant	
1	e	convex	smooth	yellow	have bruises	almond	free	close	broad	black	...	smooth	white	white	partial	white	one	pendant	
2	e	bell	smooth	white	have bruises	anise	free	close	broad	brown	...	smooth	white	white	partial	white	one	pendant	
3	p	convex	scaly	white	have bruises	pungent	free	close	narrow	brown	...	smooth	white	white	partial	white	one	pendant	
4	e	convex	smooth	grey	no bruises	none	free	crowded	broad	black	...	smooth	white	white	partial	white	one	evanescent	
...	
8119	e	knobbed	smooth	brown	no bruises	none	attached	close	broad	yellow	...	smooth	orange	orange	partial	orange	one	pendant	
8120	e	convex	smooth	brown	no bruises	none	attached	close	broad	yellow	...	smooth	orange	orange	partial	brown	one	pendant	
8121	e	flat	smooth	brown	no bruises	none	attached	close	broad	brown	...	smooth	orange	orange	partial	orange	one	pendant	
8122	p	knobbed	scaly	brown	no bruises	fishy	free	close	narrow	buff	...	silky	white	white	partial	white	one	evanescent	
8123	e	convex	smooth	brown	no bruises	none	attached	close	broad	yellow	...	smooth	orange	orange	partial	orange	one	pendant	

8124 rows × 23 columns

Data Cleaning

3) Split the data into their classes, Poisonous and Edible

Edible mushrooms

index	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	...	stalk-surface-below-ring	stalk-color-above-ring	stalk-color-below-ring	veil-type	veil-color	ring-number	ring-type	spc	
0	1	e	convex	smooth	yellow	have bruises	almond	free	close	broad	...	smooth	white	white	partial	white	one	pendant	br
1	2	e	bell	smooth	white	have bruises	anise	free	close	broad	...	smooth	white	white	partial	white	one	pendant	br
2	4	e	convex	smooth	grey	no bruises	none	free	crowded	broad	...	smooth	white	white	partial	white	one	evanescent	br
3	5	e	convex	scaly	yellow	have bruises	almond	free	close	broad	...	smooth	white	white	partial	white	one	pendant	b
4	6	e	bell	smooth	white	have bruises	almond	free	close	broad	...	smooth	white	white	partial	white	one	pendant	b
...	
4203	8115	e	convex	smooth	brown	no bruises	none	attached	close	broad	...	smooth	orange	orange	partial	orange	one	pendant	ora
4204	8119	e	knobbed	smooth	brown	no bruises	none	attached	close	broad	...	smooth	orange	orange	partial	orange	one	pendant	
4205	8120	e	convex	smooth	brown	no bruises	none	attached	close	broad	...	smooth	orange	orange	partial	brown	one	pendant	
4206	8121	e	flat	smooth	brown	no bruises	none	attached	close	broad	...	smooth	orange	orange	partial	orange	one	pendant	
4207	8123	e	convex	smooth	brown	no bruises	none	attached	close	broad	...	smooth	orange	orange	partial	orange	one	pendant	

4208 rows × 24 columns

Poisonous mushrooms

index	class	cap-shape	cap-surface	cap-color	bruises	odor	gill-attachment	gill-spacing	gill-size	...	stalk-surface-below-ring	stalk-color-above-ring	stalk-color-below-ring	veil-type	veil-color	ring-number	ring-type	ring
0	0	p	convex	smooth	brown	have bruises	pungent	free	close	narrow	...	smooth	white	white	partial	white	one	pungent
1	3	p	convex	scaly	white	have bruises	pungent	free	close	narrow	...	smooth	white	white	partial	white	one	pungent
2	8	p	convex	scaly	white	have bruises	pungent	free	close	narrow	...	smooth	white	white	partial	white	one	pungent
3	13	p	convex	scaly	white	have bruises	pungent	free	close	narrow	...	smooth	white	white	partial	white	one	pungent
4	17	p	convex	smooth	brown	have bruises	pungent	free	close	narrow	...	smooth	white	white	partial	white	one	pungent
...	
3911	8114	p	flat	scaly	cinnamon	no bruises	musty	attached	close	broad	...	scaly	cinnamon	cinnamon	partial	white	null	
3912	8116	p	knobbed	scaly	brown	no bruises	spicy	free	close	narrow	...	silky	pink	white	partial	white	one	evanescent
3913	8117	p	knobbed	smooth	red	no bruises	fishy	free	close	narrow	...	smooth	pink	white	partial	white	one	evanescent
3914	8118	p	knobbed	scaly	brown	no bruises	foul	free	close	narrow	...	smooth	pink	white	partial	white	one	evanescent
3915	8122	p	knobbed	scaly	brown	no bruises	fishy	free	close	narrow	...	silky	white	white	partial	white	one	evanescent

3916 rows × 24 columns

Analysis - Proportion

- 1) Calculate the number of poisonous and edible mushrooms for every characteristic

```
#Counting the number of instances for each variable. -filtered into poisonous and non-poisonous mushrooms
p_cap_shape_count = p_mushrooms['cap-shape'].value_counts(dropna=False)
p_cap_color_count = p_mushrooms['cap-color'].value_counts(dropna=False)
p_cap_surface_count = p_mushrooms['cap-surface'].value_counts(dropna=False)
p_bruises_count = p_mushrooms['bruises'].value_counts(dropna=False)
p odor_count = p_mushrooms['odor'].value_counts(dropna=False)
p_gill_attachment_count = p_mushrooms['gill-attachment'].value_counts(dropna=False)
p_gill_spacing_count = p_mushrooms['gill-spacing'].value_counts(dropna=False)
p_gill_size_count = p_mushrooms['gill-size'].value_counts(dropna=False)
p_gill_color_count = p_mushrooms['gill-color'].value_counts(dropna=False)
p_stalk_shape_count = p_mushrooms['stalk-shape'].value_counts(dropna=False)
p_stalk_root_count = p_mushrooms['stalk-root'].value_counts(dropna=False)
p_stalk_surface_above_ring_count = p_mushrooms['stalk-surface-above-ring'].value_counts(dropna=False)
p_stalk_surface_below_ring_count = p_mushrooms['stalk-surface-below-ring'].value_counts(dropna=False)
p_stalk_color_below_ring_count = p_mushrooms['stalk-color-below-ring'].value_counts(dropna=False)
p_stalk_color_above_ring_count = p_mushrooms['stalk-color-above-ring'].value_counts(dropna=False)
p_veil_type_count = p_mushrooms['veil-type'].value_counts(dropna=False)
p_veil_color_count = p_mushrooms['veil-color'].value_counts(dropna=False)
p_ring_number_count = p_mushrooms['ring-number'].value_counts(dropna=False)
p_ring_type_count = p_mushrooms['ring-type'].value_counts(dropna=False)
p_spore_print_color_count = p_mushrooms['spore-print-color'].value_counts(dropna=False)
p_population_count = p_mushrooms['population'].value_counts(dropna=False)
p_habitat_count = p_mushrooms['habitat'].value_counts(dropna=False)

e_cap_shape_count = e_mushrooms['cap-shape'].value_counts(dropna=False)
e_cap_color_count = e_mushrooms['cap-color'].value_counts(dropna=False)
e_cap_surface_count = e_mushrooms['cap-surface'].value_counts(dropna=False)
e_bruises_count = e_mushrooms['bruises'].value_counts(dropna=False)
e odor_count = e_mushrooms['odor'].value_counts(dropna=False)
e_gill_attachment_count = e_mushrooms['gill-attachment'].value_counts(dropna=False)
e_gill_spacing_count = e_mushrooms['gill-spacing'].value_counts(dropna=False)
e_gill_size_count = e_mushrooms['gill-size'].value_counts(dropna=False)
e_gill_color_count = e_mushrooms['gill-color'].value_counts(dropna=False)
e_stalk_shape_count = e_mushrooms['stalk-shape'].value_counts(dropna=False)
e_stalk_root_count = e_mushrooms['stalk-root'].value_counts(dropna=False)
e_stalk_surface_above_ring_count = e_mushrooms['stalk-surface-above-ring'].value_counts(dropna=False)
e_stalk_surface_below_ring_count = e_mushrooms['stalk-surface-below-ring'].value_counts(dropna=False)
e_stalk_color_below_ring_count = e_mushrooms['stalk-color-below-ring'].value_counts(dropna=False)
e_stalk_color_above_ring_count = e_mushrooms['stalk-color-above-ring'].value_counts(dropna=False)
e_veil_type_count = e_mushrooms['veil-type'].value_counts(dropna=False)
e_veil_color_count = e_mushrooms['veil-color'].value_counts(dropna=False)
e_ring_number_count = e_mushrooms['ring-number'].value_counts(dropna=False)
e_ring_type_count = e_mushrooms['ring-type'].value_counts(dropna=False)
e_spore_print_color_count = e_mushrooms['spore-print-color'].value_counts(dropna=False)
e_population_count = e_mushrooms['population'].value_counts(dropna=False)
```

Analysis - Proportion

- 2) Calculate the proportion of poisonous mushrooms to edible mushrooms for every characteristic

$$\text{Proportion of Poisonous Mushrooms for every characteristic} = \frac{P_{Mushrooms}}{P_{mushrooms} + E_{Mushrooms}}$$

```
#Defining the 2 functions required for calculating proportion
#calculating the proportion
def calc_proportions(combined_df, characteristic, mushroom_types):
    proportions = {}
    for mushroom_type in mushroom_types:
        proportion = combined_df.loc[mushroom_type, characteristic] / combined_df.loc[mushroom_type].sum()
        proportions[mushroom_type] = proportion
    return proportions
#printing the proportion
def print_proportions(combined_df, characteristic, mushroom_types):
    proportions = calc_proportions(combined_df, characteristic, mushroom_types)
    for mushroom_type, proportion in proportions.items():
        print(f"\{mushroom_types[mushroom_type]\}: {proportion:.4f}")
```

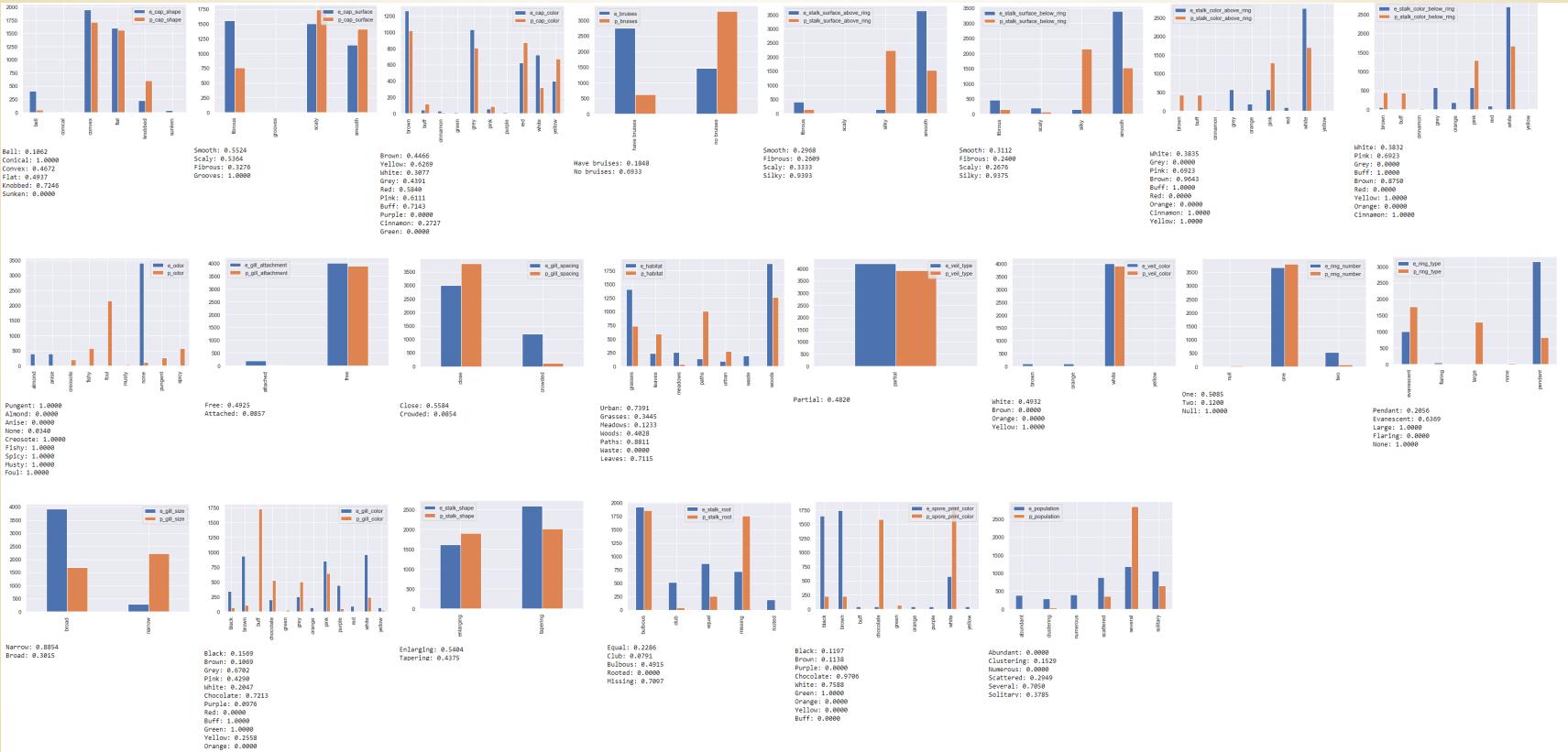
Analysis - Proportion

- 3) Use the function to calculate proportion and represent the data on a bar chart



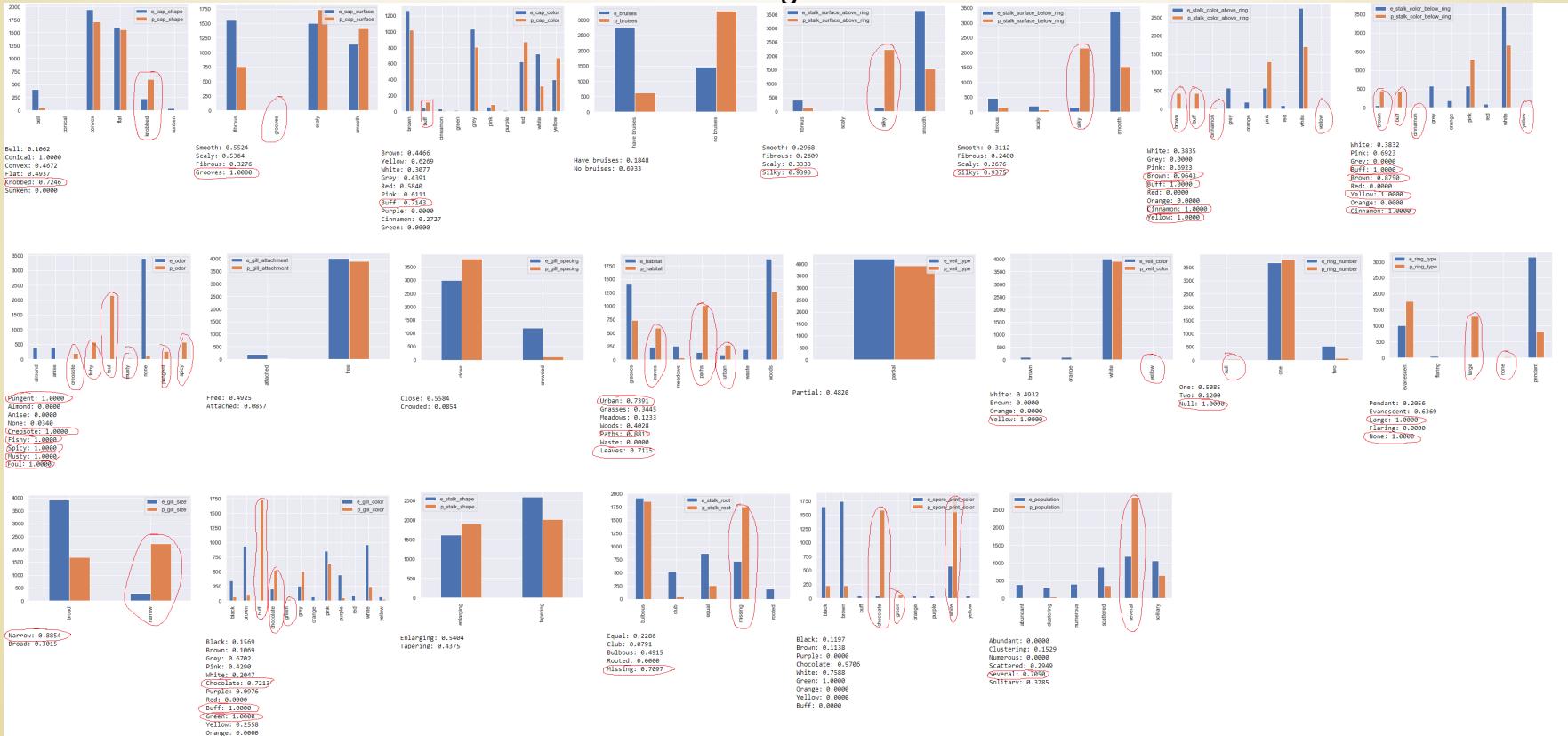
Analysis - Proportion

Findings



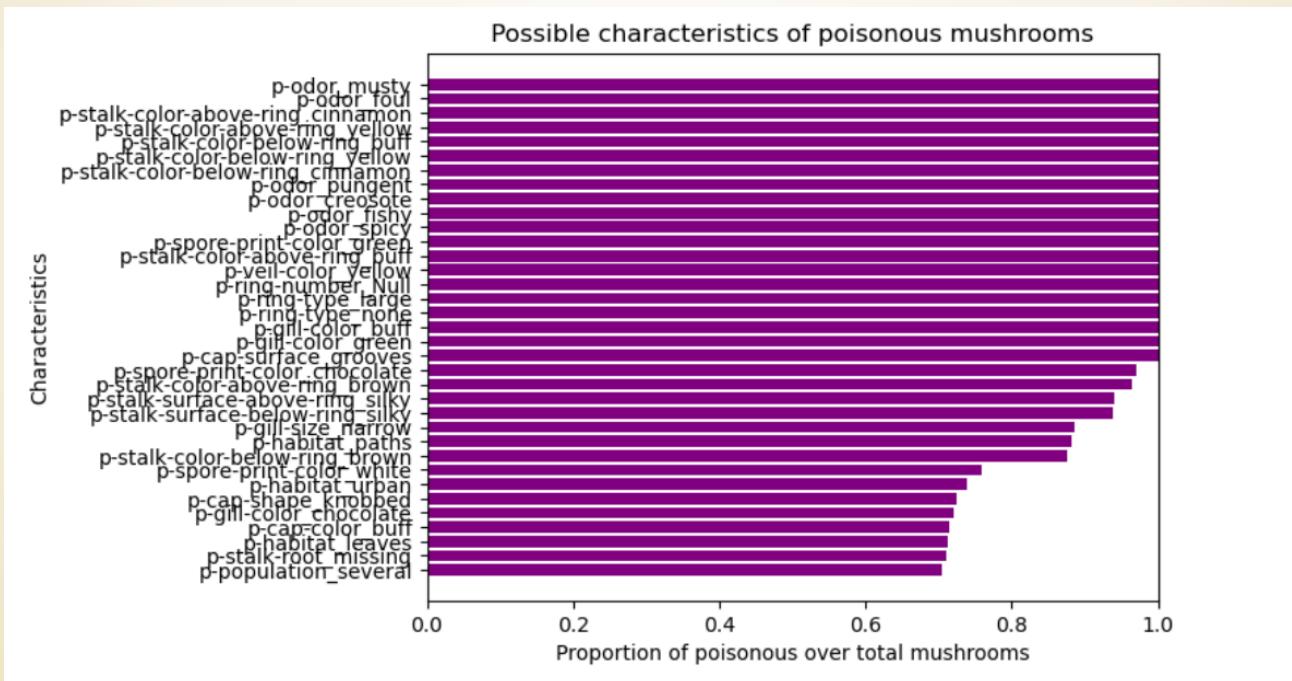
Analysis - Proportion

Findings



Analysis - Proportion

Findings



KMode

- Clustering algorithm that works with **categorical data**.
- Works by **iteratively** assigning data points to clusters based on the **similarity** of their categorical values.
- Updates the cluster centers based on the mode of the categorical values of the data points assigned to that cluster.
- The algorithm **continues iterating** until the cluster assignments **no longer change**.



Analysis - KMode

- 1) Use One-hot encoding to give a numerical value to the categorical data.
- 2) Create a Kmode object using the 'huang' algorithm and 5 clusters

```
# Select categorical columns to cluster on
cat_cols = dataset.columns

# Convert categorical variables to numerical values using one-hot encoding
one_hot = pd.get_dummies(dataset[cat_cols])

# Create KModes object
km = KModes(n_clusters=5, init='Huang', n_init=5, verbose=1)

# Fit the data to the model
clusters = km.fit_predict(one_hot)

# Add the clusters to the original dataset
dataset['cluster'] = clusters

Init: initializing centroids
Init: initializing clusters
Starting iterations...
Run 1, iteration: 1/100, moves: 2887, cost: 94594.0
Run 1, iteration: 2/100, moves: 163, cost: 94534.0
Run 1, iteration: 3/100, moves: 1, cost: 94534.0
Init: initializing centroids
Init: initializing clusters
Starting iterations...
```

Analysis - KMode

- 3) Apply PCA to reduce the number of dimensions
- 4) Create a scatter plot of the first 2 principal components.
- 5) Print the Mode for each attribute for each cluster

```
# Apply PCA to reduce the number of dimensions to 2
pca = PCA(n_components=2)
pca_result = pca.fit_transform(one_hot)

# Define the colors for each cluster
colors = ['red', 'green', 'blue', 'purple', 'orange']

# Create a scatter plot of the first two principal components
for i in range(len(set(clusters))):
    plt.scatter(pca_result[clusters==i, 0], pca_result[clusters==i, 1], c=colors[i], label=f'Cluster {i}')

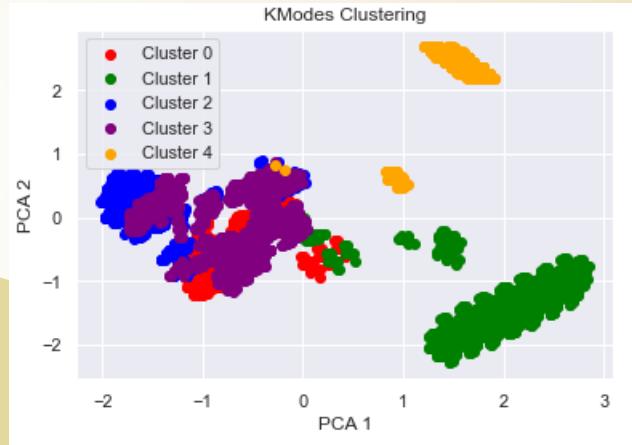
plt.title('KModes Clustering')
plt.xlabel('PCA 1')
plt.ylabel('PCA 2')
plt.legend()
plt.show()
```

```
# Print the mode (most frequent value) of each attribute for each cluster
for cluster in set(clusters):
    print(f'Cluster {cluster} mode:')
    for column in cat_cols:
        mode = dataset[dataset['cluster'] == cluster][column].mode()[0]
        print(f'\t{column}: {mode}'')
```

Analysis - KMode

Findings

Cluster 0 mode:	Cluster 1 mode:	Cluster 2 mode:
class: e	class: p	class: e
cap-shape: convex	cap-shape: flat	cap-shape: flat
cap-surface: fibrous	cap-surface: scaly	cap-surface: fibrous
cap-color: grey	cap-color: brown	cap-color: brown
bruises: no bruises	bruises: no bruises	bruises: have bruises
odor: none	odor: fishy	odor: none
gill-attachment: free	gill-attachment: free	gill-attachment: free
gill-spacing: crowded	gill-spacing: close	gill-spacing: close
gill-size: broad	gill-size: narrow	gill-size: broad
gill-color: pink	gill-color: buff	gill-color: white
stalk-shape: tapering	stalk-shape: tapering	stalk-shape: tapering
stalk-root: equal	stalk-root: missing	stalk-root: bulbous
stalk-surface-above-ring: smooth	stalk-surface-above-ring: smooth	stalk-surface-above-ring: smooth
stalk-surface-below-ring: smooth	stalk-surface-below-ring: smooth	stalk-surface-below-ring: smooth
stalk-color-above-ring: white	stalk-color-above-ring: white	stalk-color-above-ring: white
stalk-color-below-ring: white	stalk-color-below-ring: white	stalk-color-below-ring: white
veil-type: partial	veil-type: partial	veil-type: partial
veil-color: white	veil-color: white	veil-color: white
ring-number: one	ring-number: one	ring-number: one
ring-type: evanescent	ring-type: evanescent	ring-type: pendant
spore-print-color: black	spore-print-color: white	spore-print-color: brown
population: scattered	population: several	population: several
habitat: grasses	habitat: woods	habitat: woods
Cluster 3 mode:	Cluster 4 mode:	
class: e	class: p	
cap-shape: convex	cap-shape: convex	
cap-surface: smooth	cap-surface: scaly	
cap-color: white	cap-color: grey	
bruises: have bruises	bruises: no bruises	
odor: none	odor: foul	
gill-attachment: free	gill-attachment: free	
gill-spacing: close	gill-spacing: close	
gill-size: broad	gill-size: broad	
gill-color: white	gill-color: chocolate	
stalk-shape: enlarging	stalk-shape: enlarging	
stalk-root: bulbous	stalk-root: bulbous	
stalk-surface-above-ring: smooth	stalk-surface-above-ring: silky	
stalk-surface-below-ring: smooth	stalk-surface-below-ring: silky	
stalk-color-above-ring: white	stalk-color-above-ring: brown	
stalk-color-below-ring: white	stalk-color-below-ring: brown	
veil-type: partial	veil-type: partial	
veil-color: white	veil-color: white	
ring-number: one	ring-number: one	
ring-type: pendant	ring-type: large	
spore-print-color: brown	spore-print-color: chocolate	
population: scattered	population: solitary	
habitat: grasses	habitat: woods	



Analysis - KMode

Findings

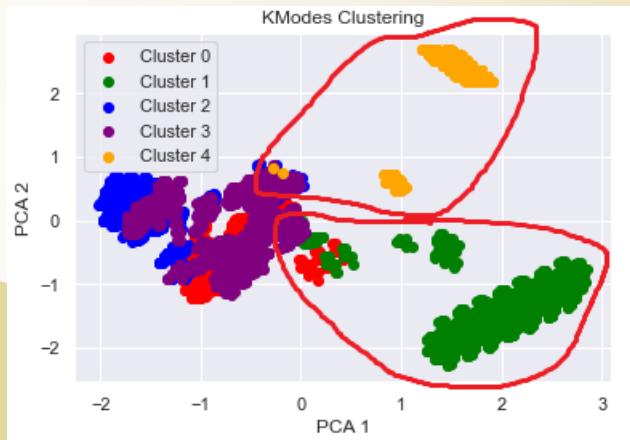
Cluster 0 mode:
class: e
cap-shape: convex
cap-surface: fibrous
cap-color: grey
bruises: no
odor: none
gill-attachment: free
gill-spacing: crowded
gill-size: broad
gill-color: pink
stalk-shape: tapering
stalk-root: equal
stalk-surface-above-ring: smooth
stalk-surface-below-ring: smooth
stalk-color-above-ring: white
stalk-color-below-ring: white
veil-type: partial
veil-color: white
ring-number: one
ring-type: evanescent
spore-print-color: black
population: scattered
habitat: grasses

Cluster 3 mode:
class: e
cap-shape: convex
cap-surface: smooth
cap-color: white
bruises: have
odor: none
gill-attachment: free
gill-spacing: close
gill-size: broad
gill-color: white
stalk-shape: enlarging
stalk-root: bulbous
stalk-surface-above-ring: smooth
stalk-surface-below-ring: smooth
stalk-color-above-ring: white
stalk-color-below-ring: white
veil-type: partial
veil-color: white
ring-number: one
ring-type: pendant
spore-print-color: brown
population: scattered
habitat: grasses

Cluster 1 mode:
class: p
cap-shape: flat
cap-surface: scaly
cap-color: brown
bruises: no
odor: fishy
gill-attachment: free
gill-spacing: close
gill-size: narrow
gill-color: buff
stalk-shape: tapering
stalk-root: missing
stalk-surface-above-ring: smooth
stalk-surface-below-ring: smooth
stalk-color-above-ring: white
stalk-color-below-ring: white
veil-type: partial
veil-color: white
ring-number: one
ring-type: evanescent
spore-print-color: white
population: several
habitat: woods

Cluster 4 mode:
class: p
cap-shape: convex
cap-surface: scaly
cap-color: grey
bruises: no
odor: foul
gill-attachment: free
gill-spacing: close
gill-size: broad
gill-color: chocolate
stalk-shape: enlarging
stalk-root: bulbous
stalk-surface-above-ring: silky
stalk-surface-below-ring: silky
stalk-color-above-ring: brown
stalk-color-below-ring: brown
veil-type: partial
veil-color: white
ring-number: one
ring-type: large
spore-print-color: chocolate
population: solitary
habitat: woods

Cluster 2 mode:
class: e
cap-shape: flat
cap-surface: fibrous
cap-color: brown
bruises: have
odor: none
gill-attachment: free
gill-spacing: close
gill-size: broad
gill-color: white
stalk-shape: tapering
stalk-root: bulbous
stalk-surface-above-ring: smooth
stalk-surface-below-ring: smooth
stalk-color-above-ring: white
stalk-color-below-ring: white
veil-type: partial
veil-color: white
ring-number: one
ring-type: pendant
spore-print-color: brown
population: several
habitat: woods



Machine Learning

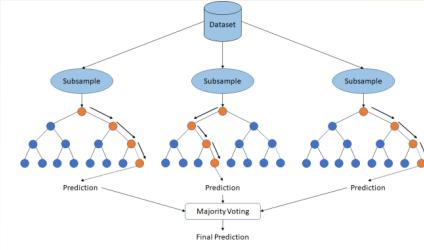
03

Models Used



*Decision
Tree*

*Simple and
Interpretable
model*



*Random
Forest*

*Complex but
Accurate model*

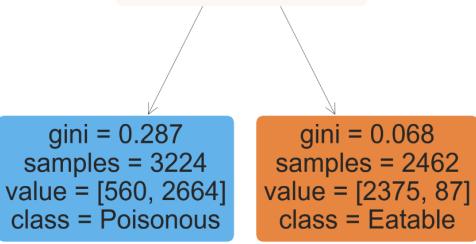
Decision Tree



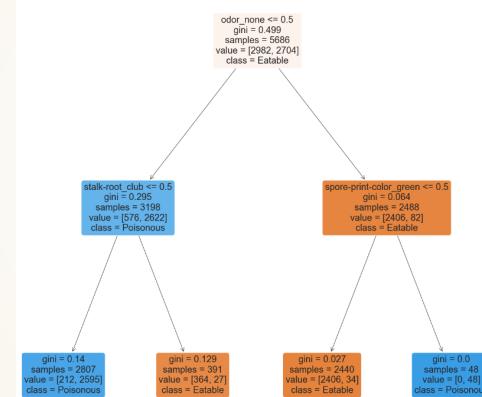
Decision Tree

Depth 1

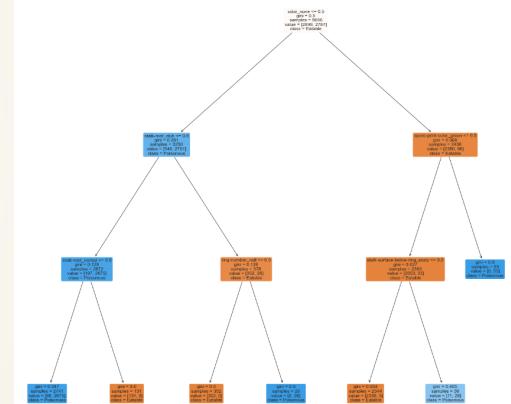
odor_none <= 0.5
gini = 0.499
samples = 5686
value = [2935, 2751]
class = Eatable



Depth 2

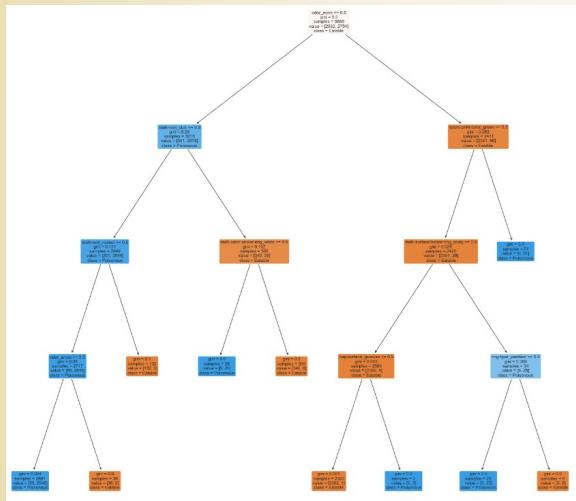


Depth 3

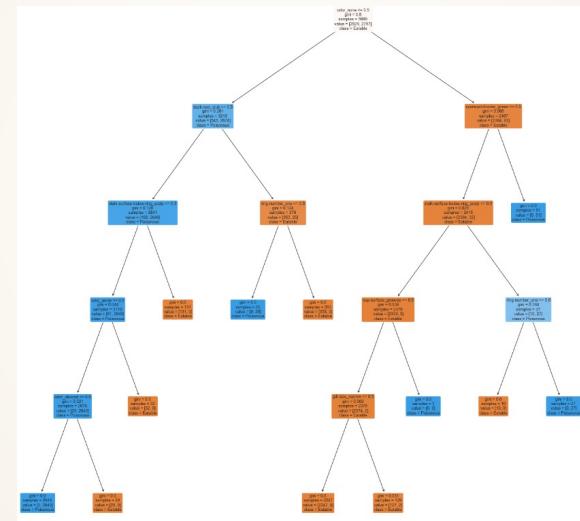


Decision Tree

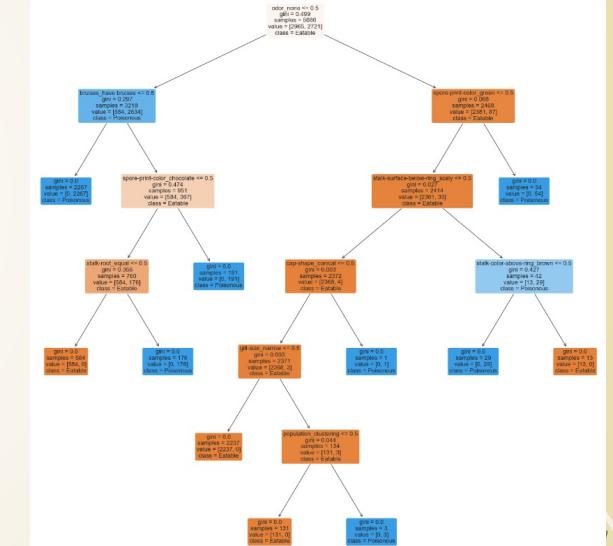
Depth 4



Depth 5



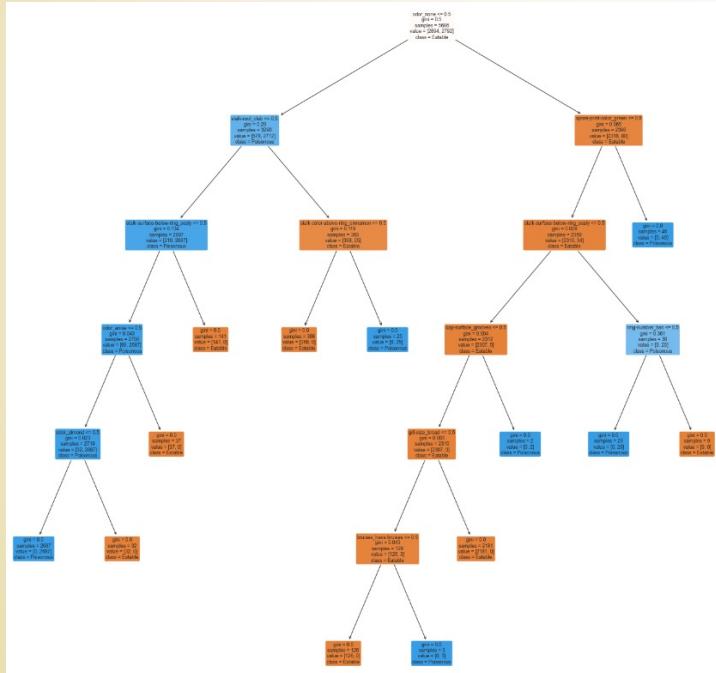
Depth 6



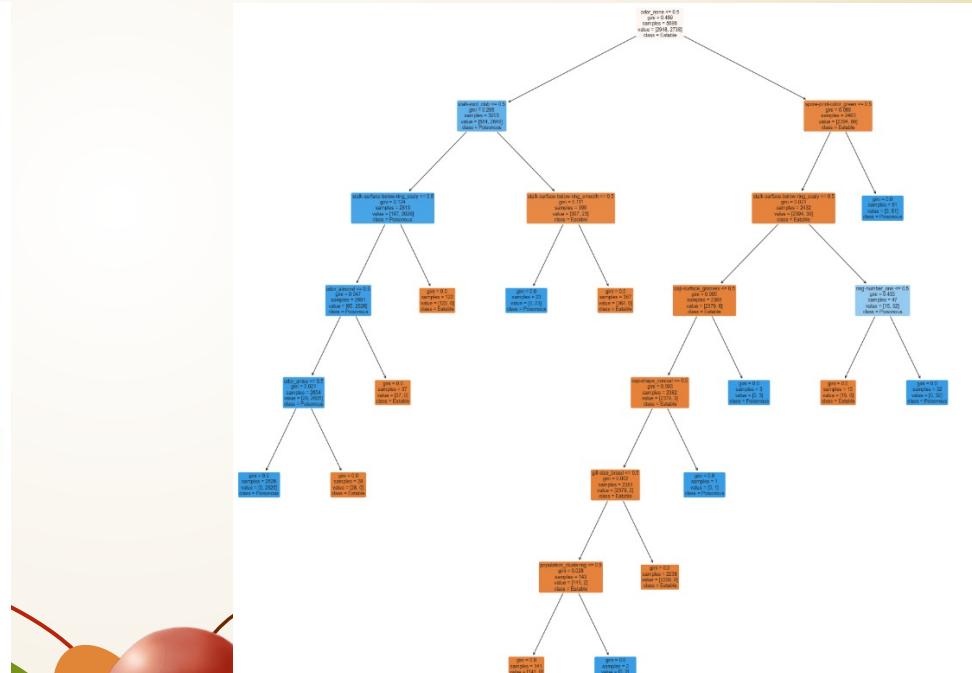


Decision Tree

Depth 7

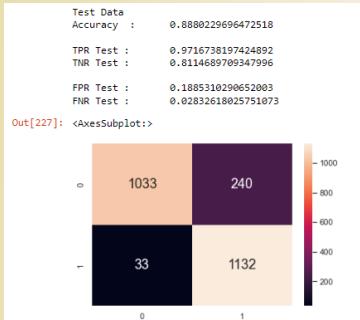


Depth 8

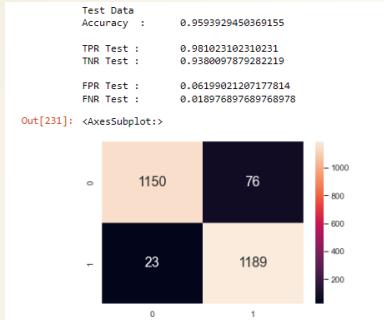


Decision Tree - Confusion Matrix (For test set)

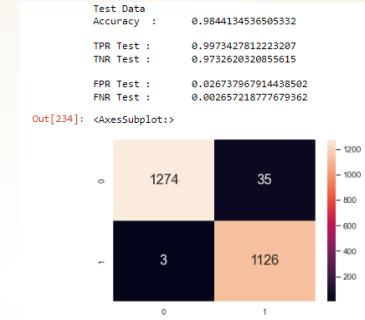
Depth 1



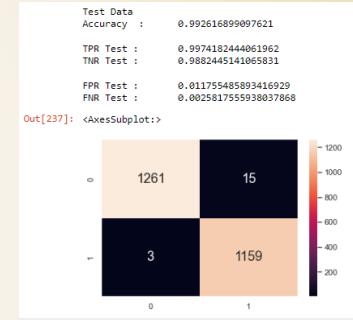
Depth 2



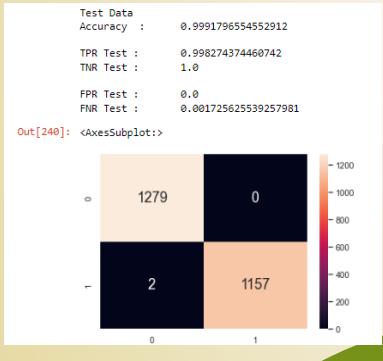
Depth 3



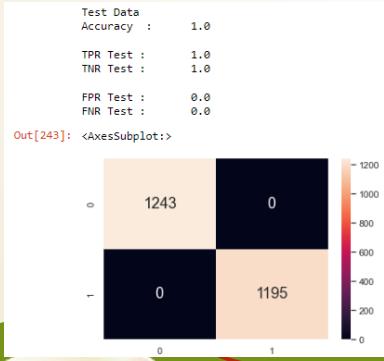
Depth 4



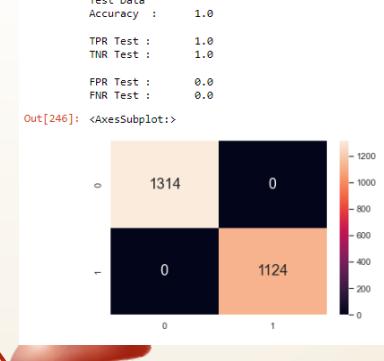
Depth 5



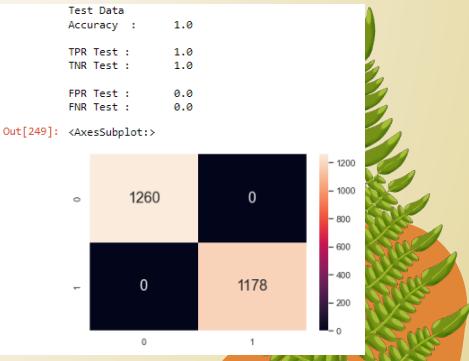
Depth 6



Depth 7



Depth 8



Depth 8

TPR rate for test

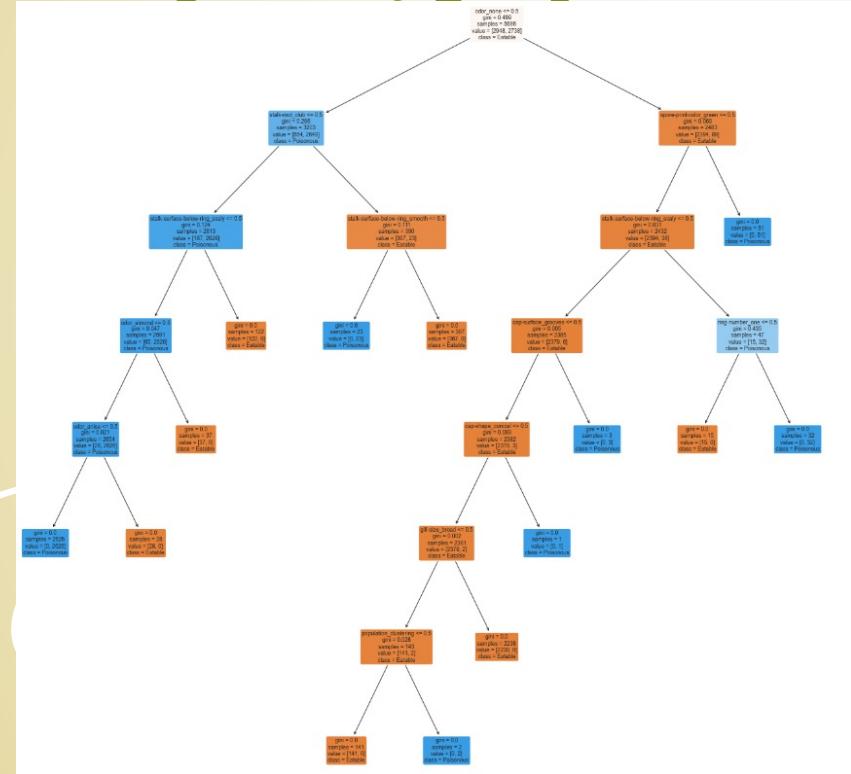
01

1.0

Important Feature we got

- odor_none
- stalk-root_club
- stalk-surface-below-ring_scaly
- odor_anise
- odor_almond
- ring-number_one
- spore-print-color_green
- stalk-surface-below-ring_scaly
- cap-surface_grooves
- cap-shape_conical
- gill-size_broad
- population_clustering
- ring-type_evanescence

02



Random Forest





First Model

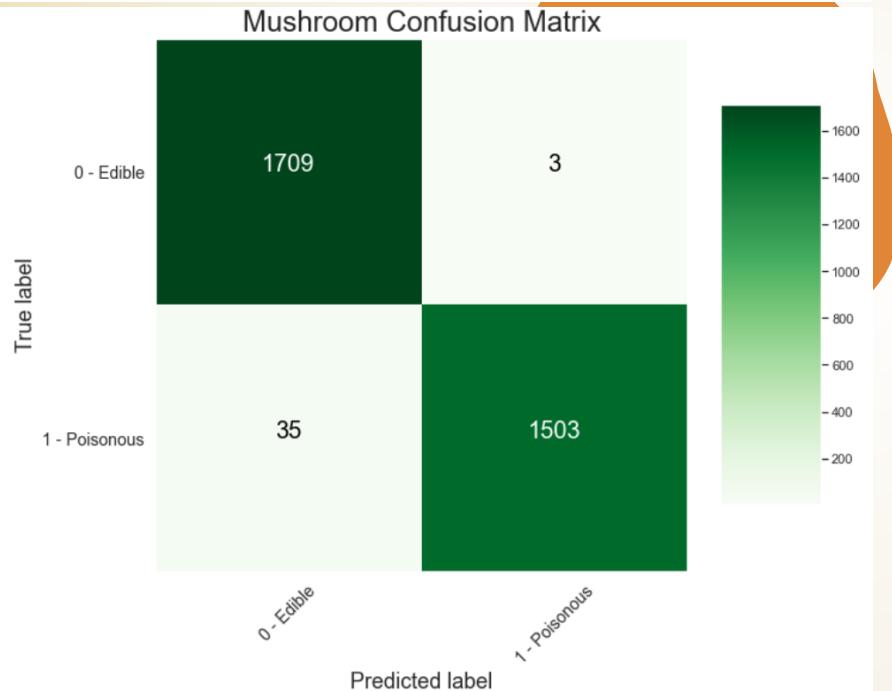
```
rf_classifier = RandomForestClassifier(  
    min_samples_leaf=50,  
    n_estimators=150,  
    bootstrap=True,  
    oob_score=True,  
    n_jobs=-1,  
    random_state=seed,  
    max_features='auto' )
```

We construct the random forest
with **150 decision trees**.

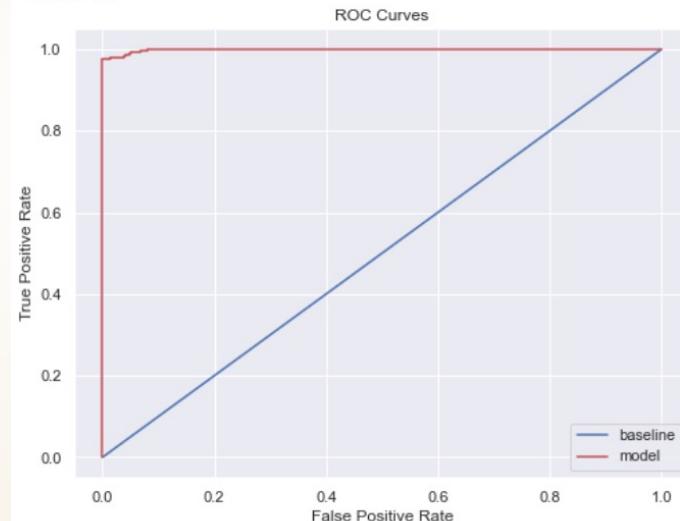


ROC Curve & Confusion Matrix

Train ROC AUC Score: 0.9989009846308069
Test ROC AUC Score: 0.999158774565623

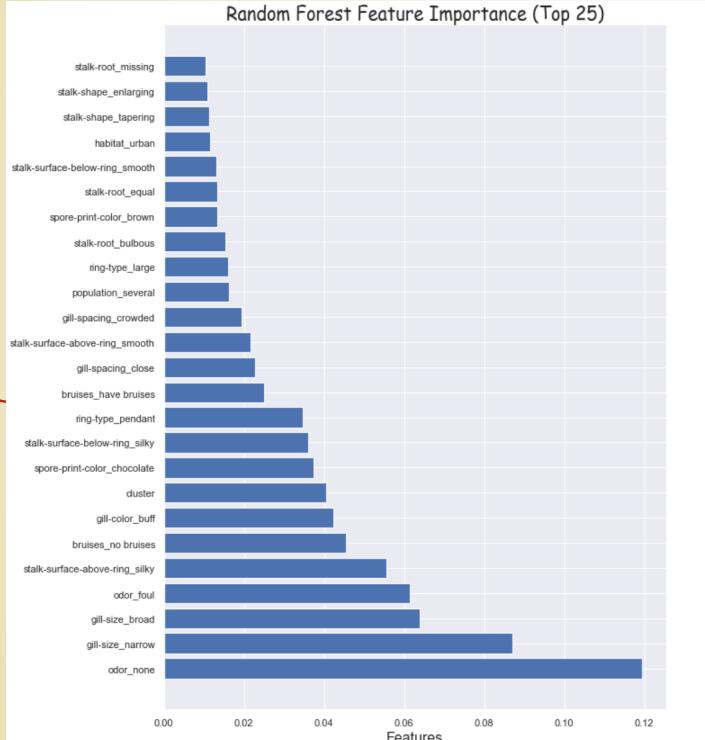


Baseline: 1.0
Test: 0.98
Train: 0.98
Baseline: 0.47
Test: 1.0
Train: 1.0
Baseline: 0.5
Test: 1.0
Train: 1.0



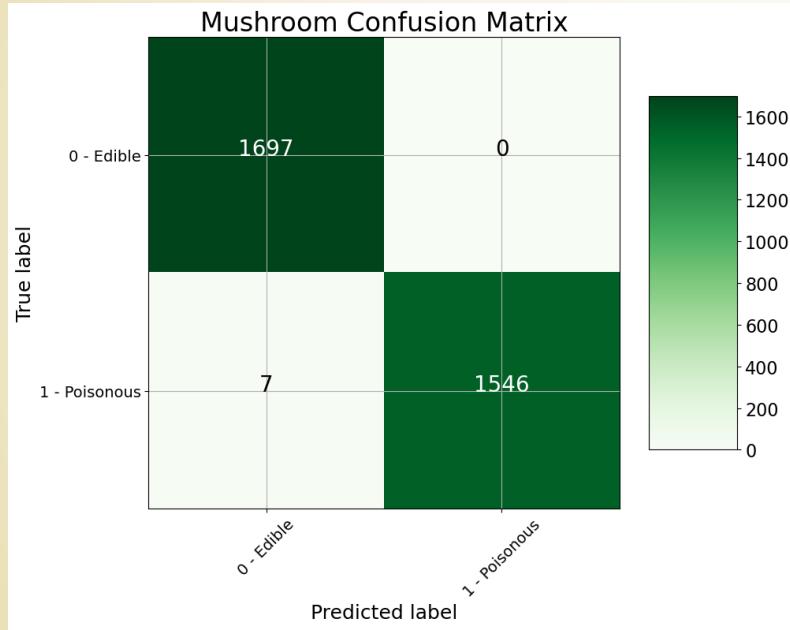
The accuracy of the model is 99.0 %

Important characteristics From Random Forest

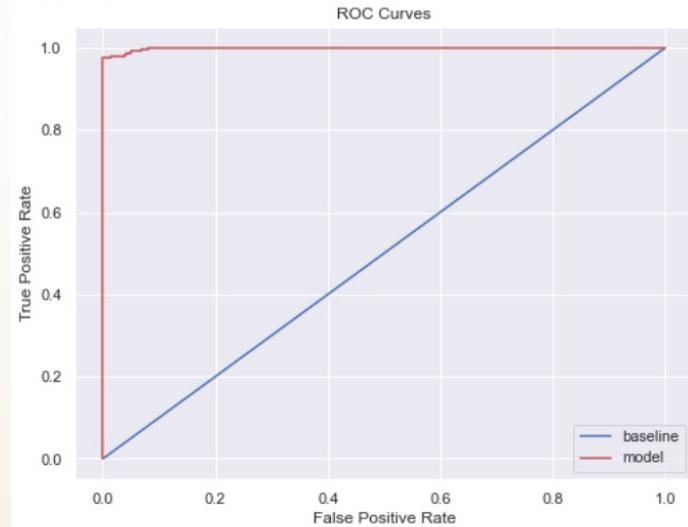


- Odor_none
- Gill-size_narrow
- Gill-size_broad
- Odor_foul
- Stalk-surface-above-ring_silky
- Bruises_no_bruises
- Gill-color_buff
- Cluster
- Spore-print-color_chocolate
- Stalk-surface-below-ring_silky
- Ring-type_pendant
- Bruises_have_bruises
- Gill-spacing_close
- Stalk-surface-above-ring_smooth
- Gill-spacing_crowded
- Population_several
- Ring-type_large
- Stalk-root_bulbous
- Spore-print-color_brown
- Stalk-root_equal
- Stalk-surface-below-ring_smooth
- Habitat_urban
- Stalk-shape_tapering
- Stalk-shape_enlarging
- Stalk-root_missing

To be BETTER ...



Baseline: 1.0
Test: 0.98
Train: 0.98
Baseline: 0.47
Test: 1.0
Train: 1.0
Baseline: 0.5
Test: 1.0
Train: 1.0



Adjusting the parameters to improve our model.

04

AI model



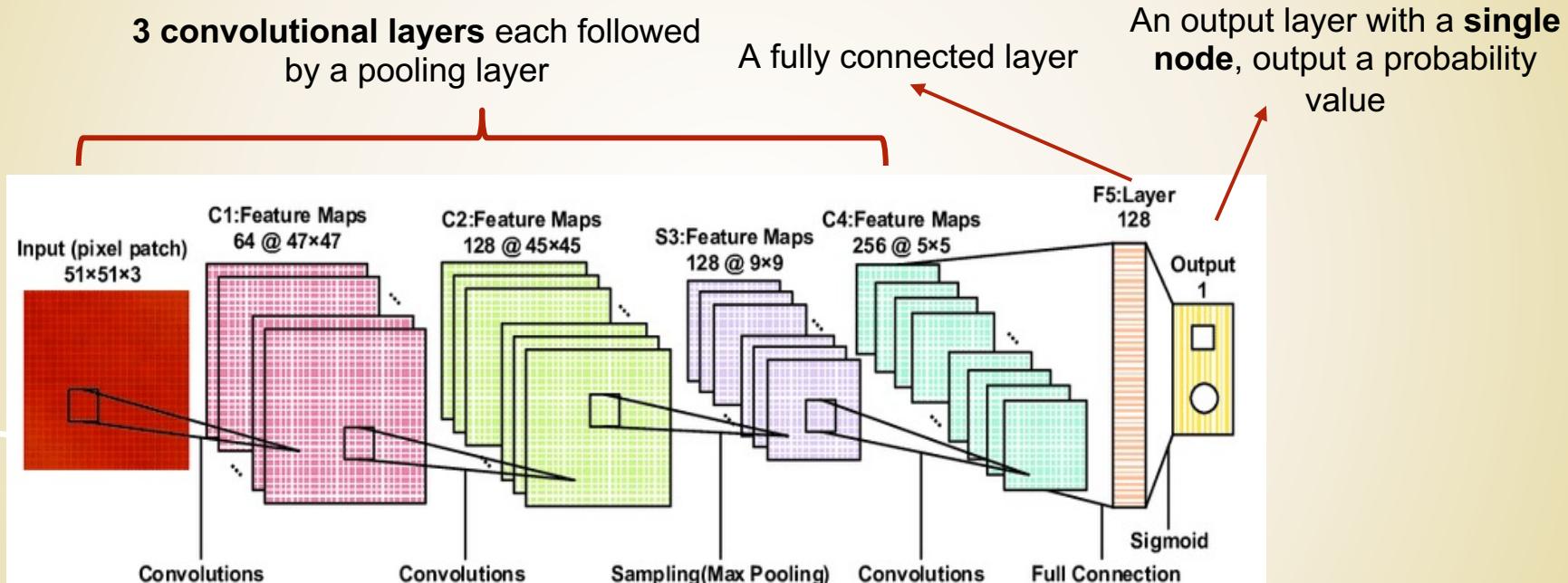
Image Manipulation



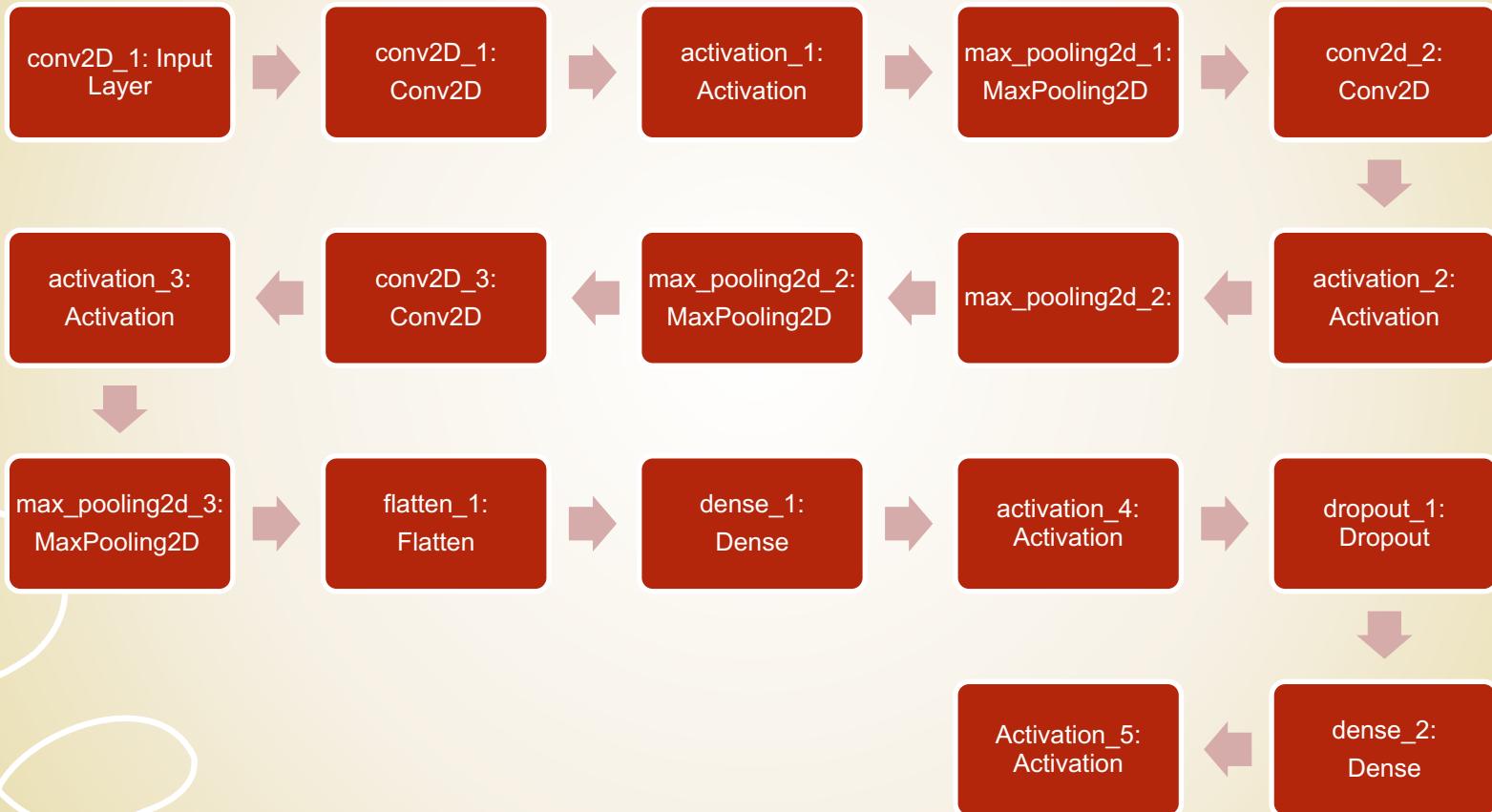
Increase the number of unique training examples by introducing small **distortions** to the images



CNN Model Architecture



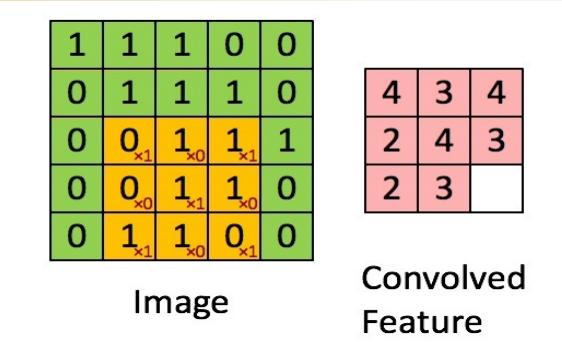
CNN Model Architecture



Model Explanation -- Convolutional layers

1	1	1	0	0
0	1	1	1	0
0	0	1	1	1
0	0	1	1	0
0	1	1	0	0

1	0	1
0	1	0
1	0	1



```
model.add(Conv2D 32, (3, 3))  
model.add(Conv2D(32, (3, 3)))  
model.add(Conv2D 64, (3, 3)))
```

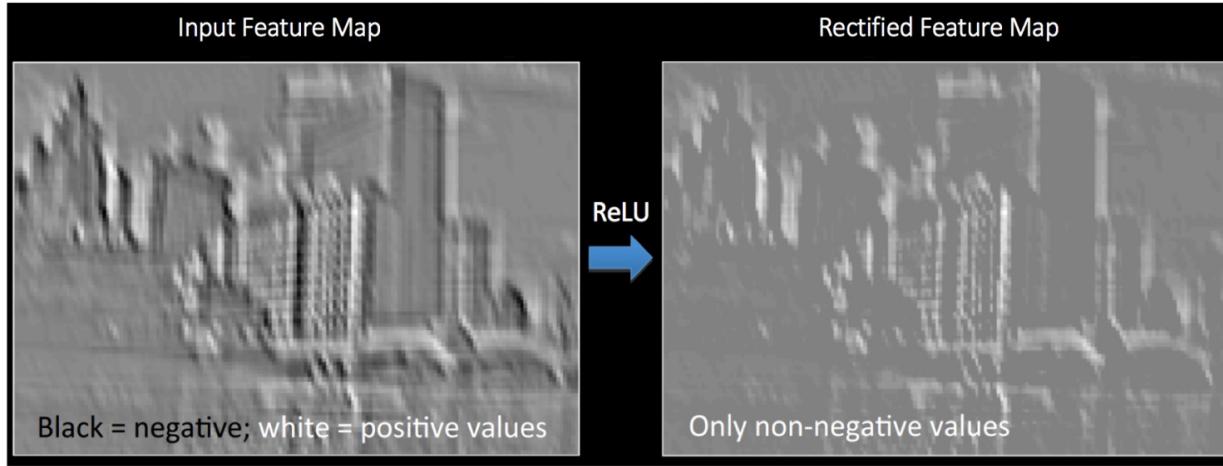
Matrix Convolution

- Every image can be considered as a matrix of pixel values.
- We use the 3*3 matrix (**filter**) to slide over the original image by 1 pixel (**stride**) and for every position we will compute an integer which forms a single element of the output matrix (**Feature Map**)

Our Model

- The depths of our three convolutional layers are 32,32 and 64.

ReLU activation & Max Pooling



ReLU: Introduce non-linearity in ConvNet.

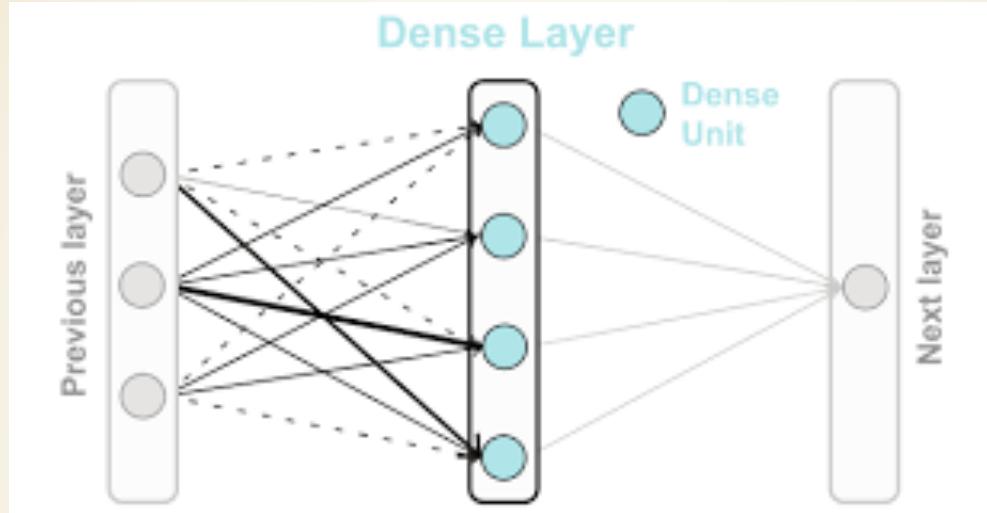
12	20	30	0
8	12	2	0
34	70	37	4
112	100	25	12

2×2 Max-Pool

20	30
112	37

Max Pooling: Reduces the dimensionality of each feature map but remains the most important information

Dense Layers & Output



Dense Layer: Receive input from all the previous layer and classify image.

Output: Probability between 0 and 1

Final Model

```
Epoch 44/50
280/280 [=====] - 313s 1s/step - loss: 0.4223 - accuracy: 0.8287
- val_loss: 0.4899 - val_accuracy: 0.8062
Epoch 45/50
280/280 [=====] - 314s 1s/step - loss: 0.3881 - accuracy: 0.8412
- val_loss: 0.3850 - val_accuracy: 0.8634
Epoch 46/50
280/280 [=====] - 318s 1s/step - loss: 0.3934 - accuracy: 0.8448
- val_loss: 0.5451 - val_accuracy: 0.8375
Epoch 47/50
280/280 [=====] - 314s 1s/step - loss: 0.4152 - accuracy: 0.8410
- val_loss: 1.5599 - val_accuracy: 0.7384
Epoch 48/50
280/280 [=====] - 313s 1s/step - loss: 0.3761 - accuracy: 0.8428
- val_loss: 0.4646 - val_accuracy: 0.8045
Epoch 49/50
280/280 [=====] - 307s 1s/step - loss: 0.4103 - accuracy: 0.8442
- val_loss: 0.3176 - val_accuracy: 0.8527
Epoch 50/50
280/280 [=====] - 315s 1s/step - loss: 0.3984 - accuracy: 0.8381
- val_loss: 0.8348 - val_accuracy: 0.7286
```

Final Model

```
Epoch 50/50
280/280 [=====] - 315s 1s/step - loss: 0.3984 - accuracy: 0.8381
- val_loss: 0.8348 - val_accuracy: 0.7286
```

- **Val_**: test set
- **Loss**: The difference between the predicted output and the true output.
- **Accuracy**: It is calculated by dividing the number of correct predictions by the total number of predictions.

Training and Test

```
epochs = 50 # the  
batch_size = 16 #
```



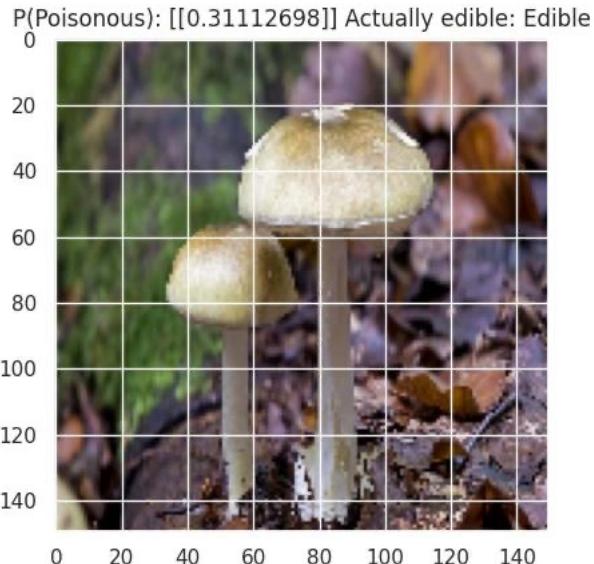
- We split the image into train and test sets with 0.8:0.2 portion.
- Then the model will be trained for a total of 50 passes over the entire training dataset. (i.e., the network was trained on 50 epochs)
- During each iteration of training, the model will process and update its weights based on 16 samples from the training dataset.
- As the train accuracy reaches a stage at **85%** , the testing accuracy waves **around 80%**.

05

Applications



AI Prediction-Application



- User can upload an image, and our AI model will output a single value describing the probability that a mushroom is poisonous
- The left image shows the prediction of one test case (outside the original image set).

User input

```
new_mushroom['ring-number'] = input('Enter the ring number of the mushroom (none,one,two): ')
new_mushroom['ring-type'] = input('Enter the ring type of the mushroom (cobwebby, evanescent, flaring, large, none, pendant, sheathing,
new_mushroom['spore-print-color'] = input('Enter the spore print color of the mushroom (black, brown, buff, chocolate, green, orange,
new_mushroom['population'] = input('Enter the population of the mushroom (abundant, clustered, numerous, scattered, several, solitary)
new_mushroom['habitat'] = input('Enter the habitat of the mushroom (grasses, leaves, meadows, paths, urban, waste, woods): ')
```

```
Enter the cap shape of the mushroom (bell, conical, convex, flat, knobbed, sunken):
```

```
Enter the cap shape of the mushroom (bell, conical, convex, flat, knobbed, sunken): convex
Enter the cap surface of the mushroom (fibrous, grooves, scaly, smooth): scaly
Enter the cap color of the mushroom (brown, buff, cinnamon, gray, green, pink, purple, red, white, yellow): white
Does the mushroom have bruises? (have bruises/no bruises): have bruises
Enter the odor of the mushroom (almond, anise, creosote, fishy, foul, musty, none, pungent, spicy): pungent
Enter the gill attachment of the mushroom (attached, descending, free, notched): free
Enter the gill spacing of the mushroom (close, crowded, distant): close
Enter the gill size of the mushroom (broad, narrow): narrow
Enter the gill color of the mushroom (black, brown, buff, chocolate, gray, green, orange, pink, purple, red, white, yellow): pink
Enter the stalk shape of the mushroom (enlarging, tapering): enlarging
Enter the stalk root of the mushroom (bulbous, club, cup, equal, rhizomorphs, rooted, missing): equal
Enter the stalk surface above the ring of the mushroom (fibrous, scaly, silky, smooth): smooth
Enter the stalk surface below the ring of the mushroom (fibrous, scaly, silky, smooth): smooth
Enter the stalk color above the ring of the mushroom (brown, buff, cinnamon, gray, orange, pink, red, white, yellow): white
Enter the stalk color below the ring of the mushroom (brown, buff, cinnamon, gray, orange, pink, red, white, yellow): white
Enter the veil type of the mushroom (partial, universal): partial
Enter the veil color of the mushroom (brown, orange, white, yellow): white
Enter the ring number of the mushroom (none, one, two): one
Enter the ring type of the mushroom (cobwebby, evanescent, flaring, large, none, pendant, sheathing, zone): pendant
Enter the spore print color of the mushroom (black, brown, buff, chocolate, green, orange, purple, white, yellow): black
Enter the population of the mushroom (abundant, clustered, numerous, scattered, several, solitary): several
Enter the habitat of the mushroom (grasses, leaves, meadows, paths, urban, waste, woods): grasses
```

```
1 new_mushroom_df = pd.DataFrame(new_mushroom, index=[0])
2
3 new_mushroom_df = new_mushroom_df.reindex(columns=X.columns, fill_value=0) # align with training data columns
4
```

Result

- **Prediction '0':** the mushroom is classified as **edible**
- **Otherwise,** classified as **poisonous.**

```
1 prediction = tree_clf.predict(encoded_new_mushroom_df)
2 if prediction == 0:
3     print('The mushroom is edible.')
4 else:
5     print('The mushroom is poisonous.')
6
```

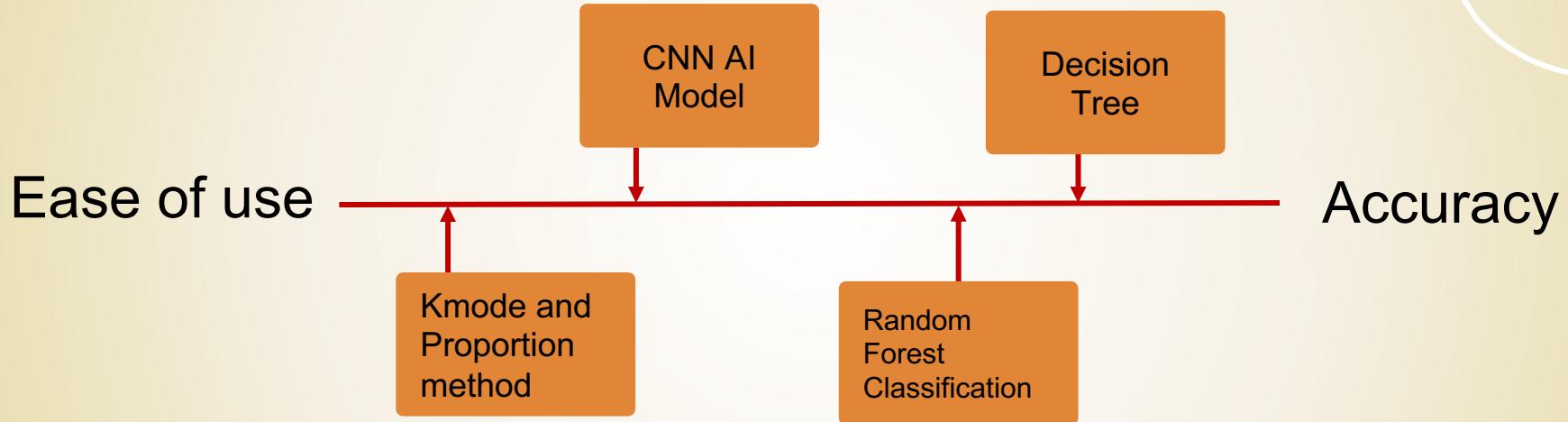
The mushroom is poisonous.

06

Conclusion and Evaluation



Findings



Takeaways

Utility Methods

1. **OneHotEncoder** (Transformation technique to convert categorical data into numerical format)
2. **PipeLine** (Chaining together multiple machine learning steps into a single object)
3. **KMode** (Method to analyse categorical data)
4. **Fit-Transform** (Standardise data)

Models

1. **Random forest classification** (Machine Learning Algorithm)
2. **CNN** (artificial neural network specializes in visual data)



Future Improvements

Dataset's flaw

- Only 1 set of data on 2 families of mushrooms



AI model's flaw

- Since the accuracy of the AI model is **80%** which can still be improve (compare with the decision tree and random forest)



Dataset's improvement

- Use a larger and more balanced dataset



AI improvement

- adjust some parameters (e.g.: epoch num)
- More complete image set

Thanks!

Risk Warning: Although our model's accuracy is high, we still strongly advise against eating any wild mushrooms.



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