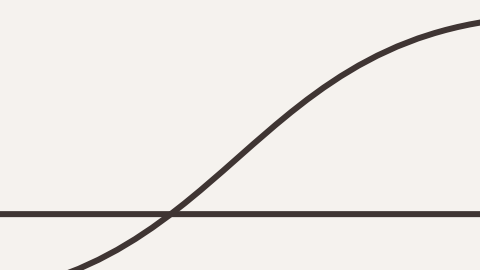
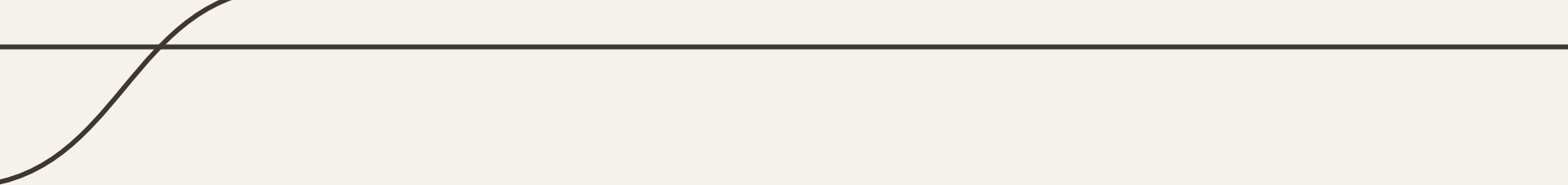




Mushroom Edibility Classification

Anieesh Saravanan and Pranav Akiri





**“All mushrooms are edible; but
some only once.”**

– Croatian Proverb



Table of contents

01

Project Overview

Relevance and Dataset
Characteristics

02

Preprocessing

Preparing the Dataset for
Manipulation

03

Manipulation

Eliminating attributes
and classification

04

Conclusion

Results and Future Work



00

Introduction

Project Goal

- Develop a binary classification model for mushrooms
- Predict if mushrooms are edible or poisonous based on physical attributes
- Ensure public safety through accurate classification



Mushroom Overview

- Mushrooms are a section of a fungus
- Toxins used to prevent consumption
- **No** simple guidelines to identify mushrooms as poisonous
- Difference between edible and poisonous mushrooms are **extremely slight**
- Experienced mycologists make mistakes



Common Myths

Folklore has created many false truths about mushrooms:

Myth: Poisonous mushrooms always have bright and flashy colors

Myth: Snails, insects, or other animals won't eat poisonous mushrooms

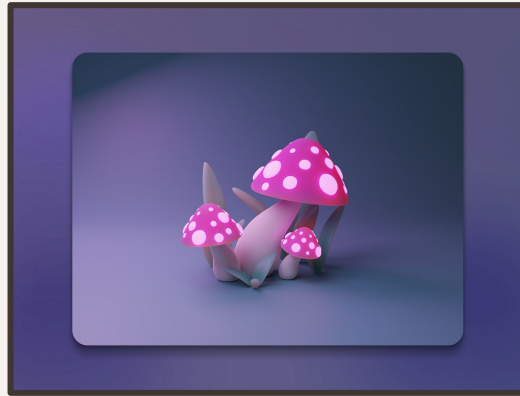
Myth: Toxic mushrooms smell and taste horrible

Myth: Any mushroom becomes safe if cooked/processed enough



Impact

There are around **7,428** cases of exposure to toxic mushrooms, mostly by ingestion, each year.



01 Project Overview



Dataset Overview

- **Categorical** dataset with **8,124 instances** and **21 attributes**
- Class attribute is the edibility of the mushroom
- Sourced from **The Audubon Society Field Guide to North American Mushrooms**
- Missing values: 2,480 instances in the stalk-root attribute
- Class distribution: 52% edible, 48% poisonous (includes unknown classifications)



Attributes

class: edible = e, poisonous = p

cap-shape: bell = b, conical = c, convex = x, flat = f, knobbed = k, sunken = s

cap-surface: fibrous = f, grooves = g, scaly = y, smooth = s

cap-color: brown = n, buff = b, cinnamon = c, gray = g, green = r, pink = p, purple = u, red = e, white = w, yellow = y

bruises: true = t, false = f

odor: almond = a, anise = l, creosote = c, fishy = y, foul = f, musty = m, none = n, pungent = p, spicy = s

gill-attachment: attached = a, descending = d, free = f, notched = n

gill-spacing: close = c, crowded = w, distant = d

gill-size: broad = b, narrow = n

gill-color: black = k, brown = n, buff = b, chocolate = h, gray = g, green = r, orange = o, pink = p, purple = u, red = e, white = w, yellow = y

stalk-shape: enlarging = e, tapering = t

stalk-root: bulbous = b, club = c, cup = u, equal = e, rhizomorphs = z, rooted = r

stalk-surface-above-ring: fibrous = f, scaly = y, silky = k, smooth = s

stalk-surface-below-ring: fibrous = f, scaly = y, silky = k, smooth = s

stalk-color-above-ring: brown = n, buff = b, cinnamon = c, gray = g, orange = o, pink = p, red = e, white = w, yellow = y

stalk-color-below-ring: brown = n, buff = b, cinnamon = c, gray = g, orange = o, pink = p, red = e, white = w, yellow = y

veil-type: partial = p, universal = u

veil-color: brown = n, orange = o, white = w, yellow = y

ring-number: none = n, one = o, two = t

ring-type: cobwebby = c, evanescent = e, flaring = f, large = l, none = n, pendant = p, sheathing = s, zone = z

spore-print-color: black = k, brown = n, buff = b, chocolate = h, green = r, orange = o, purple = u, white = w, yellow = y

population: abundant = a, clustered = c, numerous = n, scattered = s, several = v, solitary = y

habitat: grasses = g, leaves = l, meadows = m, paths = p, urban = u, waste = w, woods = d



02 Preprocessing

Missing Value Handling

- Implemented the K-Nearest-Neighbors (KNN) algorithm
- Estimates missing values by analyzing the closest neighbors based on features
- Surpasses mode/deletion (reflects underlying patterns in the data)

```
knn_imputer = KNNImputer(n_neighbors = 5)
x_imputed = knn_imputer.fit_transform(x_encoded)
x = pd.DataFrame(x_imputed, columns = x.columns)
```

KNN Imputer implementation using scikit-learn method and depth 5 consideration

Feature Encoding

All of the data in the mushrooms dataset are categorical variables

Cap shape: bell (b) → 0, conical (c) → 1, flat (f) → 2

Odor: almond (a) → 0, fishy (y) → 8

```
for column in x.columns:

    le = LabelEncoder()
    x[column] = le.fit_transform(x[column].round().astype(int))
    label_encoders[column] = le
```

Encodings using scikit-learn functionality

Dataset Splitting

- Training Set: 80% of data for model training
- Validation Set: 10% for hyperparameter tuning
- Testing Set: 10% for unbiased evaluation of model performance

```
x_train, x_temp_split, y_train, y_temp_split = train_test_split(  
    x, y, test_size = 0.2, random_state = 42, stratify = y  
)  
  
x_val, x_test, y_val, y_test = train_test_split(  
    x_temp_split, y_temp_split, test_size = 0.5, random_state = 42, stratify = y_temp_split  
)
```

Split with stratified distribution using scikit-learn functionality

03 Manipulation



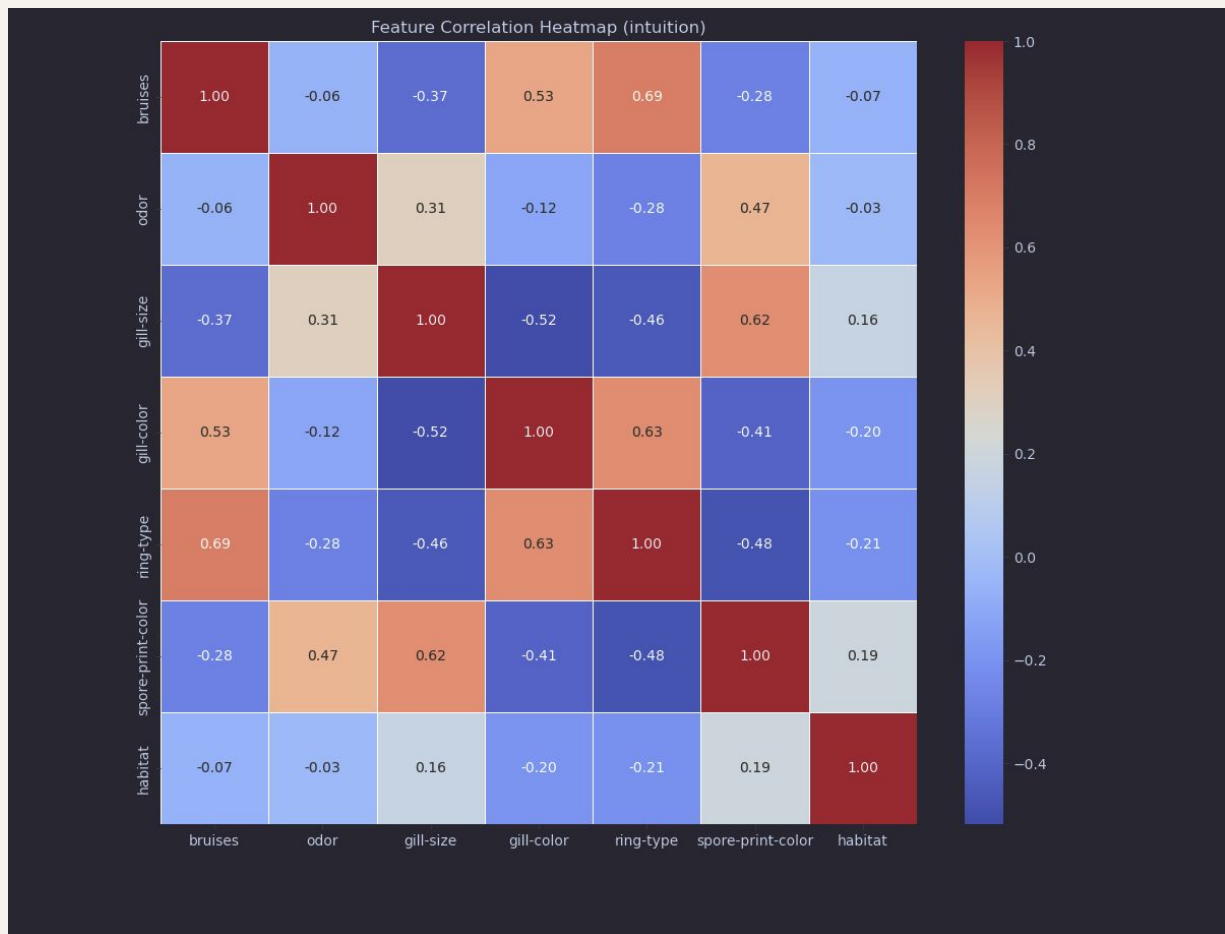
Attribute Selection Algorithms

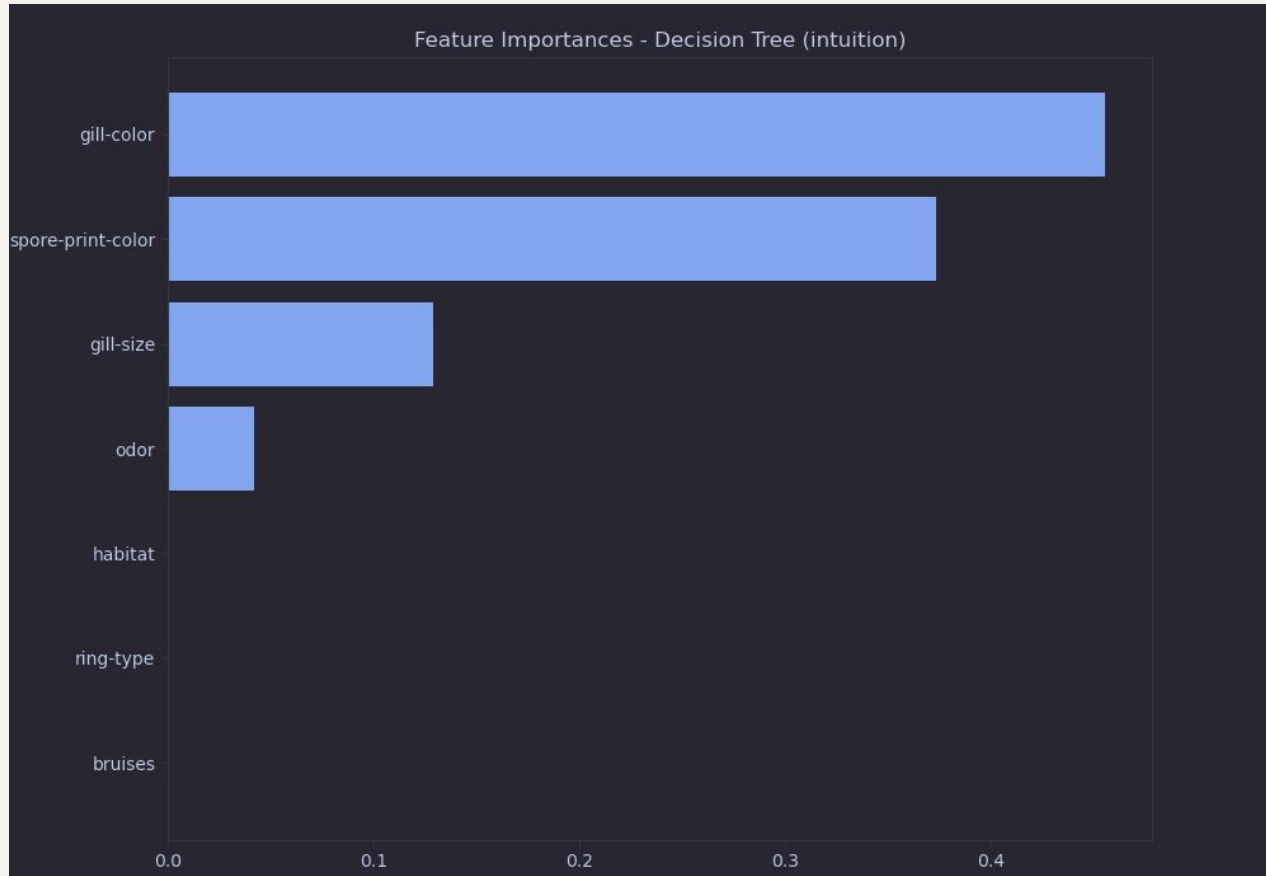
Selection Algorithm	Strengths	Weaknesses
Intuition	Simple to perform, takes the least amount of time	Prone to bias, can't be reproduced
Correlation Attribute Evaluation	Computationally efficient calculation in a straightforward way	Can only detect linear relationships, skewed by outliers
Gain Ratio Attribute Evaluation	Reduces overfitting, useful for Decision Trees	Ineffective with attributes that have only a few unique values
Information Gain Attribute Evaluation	Works with both categorical and discrete data	Biased toward attributes with many categories
Wrapper Subset Evaluation	Selection based on the specific model	Risks overfitting, especially when dataset is small

Intuition-Based Selection

- Basic selection based on personal consideration of the influence of attributes
- We watched National Geographic as kids (unofficial experts)

No.	
1	<input type="checkbox"/> bruises
2	<input type="checkbox"/> odor
3	<input type="checkbox"/> gill-size
4	<input type="checkbox"/> gill-color
5	<input type="checkbox"/> ring-type
6	<input type="checkbox"/> spore-print-color
7	<input type="checkbox"/> habitat
8	<input type="checkbox"/> class





Correlation Attribute Evaluation

- Measures the linear correlation between attributes and class labels

$$r = \frac{\sum (x_i - \bar{x}) (y_i - \bar{y})}{\sqrt{\sum (x_i - \bar{x})^2 \sum (y_i - \bar{y})^2}}$$

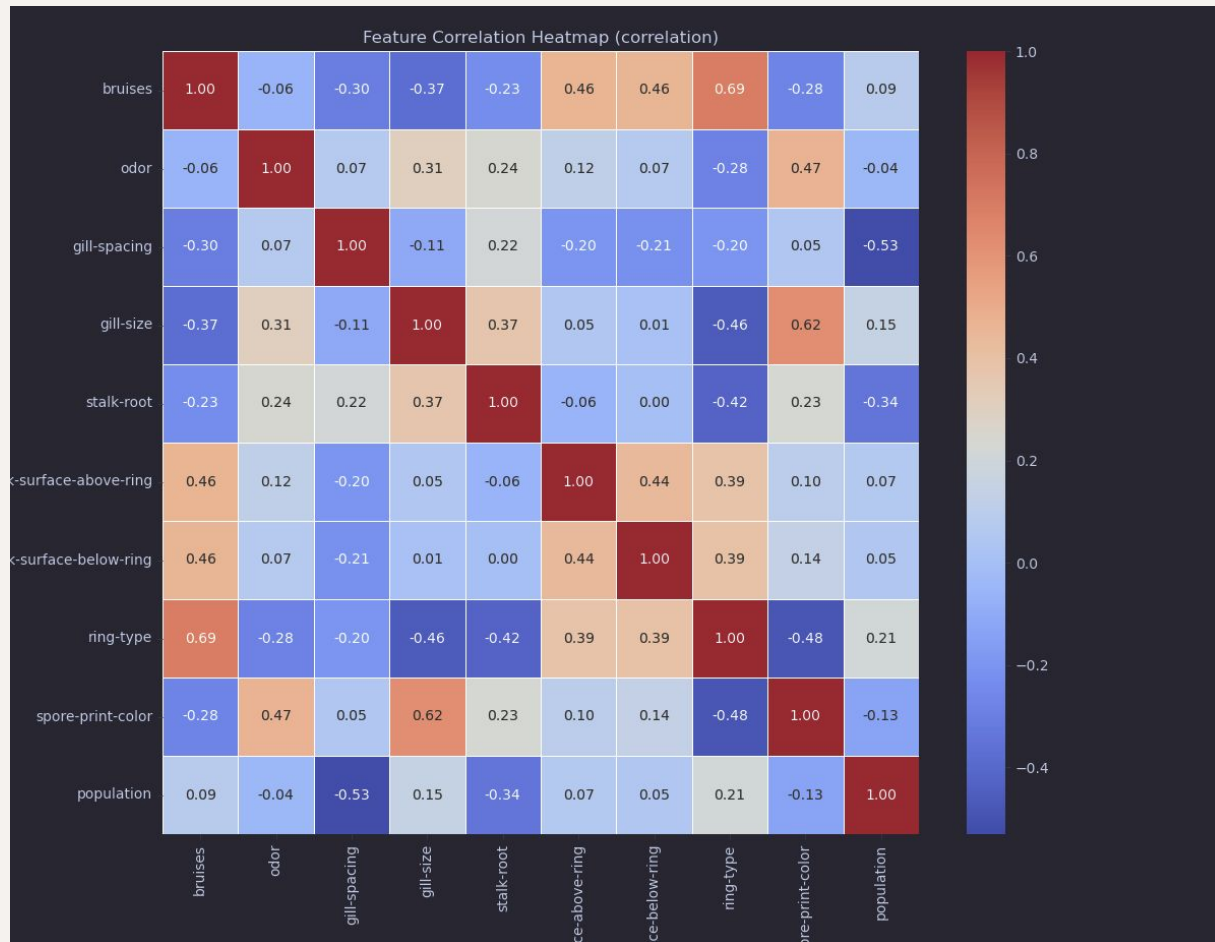
Attribute Evaluator (supervised, Class (nominal): 23 class):
Correlation Ranking Filter

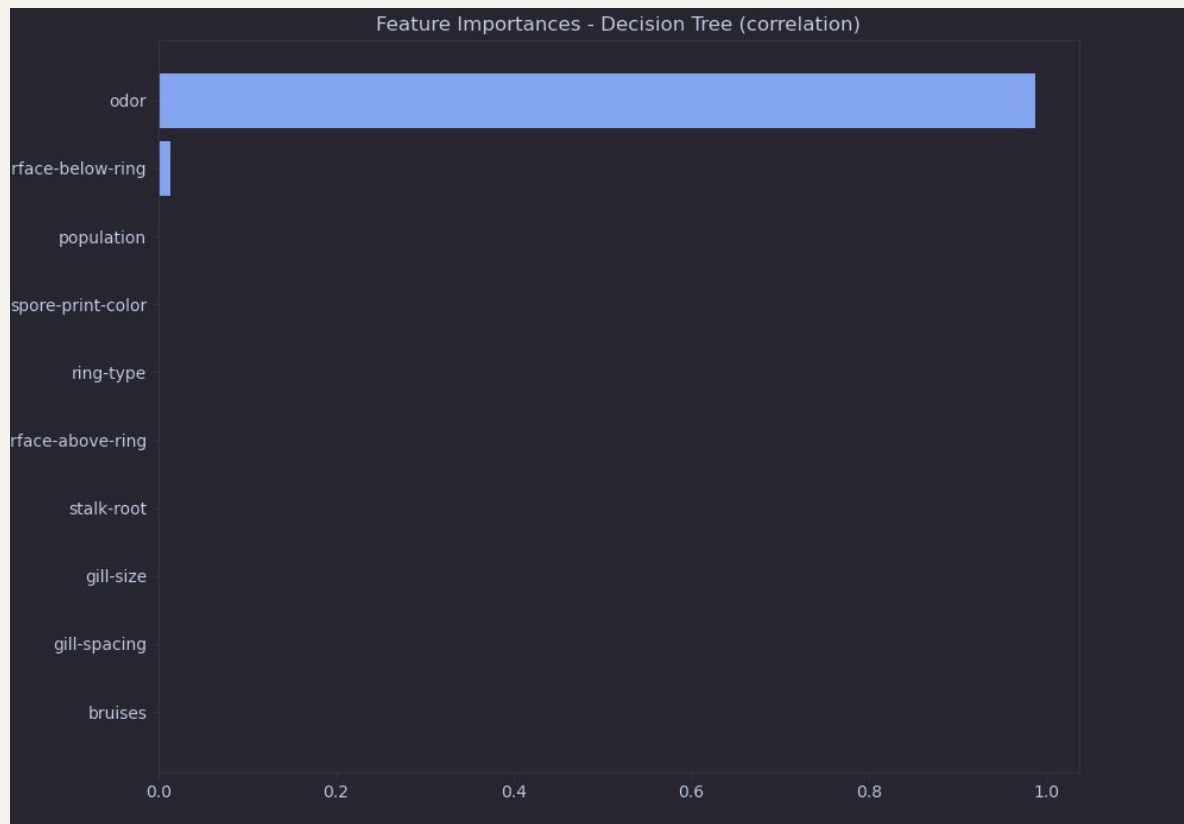
Ranked attributes:

0.5792	5	odor
0.54	8	gill-size
0.5015	4	bruises
0.4928	12	stalk-surface-above-ring
0.4341	13	stalk-surface-below-ring
0.4131	19	ring-type
0.3985	20	spore-print-color
0.3484	7	gill-spacing
0.3172	11	stalk-root
0.2945	21	population
0.242	9	gill-color
0.2227	14	stalk-color-above-ring
0.2187	15	stalk-color-below-ring
0.1833	18	ring-number
0.1675	22	habitat
0.1396	17	veil-color
0.1292	6	gill-attachment
0.1213	2	cap-surface
0.102	10	stalk-shape
0.0753	3	cap-color
0.0464	1	cap-shape
0	16	veil-type

Cutoff value: 0.25

Selected attributes: 5, 8, 4, 12, 13, 19, 20, 7, 11, 21, 9, 14, 15, 18, 22, 17, 6, 2, 10, 3, 1, 16 : 22



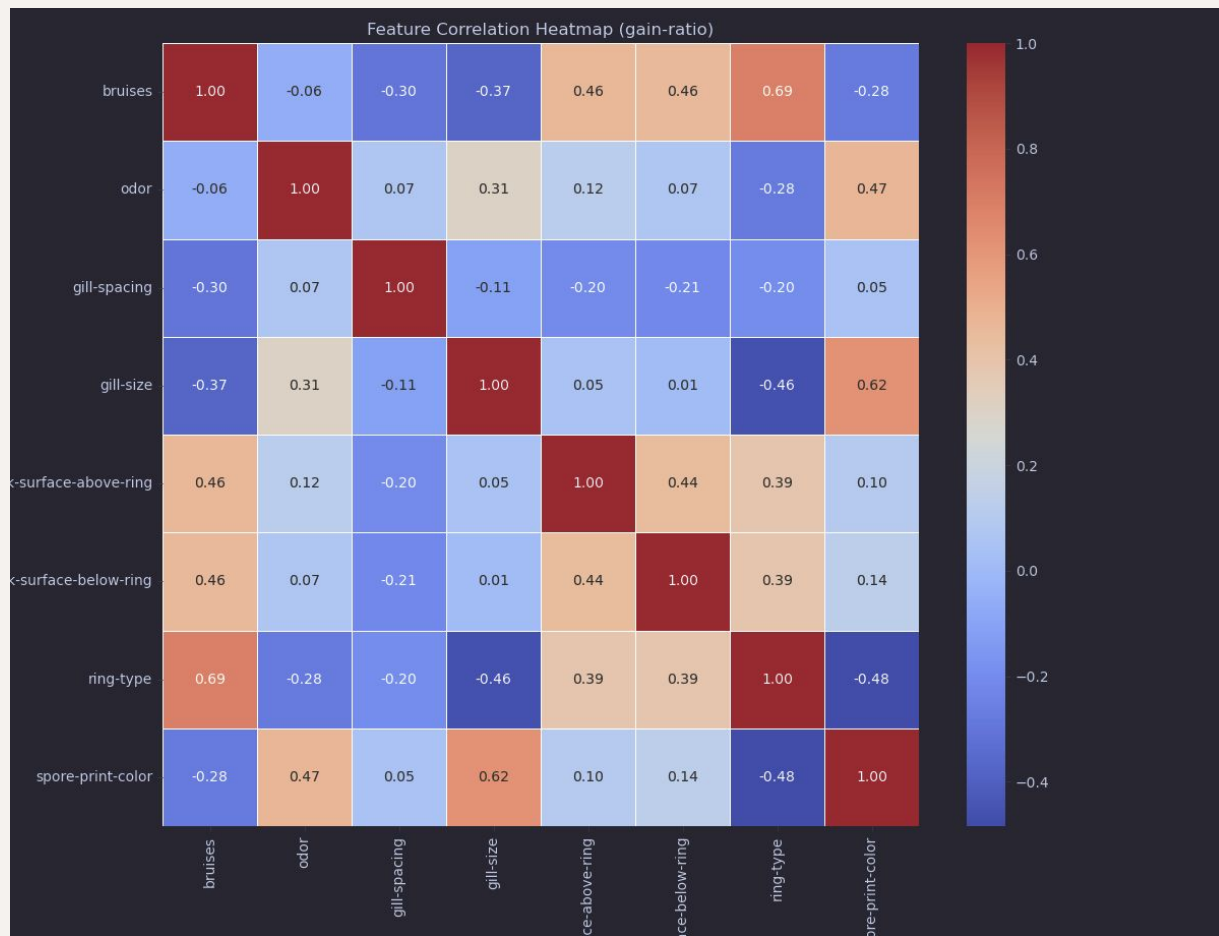


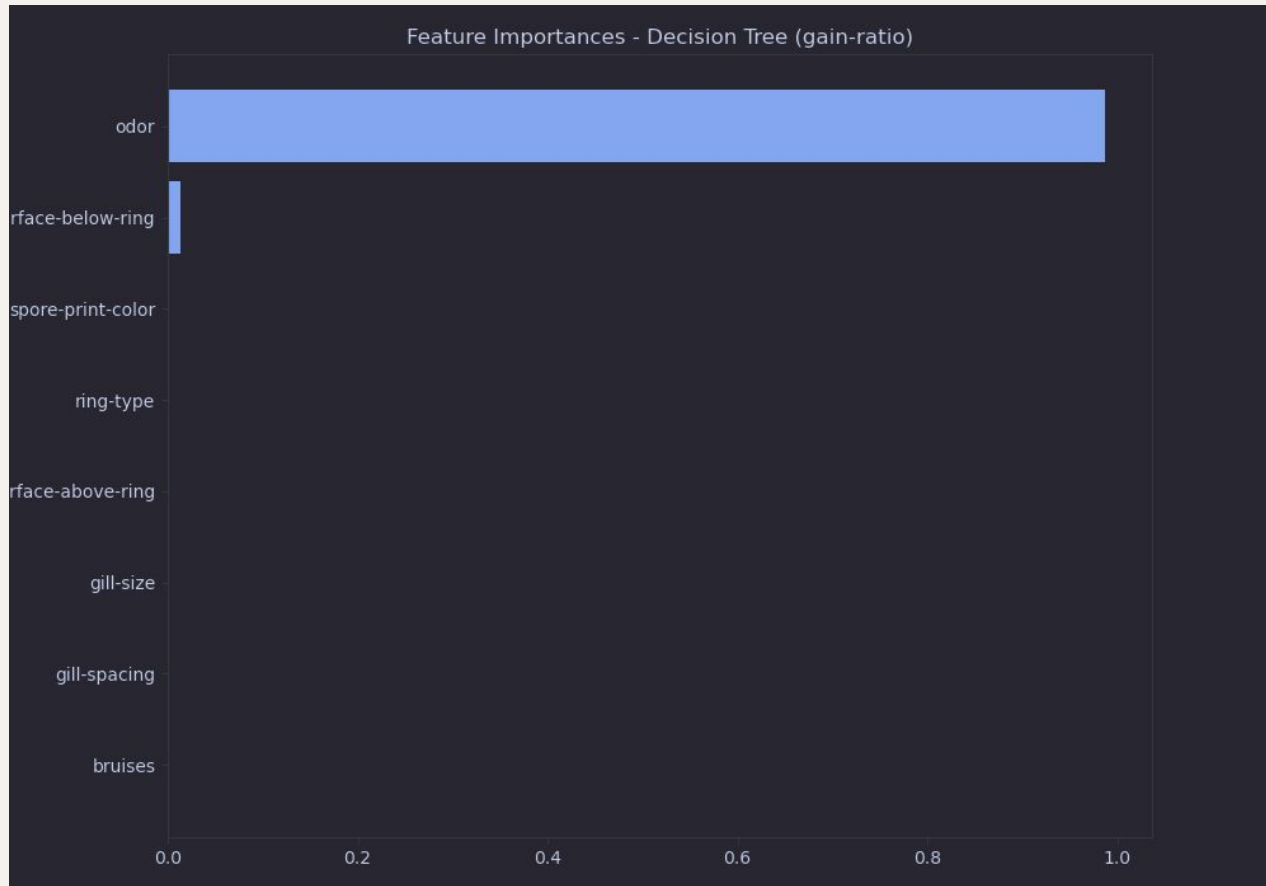
Gain Ratio Attribute Evaluation

- Ranks attributes based on their gain ratio with respect to the class
- Gain ratio reduces bias towards attributes that have many distinct values

```
Attribute Evaluator (supervised, Class (nominal): 23 class):  
Gain Ratio feature evaluator  
  
Ranked attributes:  
0.39065 5 odor  
0.25795 8 gill-size  
0.23312 12 stalk-surface-above-ring  
0.21818 20 spore-print-color  
0.20716 19 ring-type  
0.19644 4 bruises  
0.19433 13 stalk-surface-below-ring  
0.15815 7 gill-spacing  
0.1376 9 gill-color  
0.13106 14 stalk-color-above-ring  
0.12204 15 stalk-color-below-ring  
0.12137 17 veil-color  
0.10081 21 population  
0.10061 11 stalk-root  
0.09141 18 ring-number  
0.08182 6 gill-attachment  
0.06895 22 habitat  
0.02952 1 cap-shape  
0.01815 2 cap-surface  
0.01436 3 cap-color  
0.00762 10 stalk-shape  
0 16 veil-type  
  
Selected attributes: 5,8,12,20,19,4,13,7,9,14,15,17,21,11,18,6,22,1,2,3,10,16 : 22
```

Cutoff value: 0.15



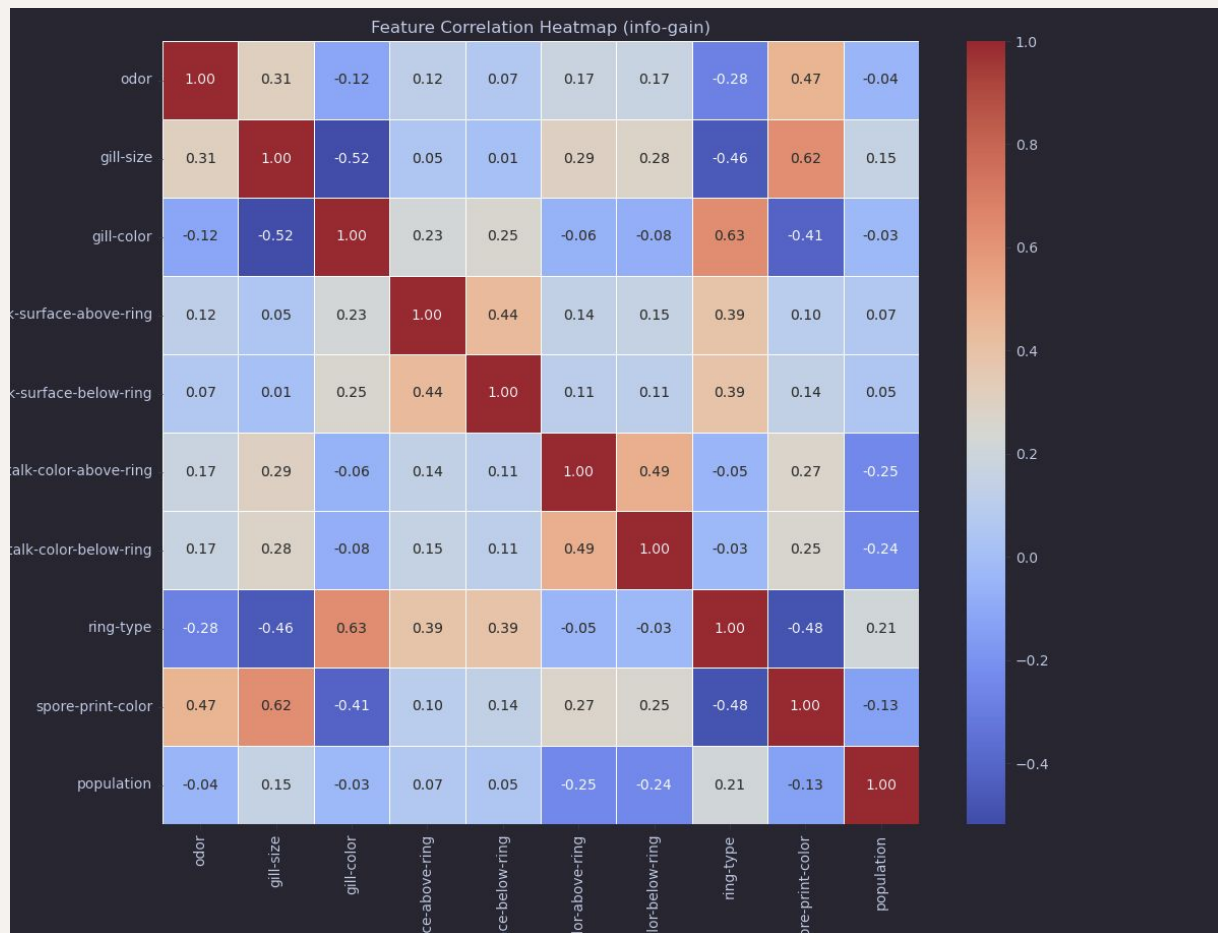


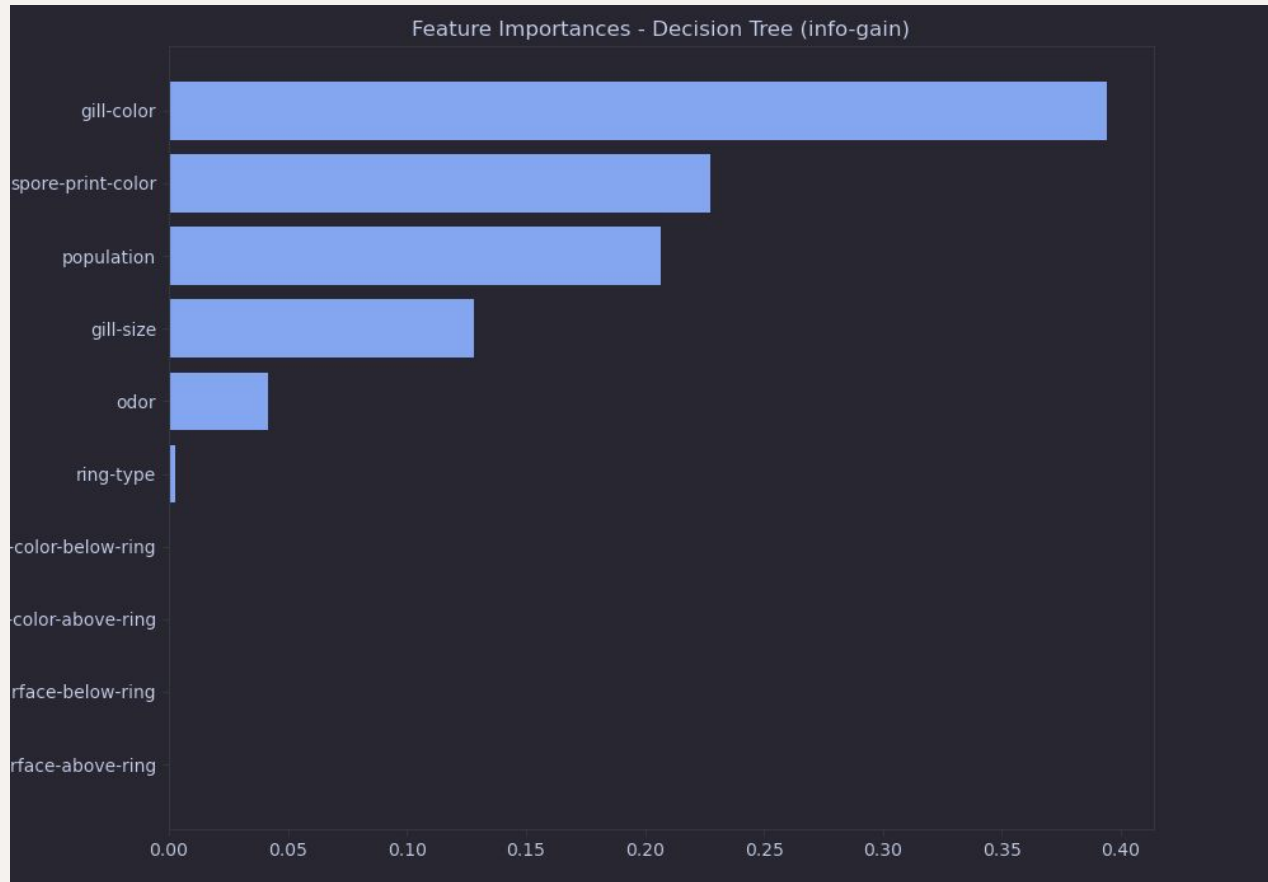
Information Gain Attribute Evaluation

- Ranks attributes based on their information gain with respect to the class
- Information gain = reduction in entropy about the class

```
Attribute Evaluator (supervised, Class (nominal): 23 class):  
Information Gain Ranking Filter  
  
Ranked attributes:  
0.90607 5 odor  
0.4807 20 spore-print-color  
0.41698 9 gill-color  
0.31802 19 ring-type  
0.28473 12 stalk-surface-above-ring  
0.27189 13 stalk-surface-below-ring  
0.25385 14 stalk-color-above-ring  
0.24142 15 stalk-color-below-ring  
0.23015 8 gill-size  
0.20196 21 population  
0.19238 4 bruises  
0.15683 22 habitat  
0.10835 11 stalk-root  
0.10088 7 gill-spacing  
0.0488 1 cap-shape  
0.03845 18 ring-number  
0.03605 3 cap-color  
0.02859 2 cap-surface  
0.02382 17 veil-color  
0.01417 6 gill-attachment  
0.00752 10 stalk-shape  
0 16 veil-type  
  
Selected attributes: 5,20,9,19,12,13,14,15,8,21,4,22,11,7,1,18,3,2,17,6,10,16 : 22
```

Cutoff value: 0.2





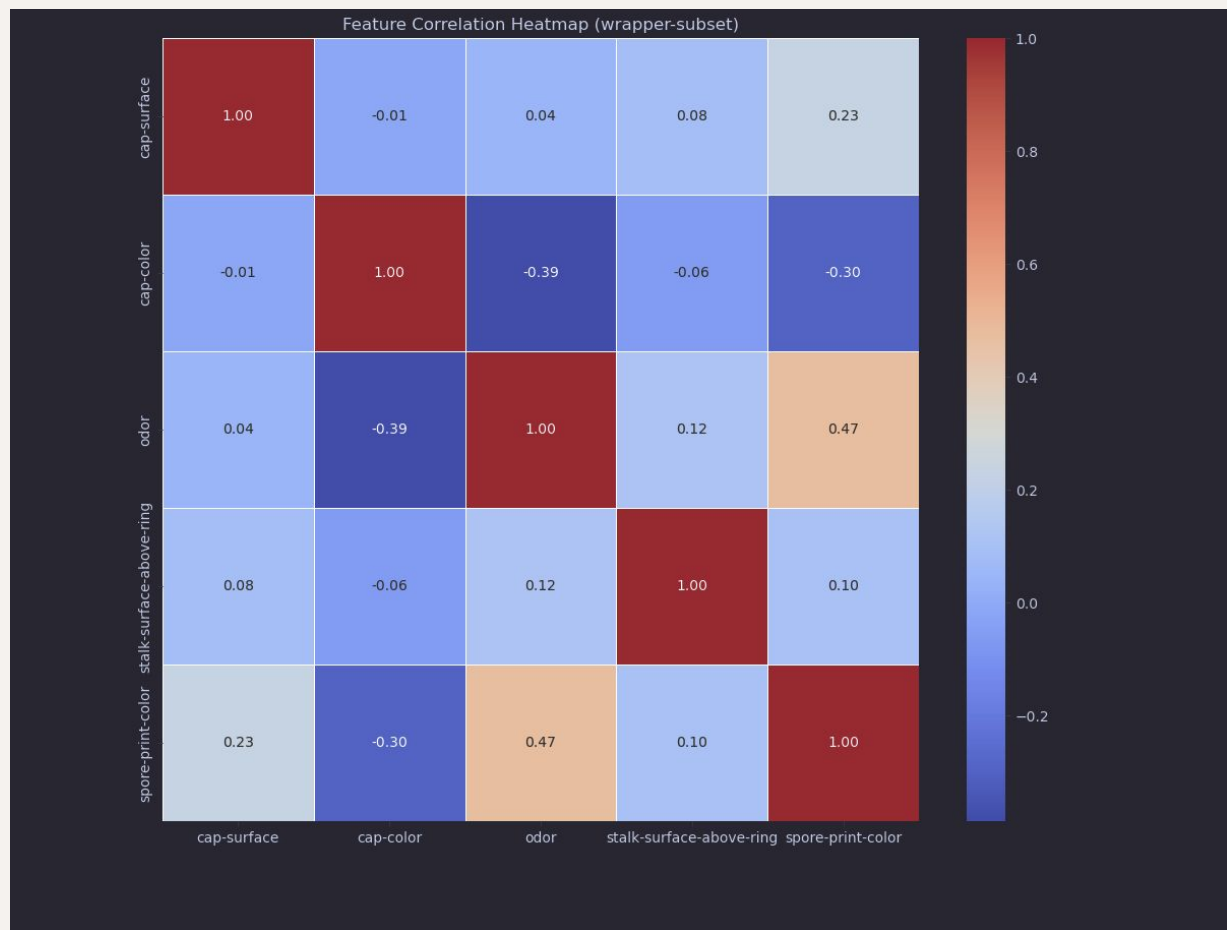
Wrapper Subset Evaluation

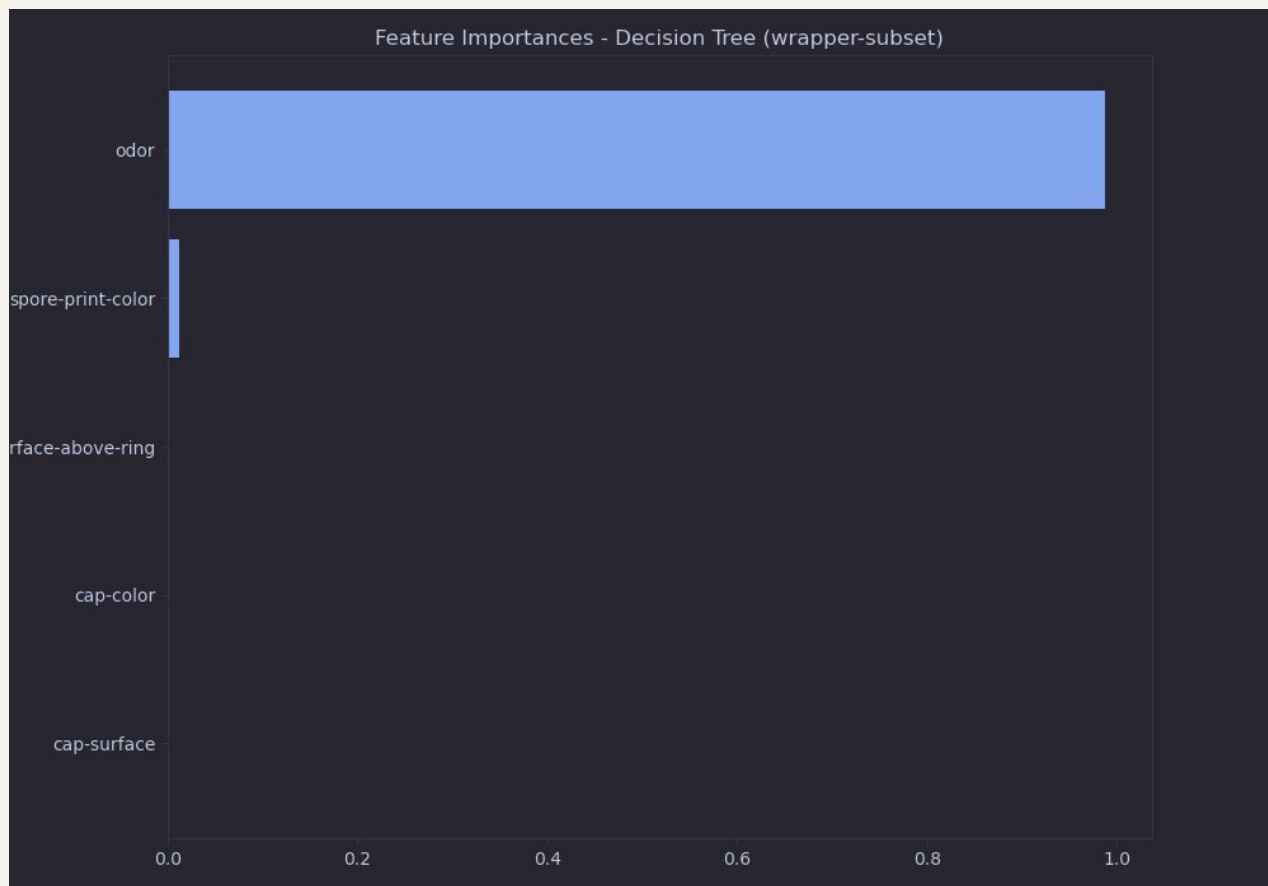
- Evaluates the performance of a subset of attributes using J48 Decision Tree classifier
- Direct measure of the impact of selected attributes on model performance

```
Search Method:
Best first.
Start set: no attributes
Search direction: forward
Stale search after 5 node expansions
Total number of subsets evaluated: 182
Merit of best subset found: 1

Attribute Subset Evaluator (supervised, Class {nominal}: 23 class):
Wrapper Subset Evaluator
Learning scheme: weka.classifiers.trees.J48
Scheme options: -C 0.25 -M 2
Subset evaluation: classification accuracy
Number of folds for accuracy estimation: 5

Selected attributes: 2,3,5,12,20 : 5
cap-surface
cap-color
odor
stalk-surface-above-ring
spore-print-color
```



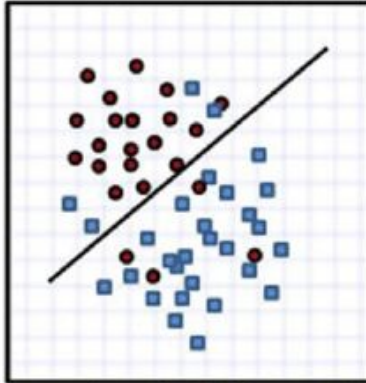


Classifier Models

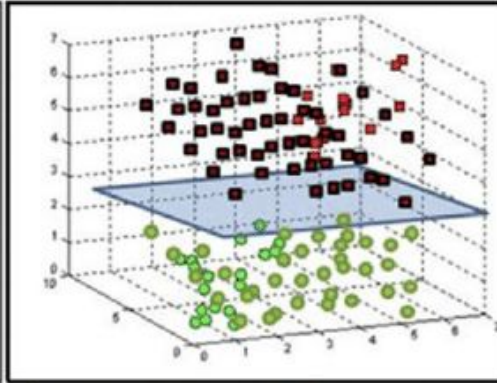
- Decision Tree (J48): Uses rules to classify data by approximating a sine curve
- Quadratic Discriminant Analysis (QDA): Generates a quadratic boundary by fitting Gaussian densities to classes
- Logistic Regression: Utilizes a Bernoulli distribution to predicts probabilities for binary outcomes
- Support Vector Classifier (SVC): Finds optimal “hyperplane” for data (the decision boundary that maximizes the distance between the closest data points of two attributes)

Models were **trained using scikit-learn** and **stored with pickle** library serialization

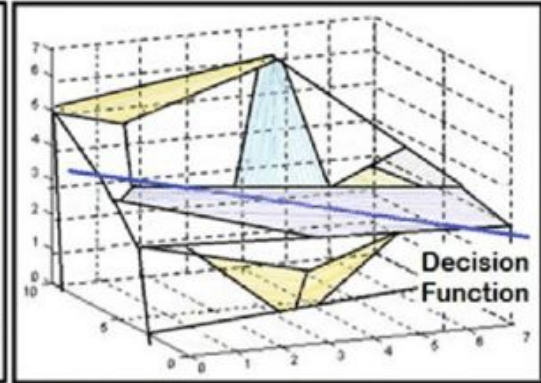
Hyperplane



Hyperplane in 2-Dimensional
Calculations (Line)



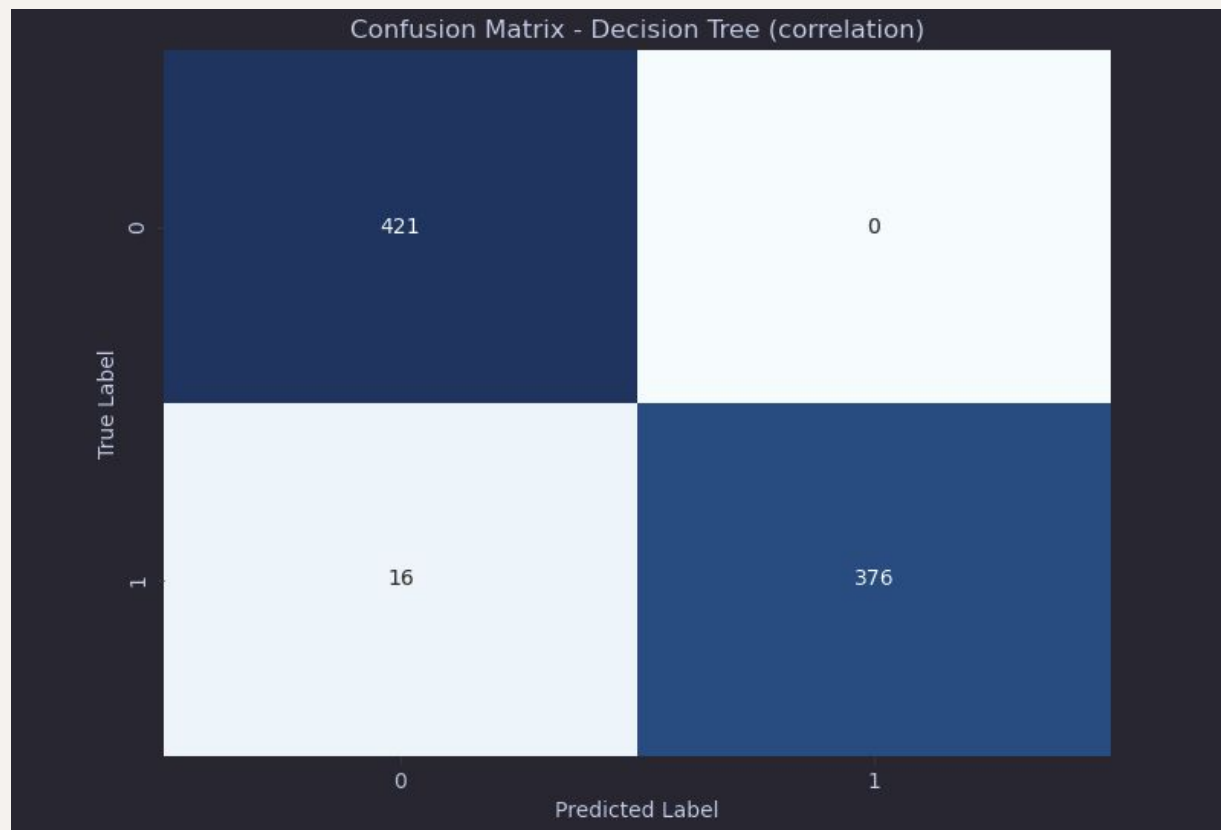
Hyperplane in 3- Dimensional
Calculations (Plane)



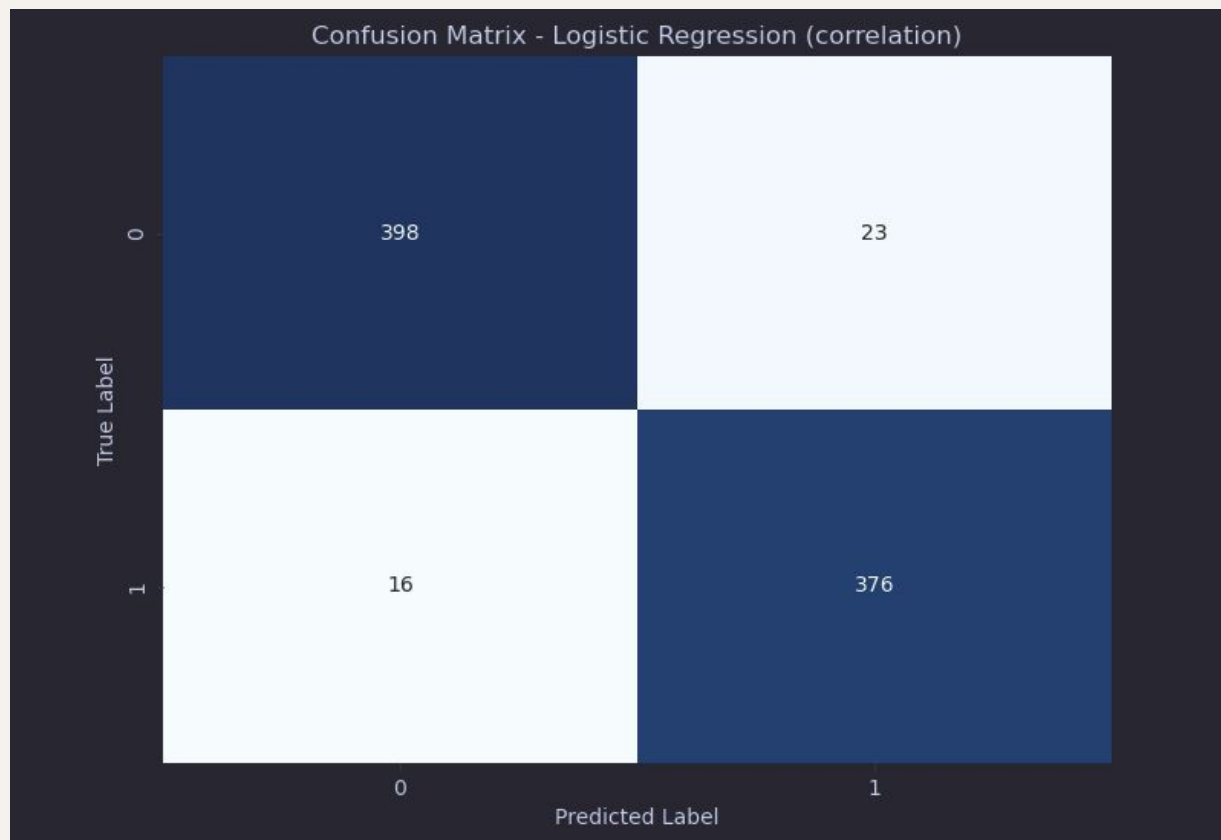
Hyperplane in n-Dimensional
Calculations (Multiple Planes)

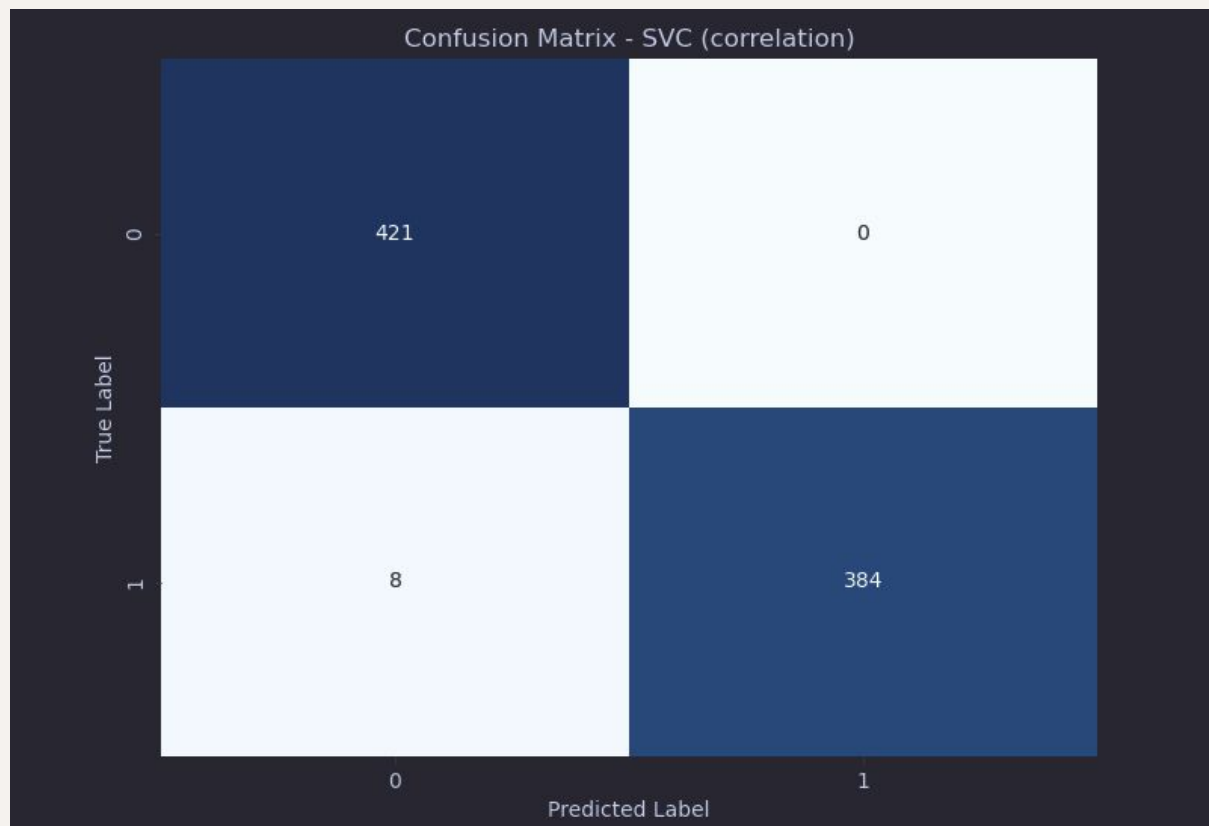
Comparison of Models

Model	Strengths	Weaknesses
J48 Decision Tree	Easy to use	Prone to overfitting
Logistic Regression	Good for binary classification	Struggles with non-linear relationships
SVC	Handles complex data well	Very slow
QDA	Works well with nonlinear relationships	Sensitive to dataset size











04 Conclusion

Accuracy Results

	<i>Decision Tree</i>	<i>QDA</i>	<i>Logistic Regression</i>	<i>SVC</i>
<i>Intuition Based Selection</i>	94.9569%	93.6039%	88.9299%	98.2780%
<i>CorrelationAttributeEval</i>	98.0320%	97.1710%	95.2030%	99.0160%
<i>GainRatioAttributeEval</i>	98.0320%	94.7109%	94.7109%	98.8930%
<i>InfoGainAttributeEval</i>	95.4490%	96.0640%	89.7909%	97.0480%
<i>WrapperSubsetEval</i>	98.0320%	86.1009%	65.5597%	98.0320%

Support Vector Classifier (SVC) with CorrelationAttributeEval performed the best

ROC Area Results

	<i>Decision Tree</i>	<i>QDA</i>	<i>Logistic Regression</i>	<i>SVC</i>
<i>Intuition Based Selection</i>	0.980328	0.962359	0.924372	0.998764
<i>CorrelationAttributeEval</i>	0.990184	0.979822	0.980125	0.999727
<i>GainRatioAttributeEval</i>	0.990184	0.969218	0.957814	0.999952
<i>InfoGainAttributeEval</i>	0.979798	0.974835	0.947125	0.997225
<i>WrapperSubsetEval</i>	0.996801	0.938454	0.753908	0.999436

Support Vector Classifier (SVC) with GainRatioAttributeEval performed the best

Metrics for Chosen Model (SVC + Correlation)

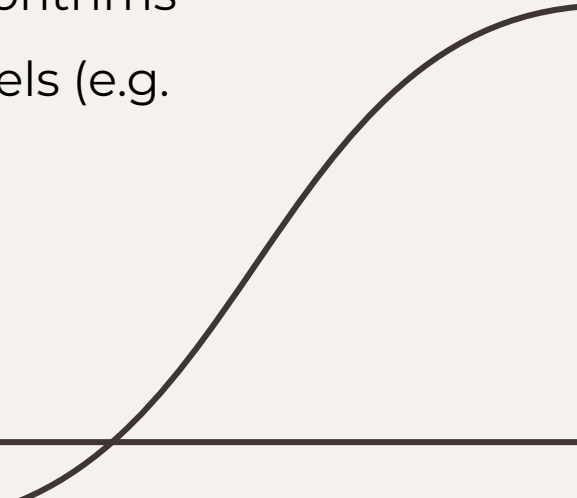
Accuracy: 99.0160%
Correctly Classified Instances: 805
Incorrectly Classified Instances: 8
Kappa Statistic: 0.9803
Mean Absolute Error (MAE): 0.0098
Root Mean Squared Error (RMSE): 0.0992
Relative Absolute Error (RAE): 0.0197
Root Relative Squared Error (RRSE): 0.1985
Total Number of Instances: 813

	TP Rate	FP Rate	Precision	Recall	F-Measure	MCC	ROC Area	PRC Area
0	1.000000	0.018648	0.981352	1.000000	0.990588	0.980472	0.999727	0.999711
1	0.979592	0.000000	1.000000	0.979592	0.989691	0.980472	0.999727	0.999711
Weighted Avg	0.989796	0.009324	0.990343	0.990160	0.990155	0.980472	0.999727	0.999711

Confusion Matrix:

	Predicted 0	Predicted 1
Actual 0	421	0
Actual 1	8	384

Future Work

- Using Correlation as a selection algorithm could overlook attributes that might have high correlation when combined with other attributes
 - Exploring alternative attribute selection algorithms
 - Experimenting with different classifier models (e.g. Random Forest, Gradient Boosting)
- 

Sources

Blythe, V. (n.d.). *Mushrooms* [Image]. Dribbble. <https://dribbble.com/shots/14323122-Mushrooms>

Brandenburg, W. E., & Ward, K. J. (2018, July 31). *Mushroom poisoning epidemiology in the United States*. National Library of Medicine. Retrieved October 23, 2024, from <https://doi.org/10.1080/00275514.2018.1479561>

Colors, C. (n.d.). *Glowing Mushrooms* [Image]. Dribbble. <https://dribbble.com/shots/22519055-Glowing-Mushrooms>

DecisionTreeClassifier. (n.d.). scikit-learn. Retrieved October 22, 2024, from <https://scikit-learn.org/stable/modules/generated/sklearn.tree.DecisionTreeClassifier.html>

1.4. Support Vector Machines. (n.d.). scikit-learn. Retrieved October 22, 2024, from <https://scikit-learn.org/1.5/modules/svm.html>

Lillo, W. (n.d.). *Isometric Mushrooms* [Image]. Dribbble. <https://dribbble.com/shots/20837558-Isometric-Mushrooms>

LogisticRegression. (n.d.). scikit-learn. Retrieved October 22, 2024, from https://scikit-learn.org/1.5/modules/generated/sklearn.linear_model.LogisticRegression.html

Sources

Miminozhvili, A. (n.d.). *Mushrooms* [Image]. Dribbble. <https://dribbble.com/shots/3641736-Mushrooms>

MKL47. (n.d.). *Mushrooms set* [Image]. Dribbble. <https://dribbble.com/shots/23206484-Mushrooms-set>

Package weka.attributeSelection. (n.d.). Weka Documentation. Retrieved October 22, 2024, from

<https://weka.sourceforge.io/doc.dev/weka/attributeSelection/package-summary.html>

QuadraticDiscriminantAnalysis. (n.d.). scikit-learn. Retrieved October 22, 2024, from

https://scikit-learn.org/stable/modules/generated/sklearn.discriminant_analysis.QuadraticDiscriminantAnalysis.html

Schultz, P. (n.d.). *Mushroom Pattern* [Image]. Dribbble. <https://dribbble.com/shots/5709006-Mushroom-Pattern>

Wild Mushrooms. (n.d.). The Blue Ridge Poison Center. Retrieved October 23, 2024, from

<https://med.virginia.edu/brpc/wp-content/uploads/sites/274/2015/10/Mushrooms.pdf>

Thank you!

CREDITS: This presentation template was created by **Slidesgo**, including icons by **Flaticon**, infographics & images by **Freepik**