

Project Topic

This project explores the application of supervised learning techniques to classify mushrooms as either **edible** or **poisonous**. This is a **binary classification problem** as the task is to predict one of two discrete classes.

The primary goal of this project is to:

1. Demonstrate the process of supervised learning by applying multiple machine learning algorithms to a real-world classification task.
2. Learn and implement advanced techniques such as hyperparameter tuning, feature engineering, and model evaluation.
3. Showcase performance metrics and comparisons to determine the most effective model for the task.
4. Highlight the importance of accurate classification in practical scenarios, such as identifying potentially dangerous mushrooms.

Data

The dataset used is the **Secondary Mushroom Dataset** from the UCI Machine Learning Repository.

Dua, D., & Graff, C. (2019). UCI Machine Learning Repository [Secondary Mushroom Dataset]. Retrieved from <https://archive.ics.uci.edu/dataset/848/secondary+mushroom+datase>.

This dataset was curated as a simulated dataset for binary classification tasks, specifically focusing on the edibility of mushrooms based on their features. It provides diverse feature types and a large number of samples, making it suitable for exploring advanced machine learning techniques and evaluating model performance comprehensively.

The data is sourced into this notebook using the `ucimlrepo` package.

Data Description

- **Number of Samples:** 61,068
- **Number of Features:** 20
- **Feature Types:**
 - Categorical features (e.g., cap shape, surface, color, etc.)
 - Continuous features (e.g., numerical indicators for specific measurements: cap diameter, stem height & width)
- **Task Type:** Binary classification (edible or poisonous)

```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
from ucimlrepo import fetch_ucirepo
```

```

# Thanks, UCI_ML_Repo!
# fetch dataset
secondary_mushroom = fetch_ucirepo(id=848)
# data (as pandas dataframes)
X = secondary_mushroom.data.features
y = secondary_mushroom.data.targets

# metadata
# print(secondary_mushroom.metadata)
# variable information
print(secondary_mushroom.variables)

```

	name	role	type	demographic	description
units \					
0	class	Target	Categorical	None	None
None					
1	cap-diameter	Feature	Continuous	None	None
None					
2	cap-shape	Feature	Categorical	None	None
None					
3	cap-surface	Feature	Categorical	None	None
None					
4	cap-color	Feature	Categorical	None	None
None					
5	does-bruise-or-bleed	Feature	Categorical	None	None
None					
6	gill-attachment	Feature	Categorical	None	None
None					
7	gill-spacing	Feature	Categorical	None	None
None					
8	gill-color	Feature	Categorical	None	None
None					
9	stem-height	Feature	Continuous	None	None
None					
10	stem-width	Feature	Continuous	None	None
None					
11	stem-root	Feature	Categorical	None	None
None					
12	stem-surface	Feature	Categorical	None	None
None					
13	stem-color	Feature	Categorical	None	None
None					
14	veil-type	Feature	Categorical	None	None
None					
15	veil-color	Feature	Categorical	None	None
None					
16	has-ring	Feature	Categorical	None	None
None					
17	ring-type	Feature	Categorical	None	None
None					

18	spore-print-color	Feature	Categorical	None	None
19	habitat	Feature	Categorical	None	None
20	season	Feature	Categorical	None	None

missing_values

0	no
1	no
2	no
3	yes
4	no
5	no
6	yes
7	yes
8	no
9	no
10	no
11	yes
12	yes
13	no
14	yes
15	yes
16	no
17	yes
18	yes
19	no
20	no

'''

Exploratory Data Analysis [Part 1]

The variable information printed above shows that several features were missing values.

In order to not cut right break certain my logistic regression model or to degrade performance of my other models, I inspected the percentage of samples missing the particular features. I decided to remove features with more than 30% of values missing to avoid causing collinearity among the features (e.g., associating a missing veil-type with poisonous if by chance many poisonous records were missing a veil-type, etc.).

For the rest with missing values I added a new, unique value (?) to represent missing. This was a viable option because the features in scope were all categorical instead of continuous.

'''

```
missing_proportions = X.isnull().mean() * 100
missing_features = missing_proportions[missing_proportions >
0].sort_values(ascending=False)
```

```

print("Missing values (%) from source dataset:")
print(missing_features)
print('Cleaning data...', end='\n\n')

features_to_drop = missing_proportions[missing_proportions > 30].index
X_cleaned = X.drop(columns=features_to_drop)

features_to_mod = missing_proportions[missing_proportions <= 30].index
for f in features_to_mod:
    X_cleaned.fillna({ f: "?" }, inplace=True)

missing_proportions_check = X_cleaned.isnull().mean() * 100
missing_features_check =
missing_proportions_check[missing_proportions_check > 0]
assert len(missing_features_check) == 0, 'Data is not cleaned as
expected'
X = X_cleaned
print('Data is clean and ready to explore, train, and test!')
print(X.head())

```

Missing values (%) from source dataset:

veil-type	94.797688
spore-print-color	89.595376
veil-color	87.861272
stem-root	84.393064
stem-surface	62.427746
gill-spacing	41.040462
cap-surface	23.121387
gill-attachment	16.184971
ring-type	4.046243

dtype: float64

Cleaning data...

Data is clean and ready to explore, train, and test!

	cap-diameter	cap-shape	cap-surface	cap-color	does-bruise-or-bleed
0	15.26	x	g	o	f
1	16.60	x	g	o	f
2	14.07	x	g	o	f
3	14.17	f	h	e	f
4	14.64	x	h	o	f

	gill-attachment	gill-color	stem-height	stem-width	stem-color	has-ring
0	e	w	16.95	17.09	w	

t					
1	e	w	17.99	18.19	w
t					
2	e	w	17.80	17.74	w
t					
3	e	w	15.77	15.98	w
t					
4	e	w	16.53	17.20	w
t					

	ring-type	habitat	season
0	g	d	w
1	g	d	u
2	g	d	w
3	p	d	w
4	p	d	w

...

Exploratory Data Analysis [Part 2]

First, I graphed the distribution of the target class to check whether the dataset is well balanced between edible and poisonous samples. A balanced dataset allows me to split my test and training samples without worrying about one class dominating the other.

Next, I used a correlation matrix, boxplots, and countplots to assess whether any strong multicollinearity exists between the features and to evaluate the importance of each feature individually. Since the dataset is composed primarily of categorical features, I first encoded those feature values into numeric values. This allowed me to display a correlation matrix, which showed almost no significant correlations. However, this lack of correlations might be due to the nature of the label encoding applied to the categorical features. Because of the label encoding and the potential for feature multicollinearity, I hypothesized that my logistic regression model (see the "Models" section below) would perform the worst among the models I tested.

The boxplots (used for numerical features) and countplots (used for categorical features) provided more insightful observations. The three numerical features exhibited a similar distribution of values across each feature, with a general trend that large outliers were typically associated with edible samples. However, since most values overlapped between classes, I predicted that the numerical features would not be the most influential in the models. I reached a similar conclusion for the more balanced categorical features.

However, among the categorical features, several stood out based on their countplots as being likely to have significant predictive importance. Specifically, cap-surface, gill-attachment, gill-color,

and stem-color appeared to be particularly important features.

```
...
```

```
None #Disable cell output
```

```
print(type(y))
```

```
y_col = y.iloc[:, 0]
```

```
print(type(y_col))
```

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

```
<class 'pandas.core.series.Series'>
```

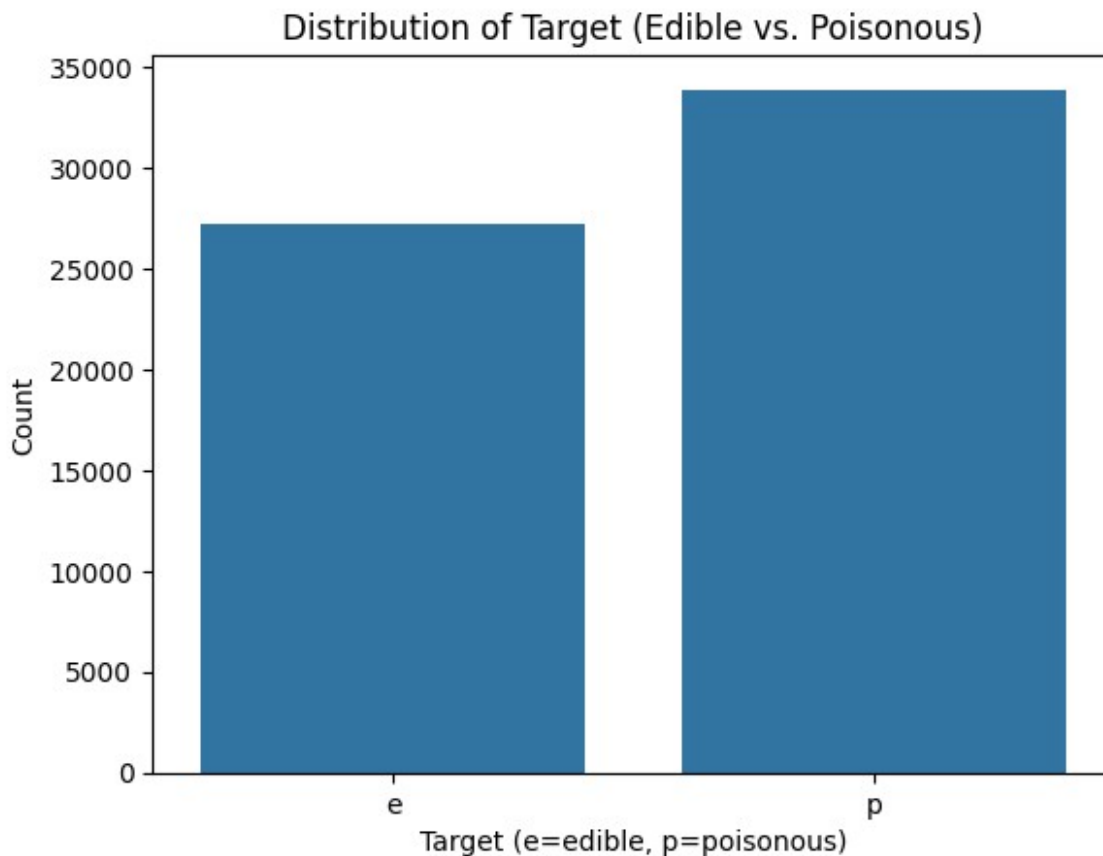
```
sns.countplot(x=y_col, order=['e', 'p'])
```

```
plt.title("Distribution of Target (Edible vs. Poisonous)")
```

```
plt.xlabel("Target (e=edible, p=poisonous)")
```

```
plt.ylabel("Count")
```

```
plt.show()
```



```
num_features = X.select_dtypes(include=['float64'])
```

```
cat_features = X.select_dtypes(include=['object'])
```

```
print(f'{len(num_features.columns)} numeric features')
```

```
print(f'{len(cat_features.columns)} categorical features')
```

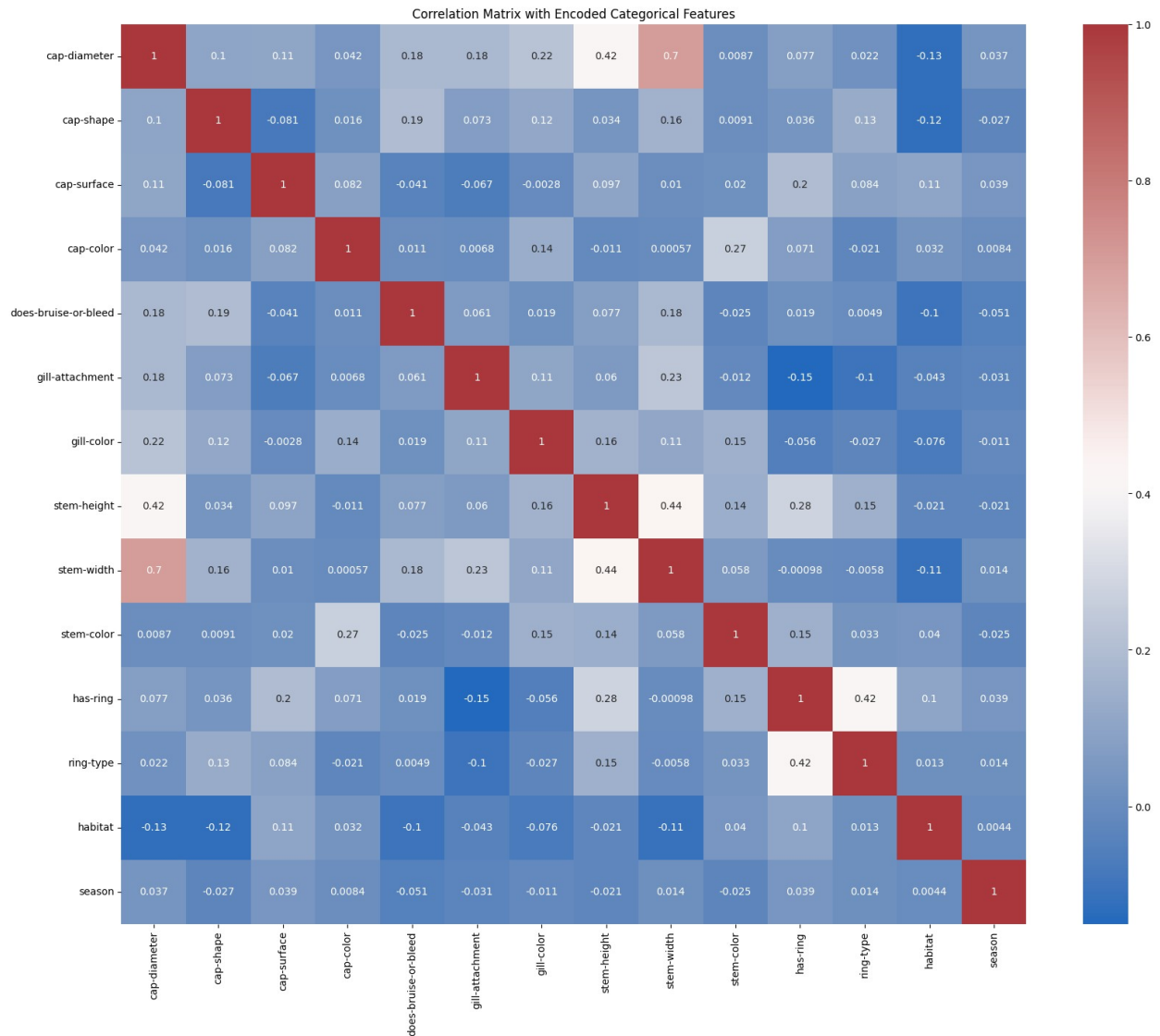
```
3 numeric features
11 categorical features

from sklearn.preprocessing import LabelEncoder

def label_encode_data(data, le_map):
    clone = data.copy()
    for col in clone.select_dtypes(include=['object']):
        le = LabelEncoder()
        clone[col] = le.fit_transform(clone[col])
        le_map[col] = le
    return clone, le_map

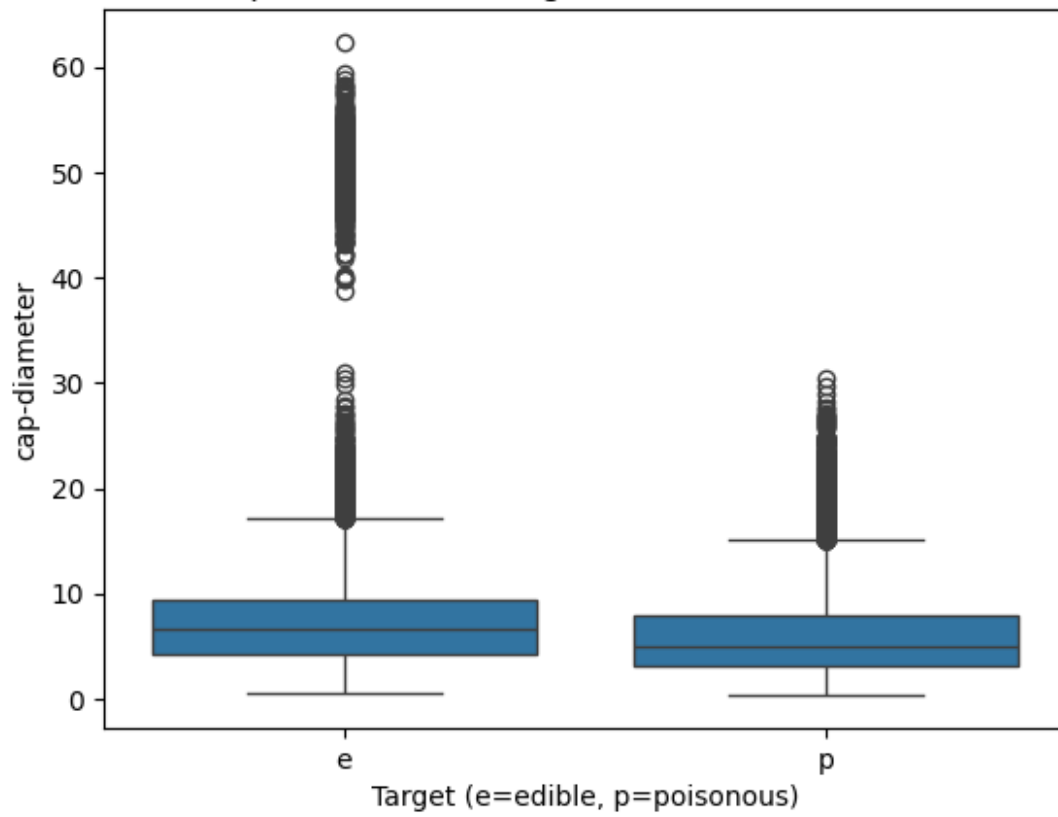
def label_decode_data(data, le_map):
    clone = data.copy()
    for col, le in le_map.items():
        clone[col] = le.inverse_transform(clone[col])
    return clone

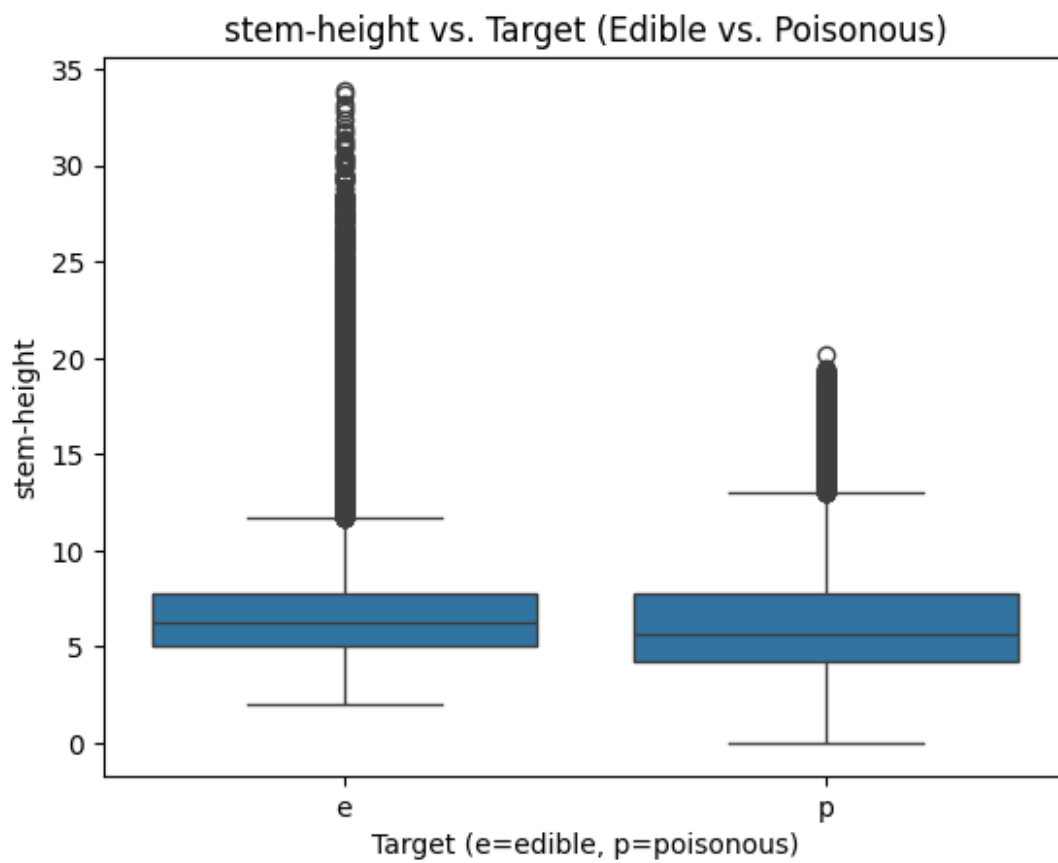
X_le, X_le_map = label_encode_data(X, {})
plt.figure(figsize=(20,16))
sns.heatmap(X_le.corr(), cmap='vlag', annot=True)
plt.title("Correlation Matrix with Encoded Categorical Features")
plt.show()
```

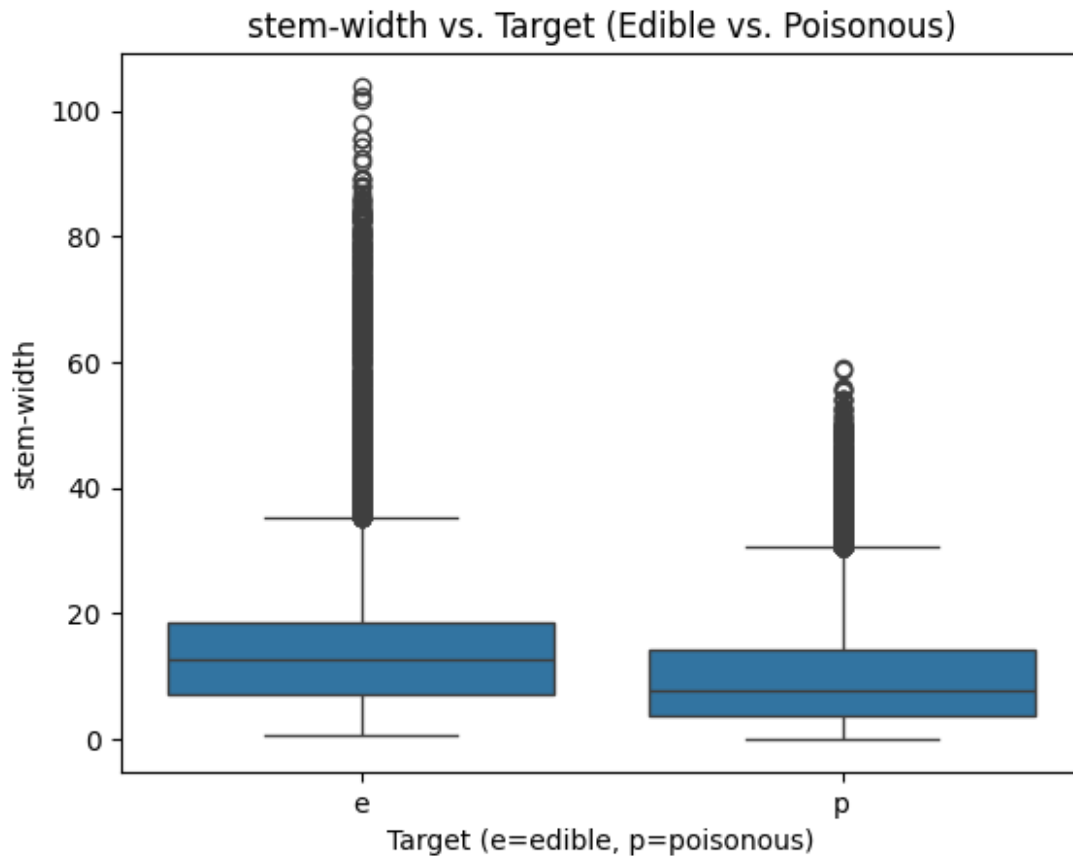


```
for f in num_features:
    sns.boxplot(x=y_col, y=f, data=X, order=['e', 'p'])
    plt.title(f + ' vs. Target (Edible vs. Poisonous)')
    plt.xlabel('Target (e=edible, p=poisonous)')
    plt.show()
```


cap-diameter vs. Target (Edible vs. Poisonous)







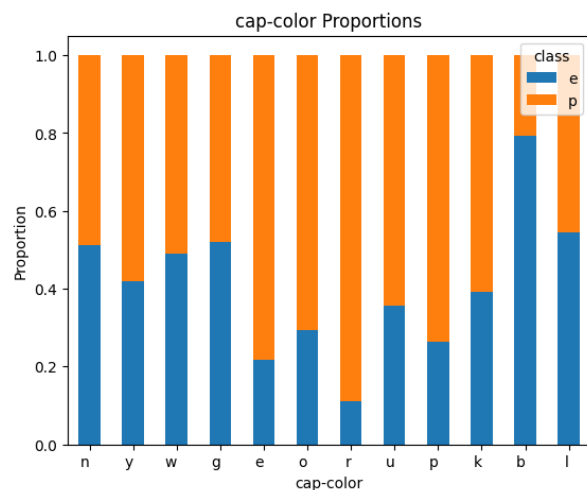
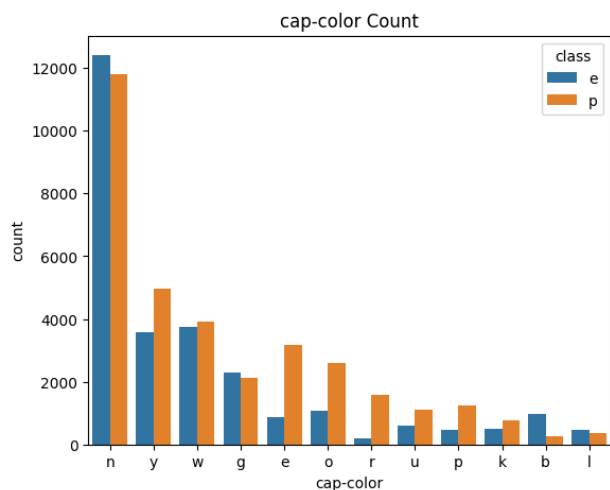
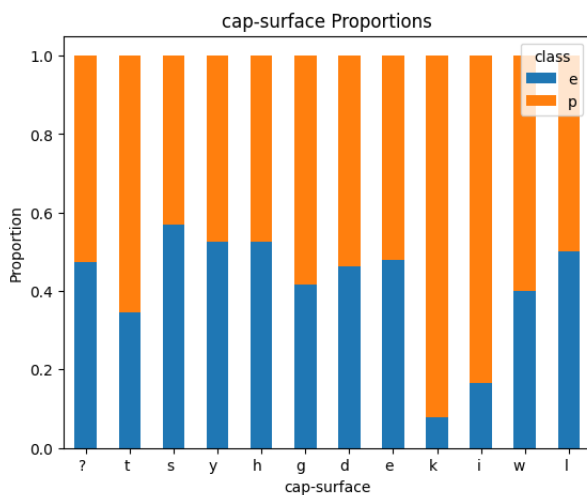
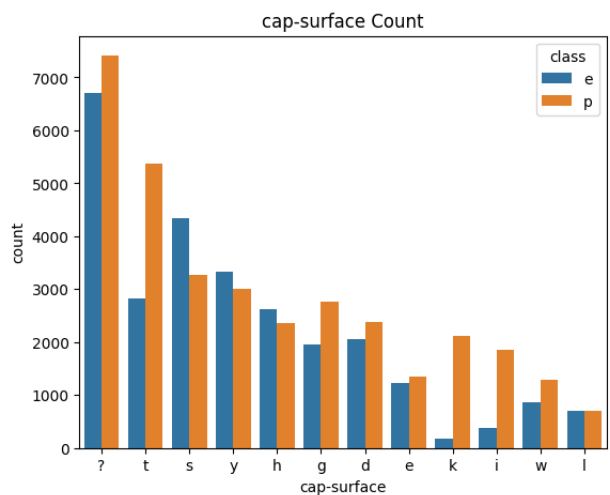
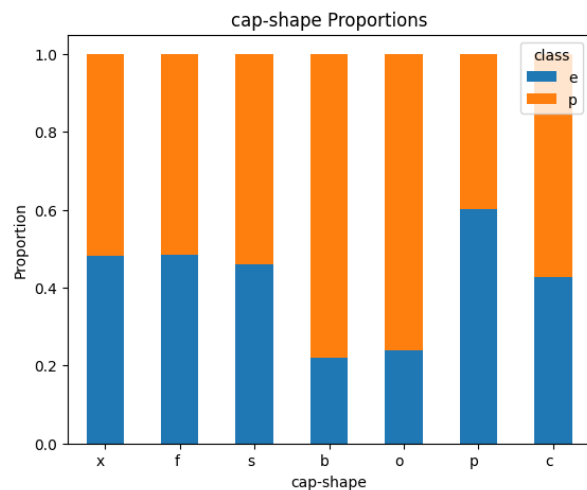
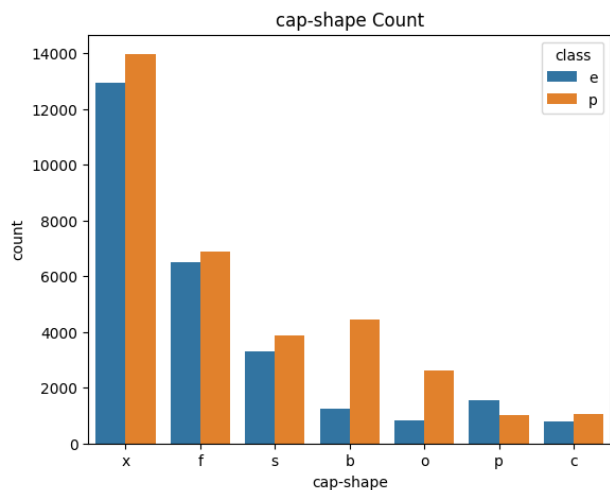
```
for f in cat_features:
    fig, axes = plt.subplots(1, 2, figsize=(14, 5))

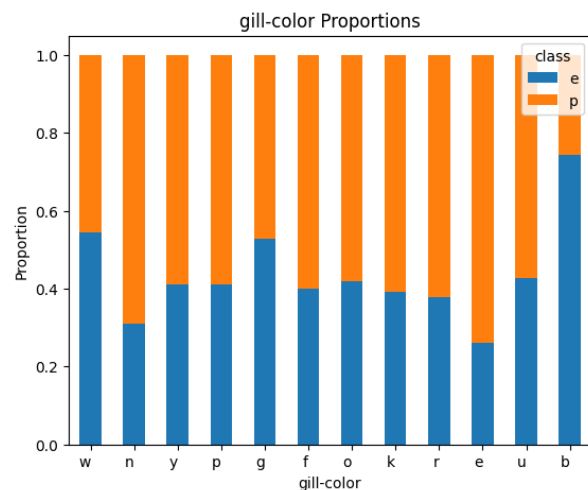
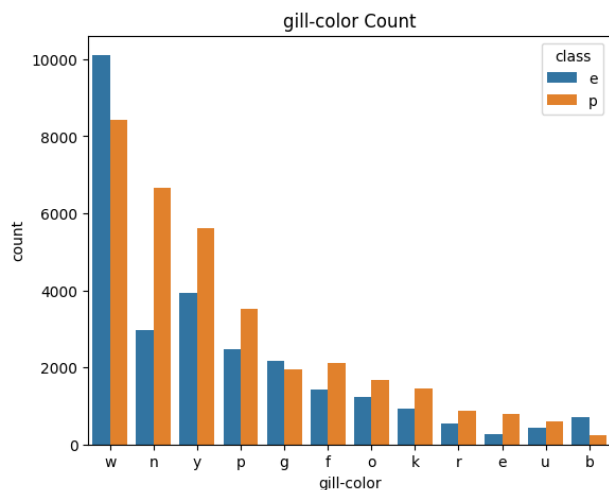
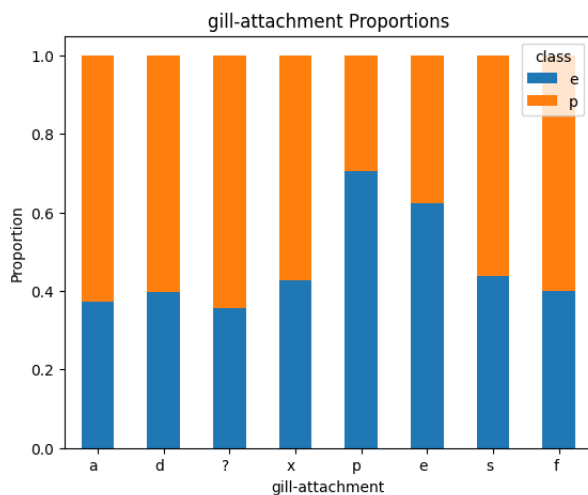
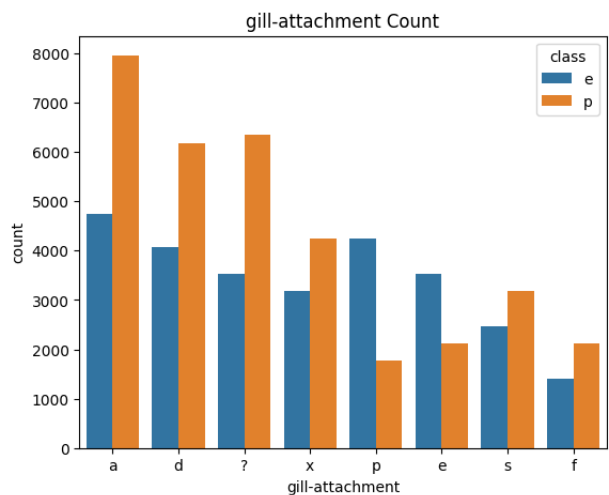
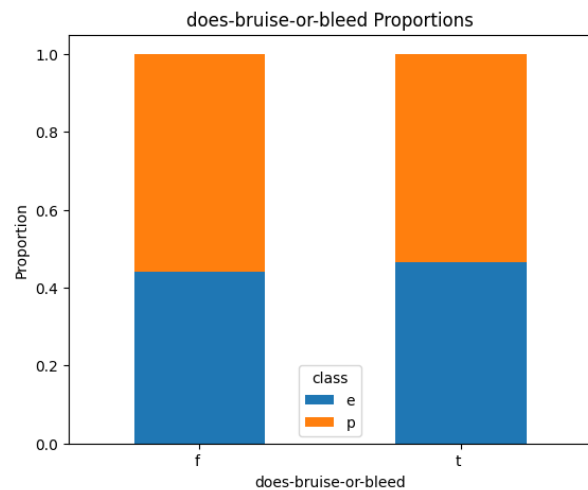
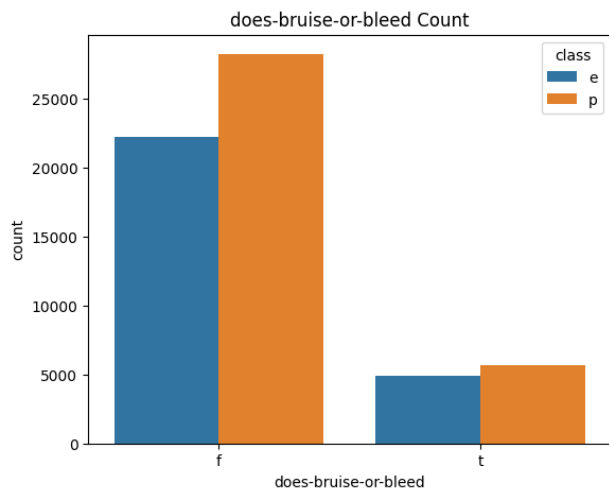
    order = X[f].value_counts().index

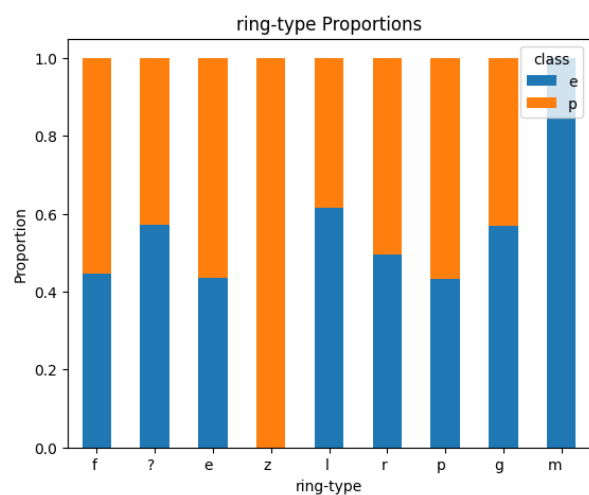
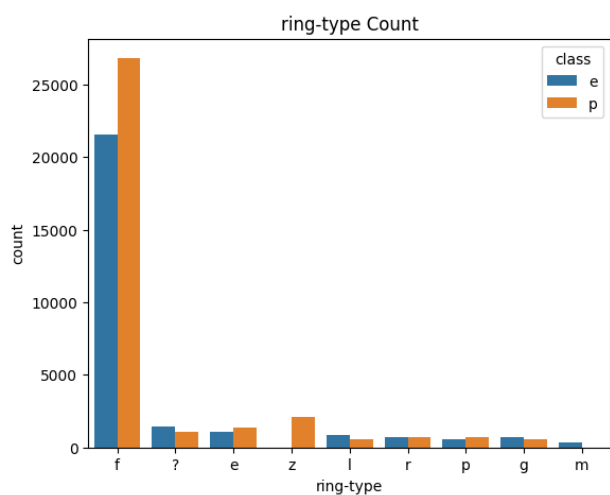
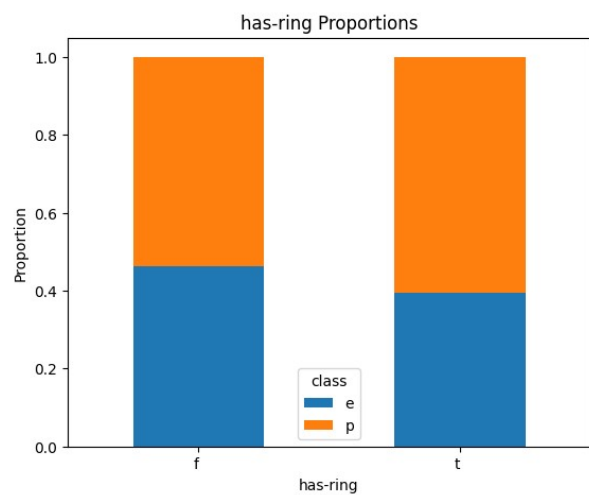
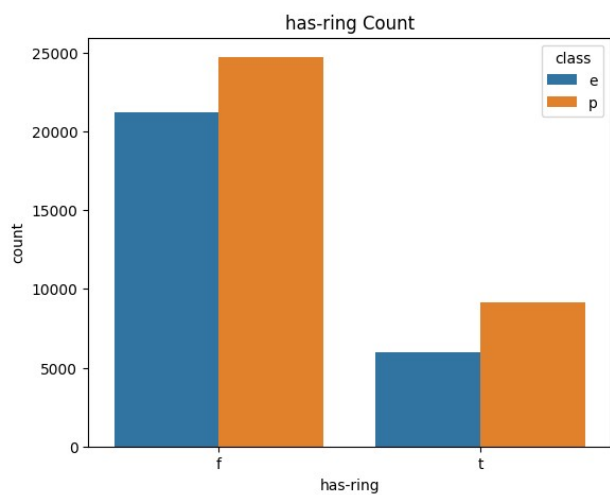
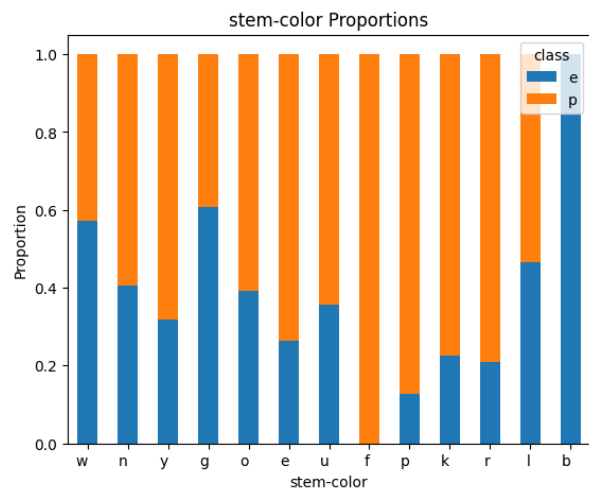
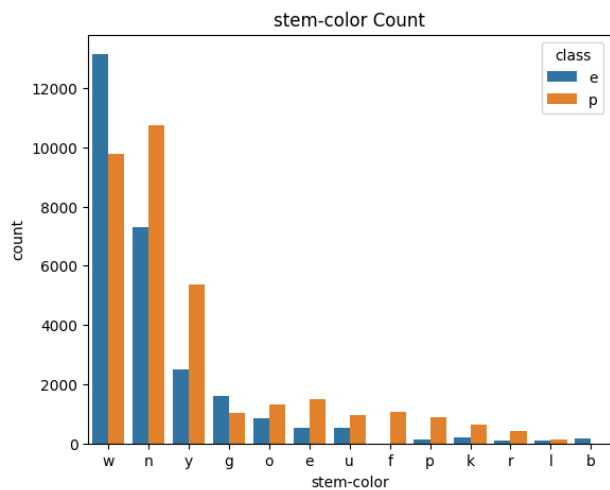
    sns.countplot(x=f, hue=y_col, data=X, ax=axes[0], order=order,
hue_order=['e', 'p'])
    axes[0].set_title(f + ' Count')

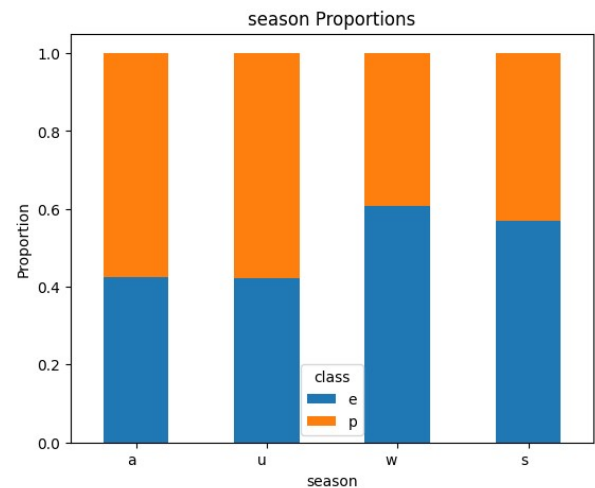
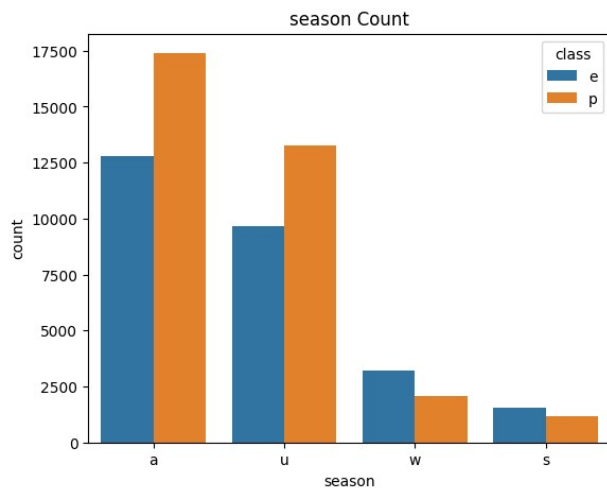
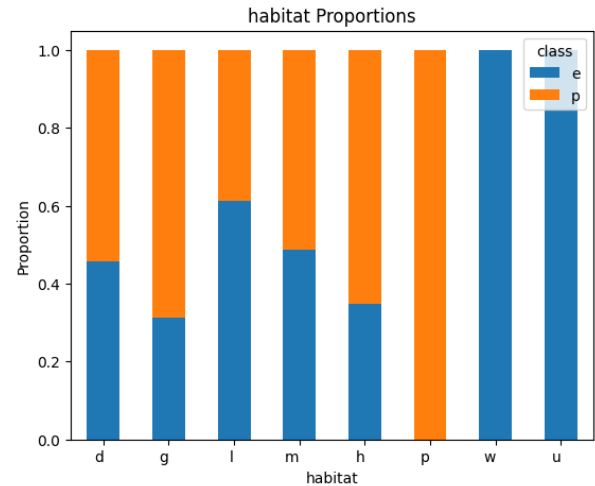
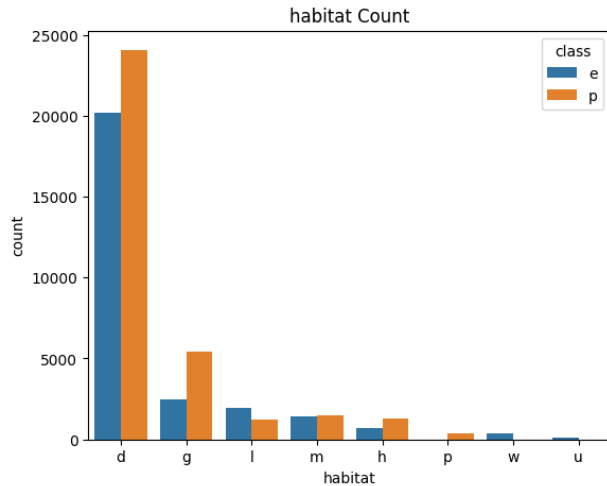
    proportions = X.groupby([f,
y_col]).size().unstack().reindex(index=order)
    proportions.div(proportions.sum(axis=1), axis=0).plot(kind='bar',
stacked=True, ax=axes[1])
    axes[1].set_title(f + ' Proportions')
    axes[1].set_ylabel("Proportion")
    axes[1].set_xticklabels(axes[1].get_xticklabels(), rotation=0,
ha='right')

    plt.show()
```









'''

Models

I chose several models to train and evaluate their performance and accuracy in classifying mushrooms as edible or poisonous. I selected Logistic Regression for its simplicity, though I anticipated it might struggle due to the label encoding and potential multicollinearity among the features.

I also selected Gradient Boosting and Random Forest because of their ability to handle non-linear relationships effectively. I wanted to compare their performance to observe the differences between these two models. Gradient Boosting is expected to be more computationally expensive due to its iterative nature, while Random Forest should train relatively quickly given the small number of features in this dataset.

Lastly, I chose a neural network (MLP Classifier) to experiment with a supervised learning model that was not covered in class.

```

'''

from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import GradientBoostingClassifier,
RandomForestClassifier
from sklearn.neural_network import MLPClassifier
from sklearn.metrics import classification_report, confusion_matrix,
ConfusionMatrixDisplay, accuracy_score
from sklearn.model_selection import train_test_split, GridSearchCV
import time

y_le, y_le_map = label_encode_data(y, {})
X_le_train, X_le_test, y_le_train, y_le_test = train_test_split(X_le,
y_le, test_size=0.25, random_state=28)

accuracy_scores = {}
def evaluate_performance(y_pred, title=None):
    if title != None:
        print(title, end='\n\n')

    disp = ConfusionMatrixDisplay(confusion_matrix(y_le_test, y_pred),
display_labels=['e', 'p'])
    disp.plot()
    plt.show()

    acc = round(accuracy_score(y_le_test, y_pred),7)
    print(f'Accuracy: {acc}', end='\n')
    if (title in training_times):
        accuracy_scores[title] = acc
        print(f'Training Time: {training_times[title]}', end='\n')

    print("\nClassification Report:")
    print(classification_report(y_le_test, y_pred))

def evaluate_features(model, title=None):
    if title != None:
        print(title, end='\n\n')

    feature_importances = pd.Series(model.feature_importances_,
index=X_le.columns)
    feature_importances =
feature_importances.sort_values(ascending=False)

    plt.figure(figsize=(10, 6))
    feature_importances.plot(kind='bar')
    plt.title("Feature Importances")
    plt.show()

```



```

def hyperparameter_tuning(model, params, X_train, y_train, cv=5):
    grid_search = GridSearchCV(
        model,
        params,
        cv=cv,
        scoring='accuracy',
        n_jobs=-1
    ).fit(X_train, y_train.iloc[:, 0])

    print(f'Best Parameters: {grid_search.best_params_}')
    return grid_search.best_estimator_

training_times = {
    # model_name: elapsed time in ms
}
def log_training_time(model_name, s, e):
    training_times[model_name] = round((e - s) * 1000)

#Logistic Regression

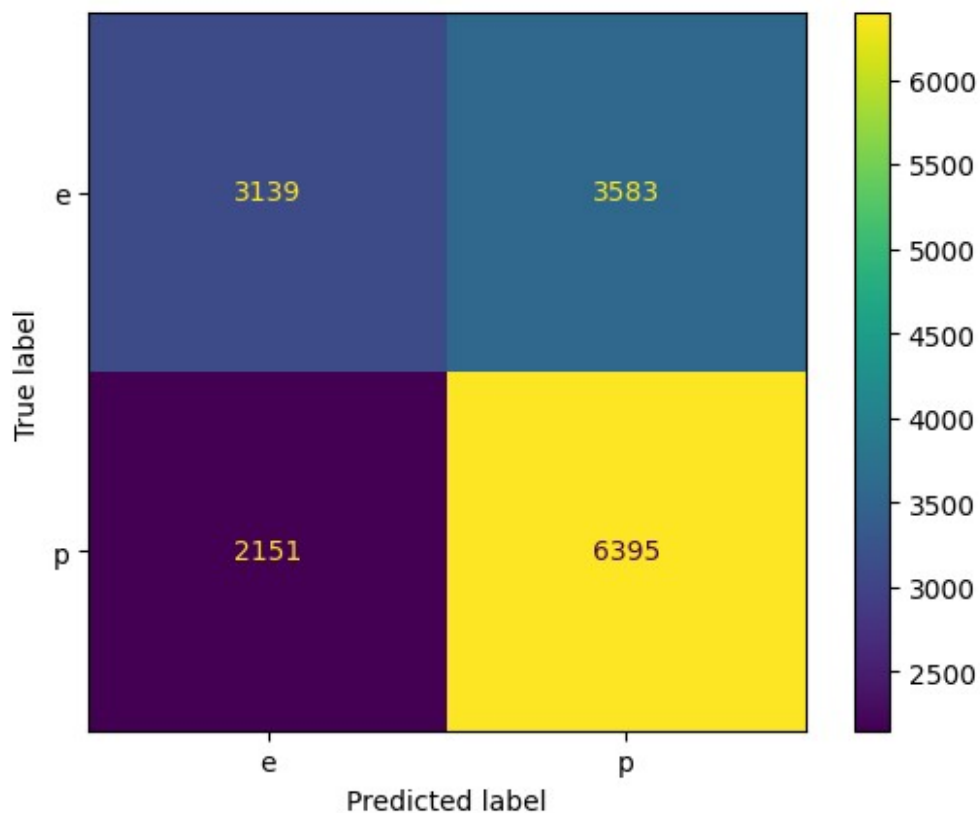
s = time.perf_counter()
lr_model = LogisticRegression(n_jobs=-1).fit(X_le_train,
y_le_train.iloc[:, 0])
log_training_time('Logistic Regression', s, time.perf_counter())

lr_pred = lr_model.predict(X_le_test)
evaluate_performance(lr_pred, 'Logistic Regression')

print('Coefficients:')
print(lr_model.coef_)

Logistic Regression

```



Accuracy: 0.6244433
Training Time: 1634

Classification Report:

	precision	recall	f1-score	support
0	0.59	0.47	0.52	6722
1	0.64	0.75	0.69	8546
accuracy			0.62	15268
macro avg	0.62	0.61	0.61	15268
weighted avg	0.62	0.62	0.62	15268

Coefficients:

```
[[ -0.04716796 -0.11097769  0.00660107  0.03805657  0.15151233 -
  0.03516807
  0.00681629 -0.03822812 -0.01789552 -0.07154598  0.32622107
  0.15393449
 -0.14328419 -0.11674118]]
```

```
lr_params = {
  'C': [0.1, 0.5, 1, 2, 5, 10],
  'class_weight': [None, {1: 2, 0: 1}],
  'solver': ['lbfgs', 'liblinear', 'newton-cg', 'newton-cholesky',
  'sag', 'saga'],
```

```

    'max_iter': [100, 250, 500],
    'n_jobs': [-1]
}
tuned_lr_model = hyperparameter_tuning(
    LogisticRegression(n_jobs=-1),
    lr_params,
    X_le_train,
    y_le_train
)

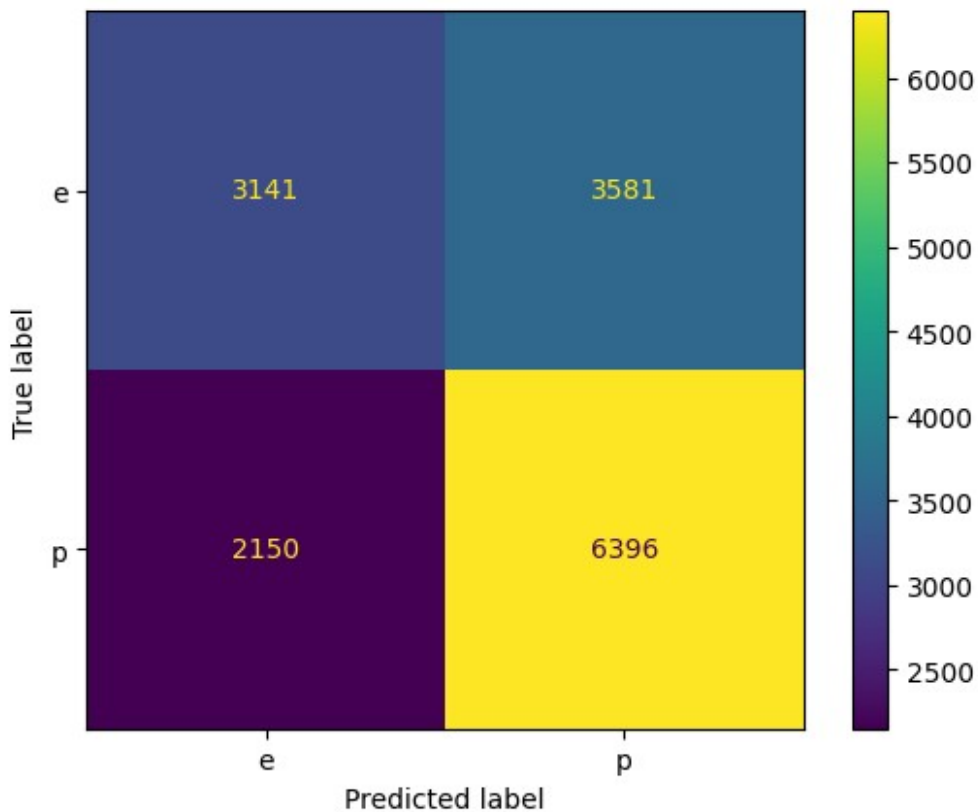
Best Parameters: {'C': 5, 'class_weight': None, 'max_iter': 100,
'n_jobs': -1, 'solver': 'lbfgs'}

tuned_lr_pred = tuned_lr_model.predict(X_le_test)
evaluate_performance(tuned_lr_pred, 'Hyperparameter Tuned Logistic
Regression')

print('Coefficients:')
print(lr_model.coef_)

Hyperparameter Tuned Logistic Regression

```



Accuracy: 0.6246398

Classification Report:

	precision	recall	f1-score	support
0	0.59	0.47	0.52	6722
1	0.64	0.75	0.69	8546
accuracy			0.62	15268
macro avg	0.62	0.61	0.61	15268
weighted avg	0.62	0.62	0.62	15268

Coefficients:

```
[[ -0.04716796 -0.11097769  0.00660107  0.03805657  0.15151233 -  
 0.03516807  
   0.00681629 -0.03822812 -0.01789552 -0.07154598  0.32622107  
 0.15393449  
 -0.14328419 -0.11674118]]
```

```
def one_hot_encode_data(data):  
    clone = data.copy()  
    oh_map = {}  
    for col in clone.select_dtypes(include=['object']):  
        oh_encoded = pd.get_dummies(clone[col], prefix=col)  
        oh_map[col] = oh_encoded.columns.tolist()  
        clone = clone.drop(columns=[col]).join(oh_encoded)  
    return clone, oh_map  
  
def oh_decode_data(data, oh_map):  
    clone = data.copy()  
    for original_col, oh_cols in oh_map.items():  
        oh_data = clone[oh_cols]  
        clone[original_col] =  
oh_data.idxmax(axis=1).str[len(original_col) + 1:] # Remove the  
prefix  
        clone = clone.drop(columns=oh_cols)  
    return clone
```

```
X_oh, X_oh_map = one_hot_encode_data(X)  
X_oh_train, X_oh_test, y_le_train, y_le_test = train_test_split(X_oh,  
y_le, test_size=0.25, random_state=28)
```

```
print(X_oh.head())
```

	cap-diameter	stem-height	stem-width	cap-shape_b	cap-shape_c	\
0	15.26	16.95	17.09	False	False	
1	16.60	17.99	18.19	False	False	
2	14.07	17.80	17.74	False	False	
3	14.17	15.77	15.98	False	False	
4	14.64	16.53	17.20	False	False	

	cap-shape_f	cap-shape_o	cap-shape_p	cap-shape_s	cap-shape_x
0	False	False	False	False	False
1	False	False	False	False	False
2	False	False	False	False	False
3	True	False	False	False	False
4	False	False	False	False	False

	habitat_h	habitat_l	habitat_m	habitat_p	habitat_u	habitat_w
0	False	False	False	False	False	False
1	False	False	False	False	False	False
2	False	False	False	False	False	False
3	False	False	False	False	False	False
4	False	False	False	False	False	False

	season_s	season_u	season_w
0	False	False	True
1	False	True	False
2	False	False	True
3	False	False	True
4	False	False	True

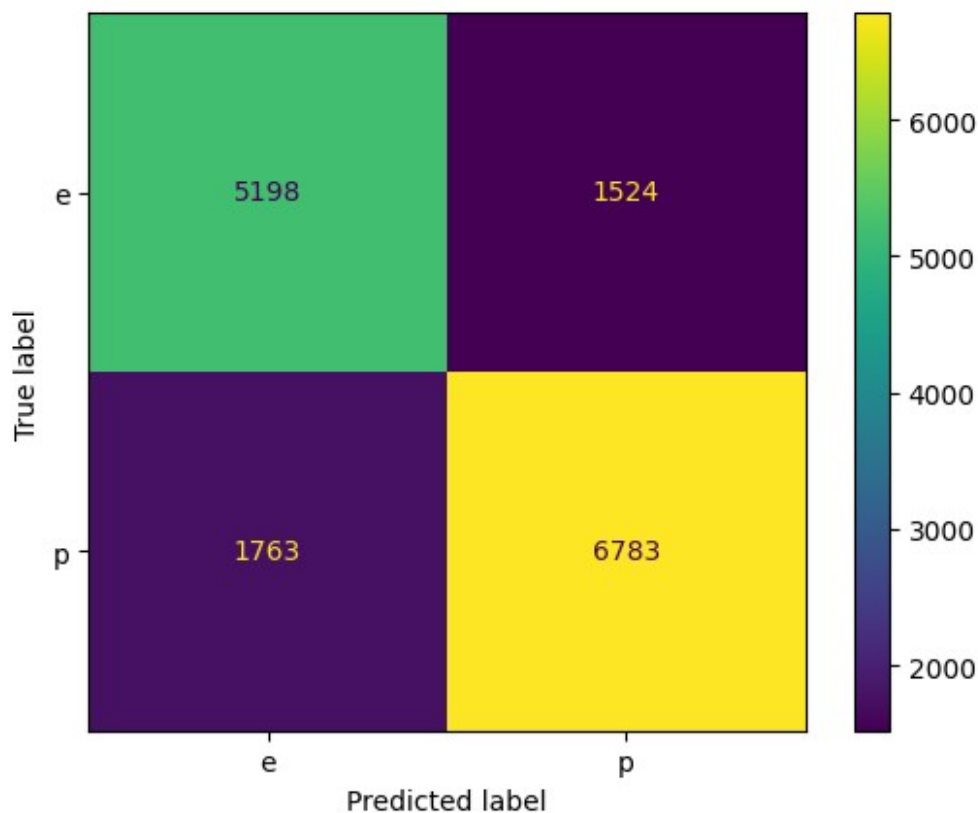
[5 rows x 92 columns]

```
s = time.perf_counter()
lr_model = LogisticRegression(n_jobs=-1).fit(X_oh_train,
y_le_train.iloc[:, 0])
log_training_time('Logistic Regression (One-Hot)', s,
time.perf_counter())

lr_pred = lr_model.predict(X_oh_test)
evaluate_performance(lr_pred, 'Logistic Regression (One-Hot)')

print('Coefficients:')
print(lr_model.coef_)

Logistic Regression (One-Hot)
```



Accuracy: 0.7847131

Training Time: 884

Classification Report:

	precision	recall	f1-score	support
0	0.75	0.77	0.76	6722
1	0.82	0.79	0.80	8546
accuracy			0.78	15268
macro avg	0.78	0.78	0.78	15268
weighted avg	0.79	0.78	0.79	15268

Coefficients:

```

[[-0.05541257  0.10342152 -0.00478196  1.10832176 -0.26035395 -
 0.39931733
  0.92464971 -0.29396218 -0.76132402 -0.34600821 -0.15917259
 0.01317117
  0.7765774  -0.71520952 -0.9459746   1.51887443  3.12490924 -
 1.50653604
 -0.87449425 -0.04587881 -0.64723163 -0.56702903 -1.52046828
 1.03537539
 -0.395653    0.55215264 -1.53578626 -0.62082615  0.68651553
 0.13585475]

```

```

1.89031149 0.42652953 -0.28953125 -0.39246861 0.03396843 -
0.06196265
0.30403035 0.40740371 0.99547299 -0.48721207 0.06458342 -
2.22051891
0.37093656 0.53730973 -1.84648657 1.12022589 0.06458342 -
0.19493094
0.04525103 0.39440153 -0.09917269 -0.11557588 -0.33547314
0.23023708
-0.09329621 0.80224225 -0.93886502 0.43531704 2.70346346 -
1.7596478
1.93791447 -1.11989062 -0.12850012 -1.43715721 1.47208559
0.25702635
0.14562628 -1.50569639 -0.08967026 -1.08319825 1.05520403 -
1.69514028
0.15515206 1.3150343 -0.33383451 -0.22384495 -3.47717025
1.12876379
-0.82492365 3.92796925 0.18297732 0.82274602 0.21037316 -
0.42634057
0.0675442 1.55873812 -0.63849128 -1.80554118 0.61522039 -
0.80136569
0.75841538 -0.6002643 ]]

```

#Gradient Boosting

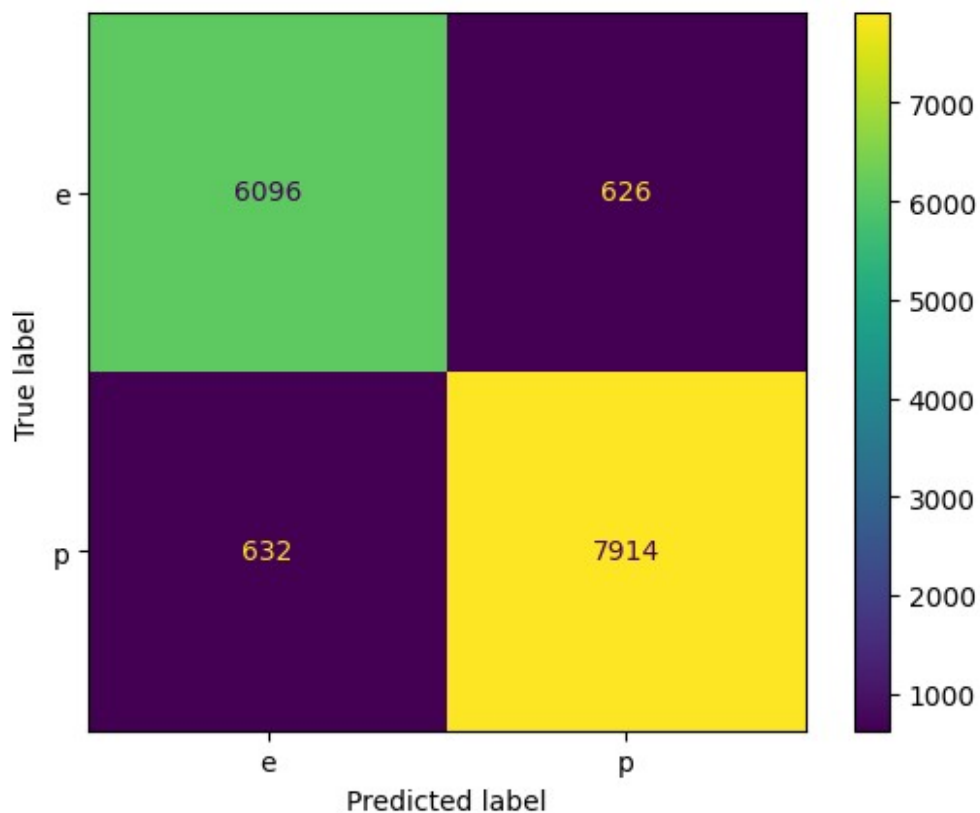
```

s = time.perf_counter()
gb_model = GradientBoostingClassifier().fit(X_le_train,
y_le_train.iloc[:, 0])
log_training_time('Gradient Boosting', s, time.perf_counter())

gb_pred = gb_model.predict(X_le_test)
evaluate_performance(gb_pred, 'Gradient Boosting')
evaluate_features(gb_model)

Gradient Boosting

```

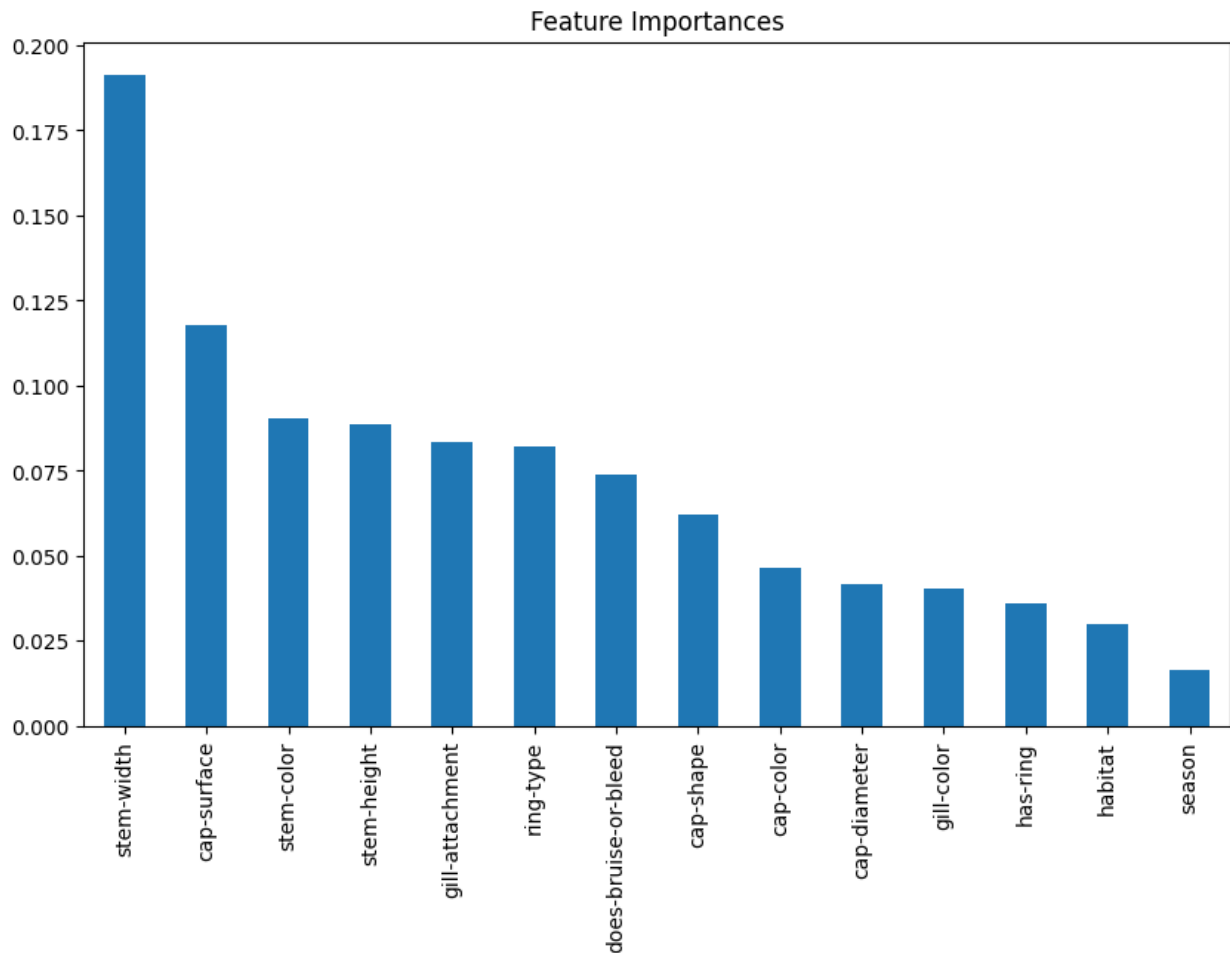


Accuracy: 0.9176054

Training Time: 4724

Classification Report:

	precision	recall	f1-score	support
0	0.91	0.91	0.91	6722
1	0.93	0.93	0.93	8546
accuracy			0.92	15268
macro avg	0.92	0.92	0.92	15268
weighted avg	0.92	0.92	0.92	15268



```
gb_params = {
    'loss': ['log_loss', 'exponential'],
    'learning_rate': [0.05, 0.1, 0.2],
    # 'n_estimators': [50, 100, 200],
    'n_estimators': [200, 300],
    # 'max_depth': [3, 5, 7],
    'max_depth': [7, 10],
    # 'min_samples_leaf': [1, 2],
    # 'max_features': ['sqrt', None],
    'max_features': ['sqrt', 'log2'],
}

X_le_train_tune, X_le_test_tune, y_le_train_tune, y_le_test_tune =
train_test_split(X_le, y_le, test_size=0.99)

hyperparameter_tuning(
    GradientBoostingClassifier(),
    gb_params,
    X_le_train_tune,
```

```

    y_le_train_tune
)

Best Parameters: {'learning_rate': 0.2, 'loss': 'log_loss',
'max_depth': 7, 'max_features': 'log2', 'n_estimators': 300}

GradientBoostingClassifier(learning_rate=0.2, max_depth=7,
max_features='log2',
                             n_estimators=300)

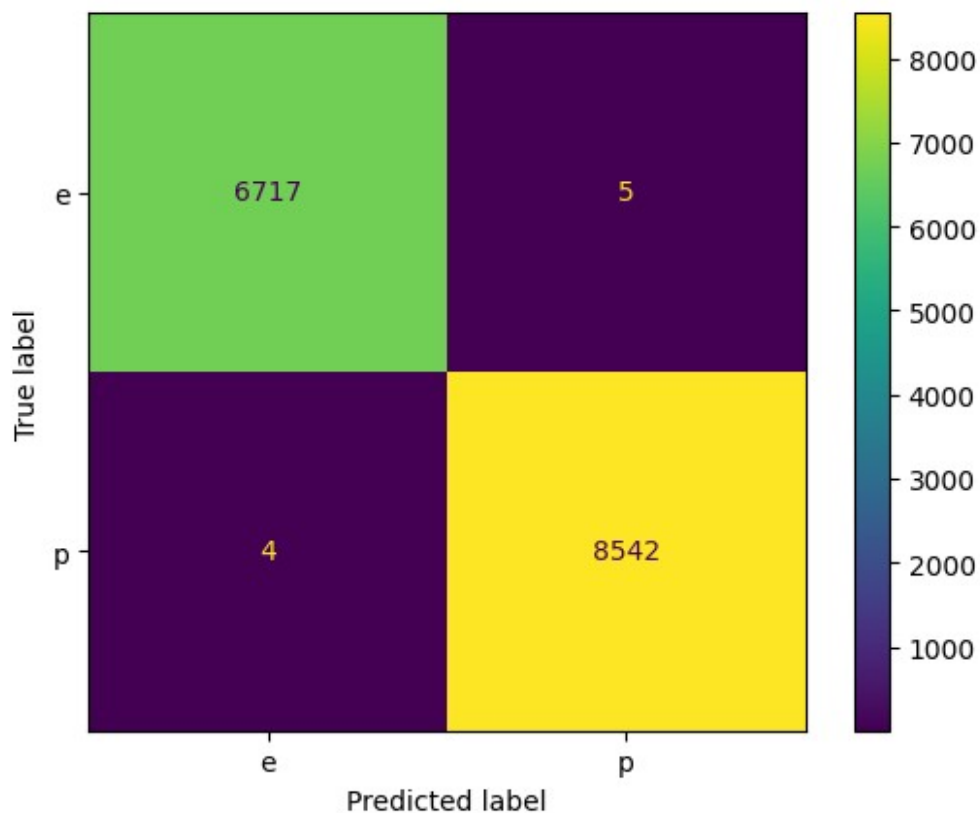
...
Best Parameters: {
    'learning_rate': 0.1,
    'loss': 'exponential',
    'max_depth': 7,
    'max_features': 'sqrt',
    'min_samples_leaf': 1,
    'n_estimators': 200
}
...

s = time.perf_counter()
tuned_gb_model_1 = GradientBoostingClassifier(
    learning_rate=0.1,
    loss='exponential',
    max_depth=7,
    max_features='sqrt',
    min_samples_leaf=1,
    n_estimators=200
).fit(X_le_train, y_le_train.iloc[:, 0])
log_training_time('Gradient Boosting (Hyperparameter Tuned)', s,
time.perf_counter())

tuned_gb_pred = tuned_gb_model_1.predict(X_le_test)
evaluate_performance(tuned_gb_pred, 'Gradient Boosting (Hyperparameter
Tuned)')
evaluate_features(tuned_gb_model_1)

Gradient Boosting (Hyperparameter Tuned)

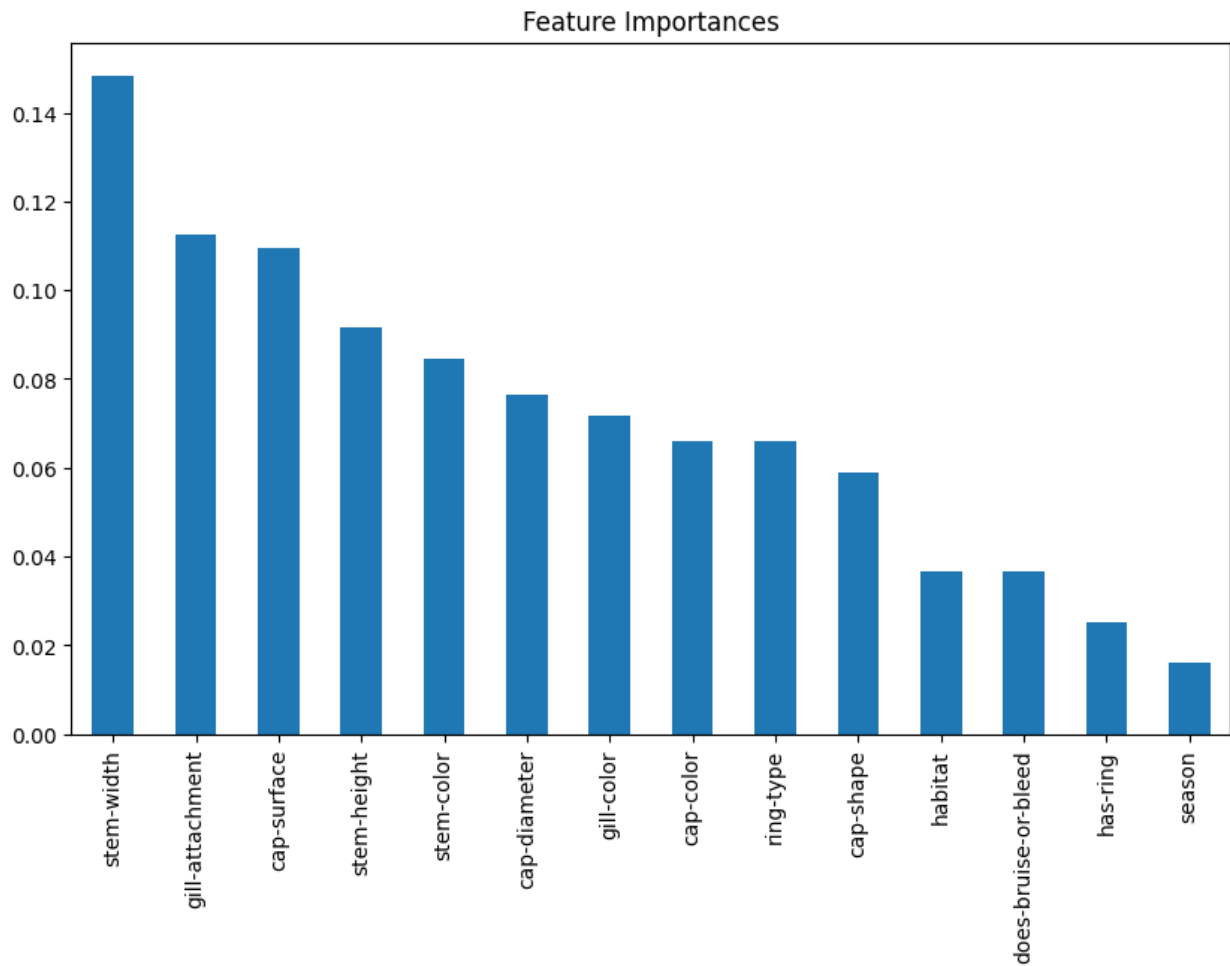
```



Accuracy: 0.9994105
 Training Time: 12281

Classification Report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	6722
1	1.00	1.00	1.00	8546
accuracy			1.00	15268
macro avg	1.00	1.00	1.00	15268
weighted avg	1.00	1.00	1.00	15268

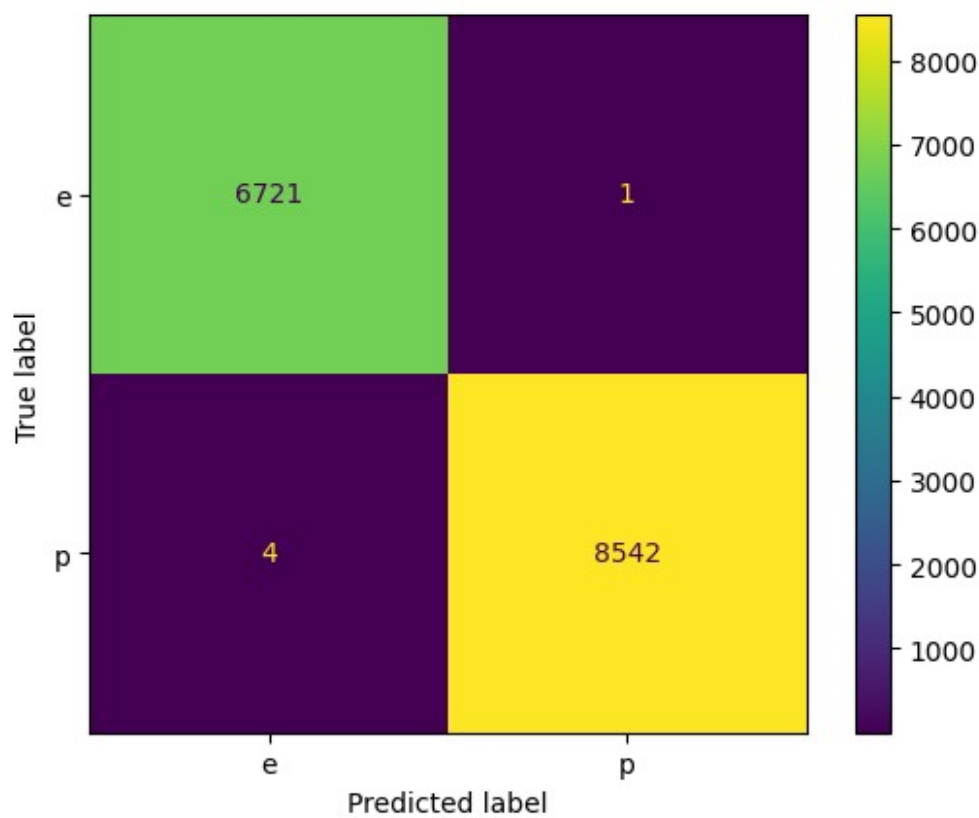


```
'''
Best Parameters: {
    'learning_rate': 0.2,
    'loss': 'log_loss',
    'max_depth': 7,
    'max_features': 'sqrt',
    'min_samples_leaf': 1,
    'n_estimators': 200
}
'''

tuned_gb_model_2 = GradientBoostingClassifier(
    learning_rate=0.2,
    loss='log_loss',
    max_depth=7,
    max_features='sqrt',
    min_samples_leaf=1,
    n_estimators=200
).fit(X_le_train, y_le_train.iloc[:, 0])
tuned_gb_pred = tuned_gb_model_2.predict(X_le_test)
```

```
evaluate_performance(tuned_gb_pred, 'Gradient Boosting (Hyperparameter Tuned) (2)')
evaluate_features(tuned_gb_model_2)
```

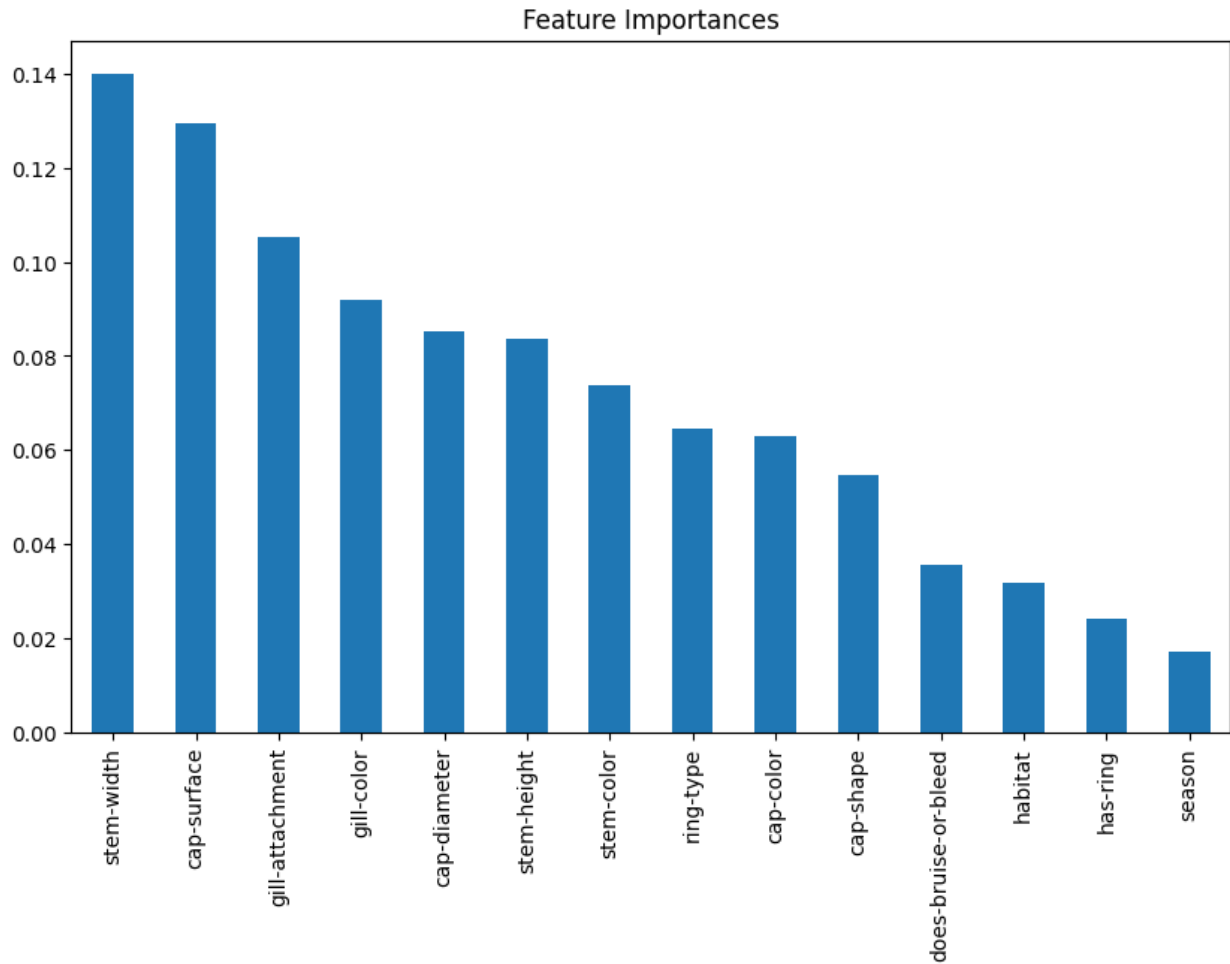
Hyperparameter Tuned Gradient Boosting Classifier (2)



Accuracy: 0.9996725176840451

Classification Report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	6722
1	1.00	1.00	1.00	8546
accuracy			1.00	15268
macro avg	1.00	1.00	1.00	15268
weighted avg	1.00	1.00	1.00	15268



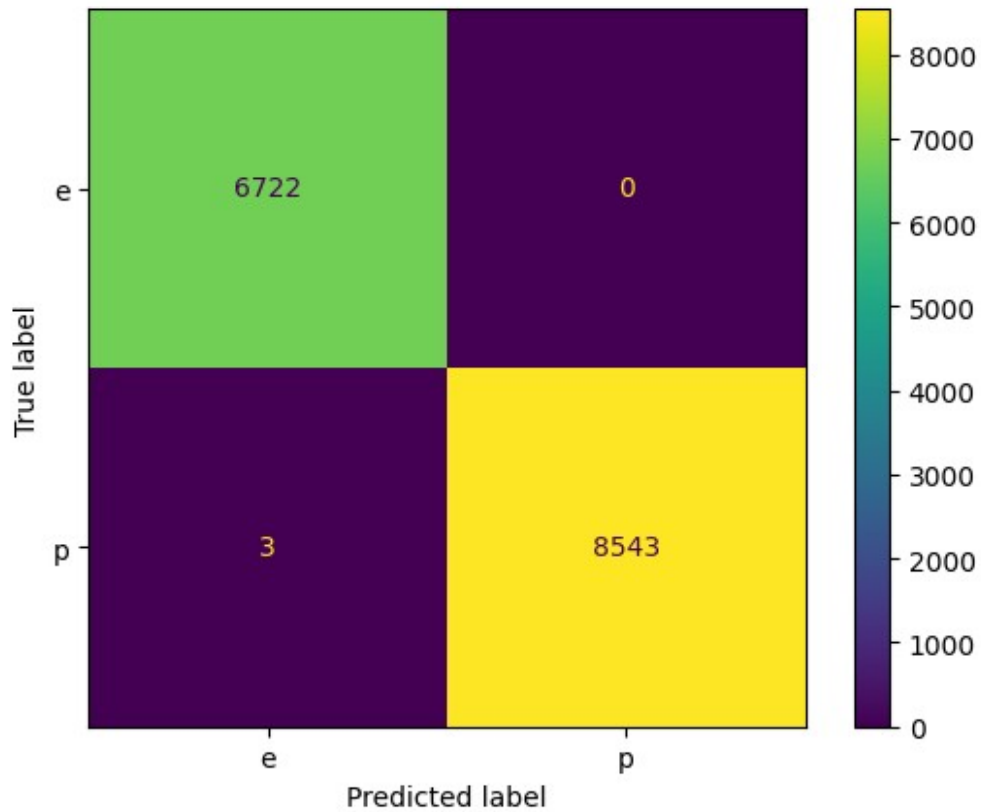
```
...
Best Parameters: {
    'learning_rate': 0.1,
    'loss': 'exponential',
    'max_depth': 10,
    'max_features': 'log2',
    'n_estimators': 300
}
...

tuned_gb_model_3 = GradientBoostingClassifier(
    learning_rate=0.1,
    loss='exponential',
    max_depth=10,
    max_features='log2',
    min_samples_leaf=1,
    n_estimators=300
).fit(X_le_train, y_le_train.iloc[:, 0])
tuned_gb_pred = tuned_gb_model_3.predict(X_le_test)
evaluate_performance(tuned_gb_pred, 'Gradient Boosting (Hyperparameter
```

```
Tuned) (3)')
```

```
evaluate_features(tuned_gb_model_3)
```

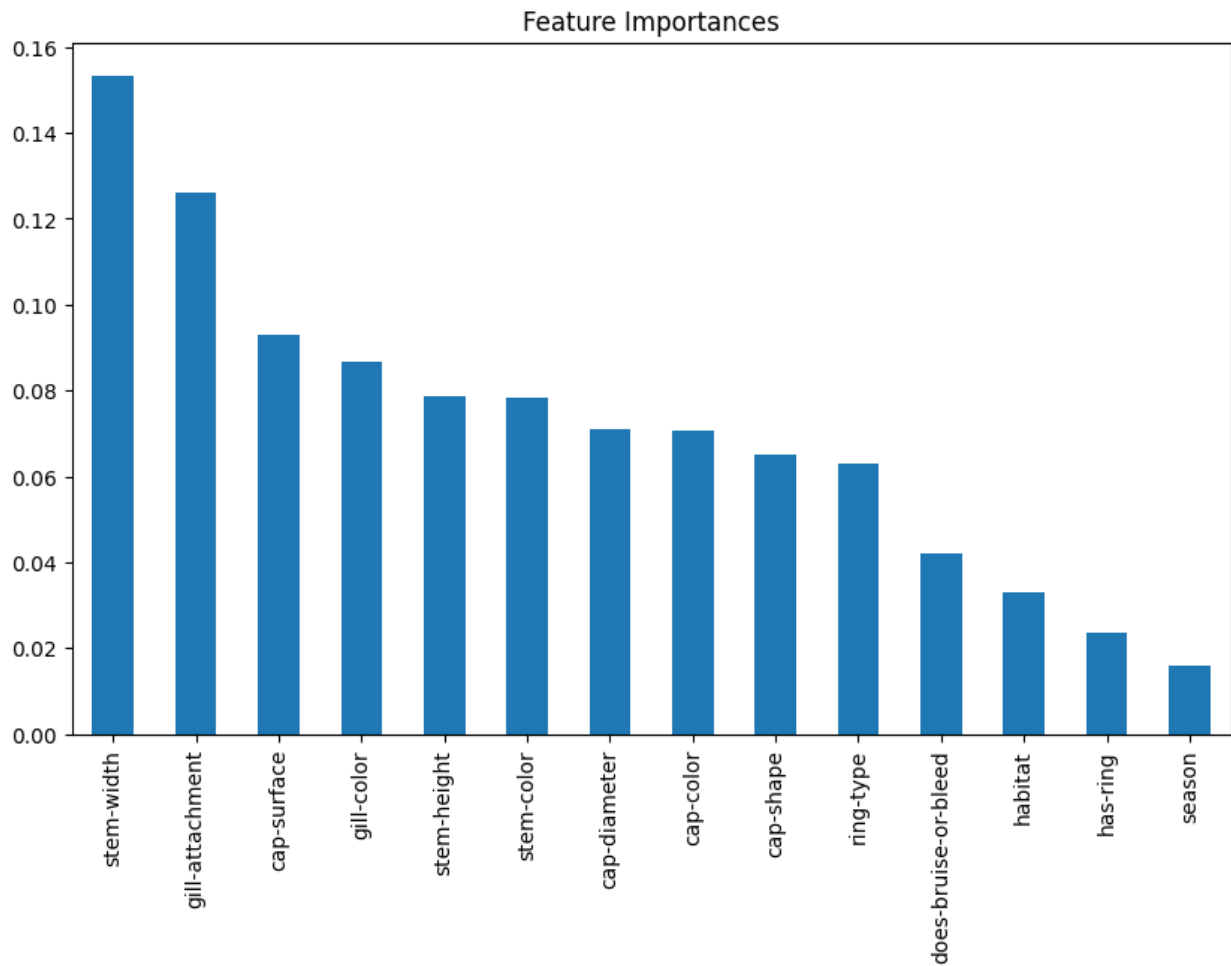
Hyperparameter Tuned Gradient Boosting Classifier (3)



Accuracy: 0.999803510610427

Classification Report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	6722
1	1.00	1.00	1.00	8546
accuracy			1.00	15268
macro avg	1.00	1.00	1.00	15268
weighted avg	1.00	1.00	1.00	15268

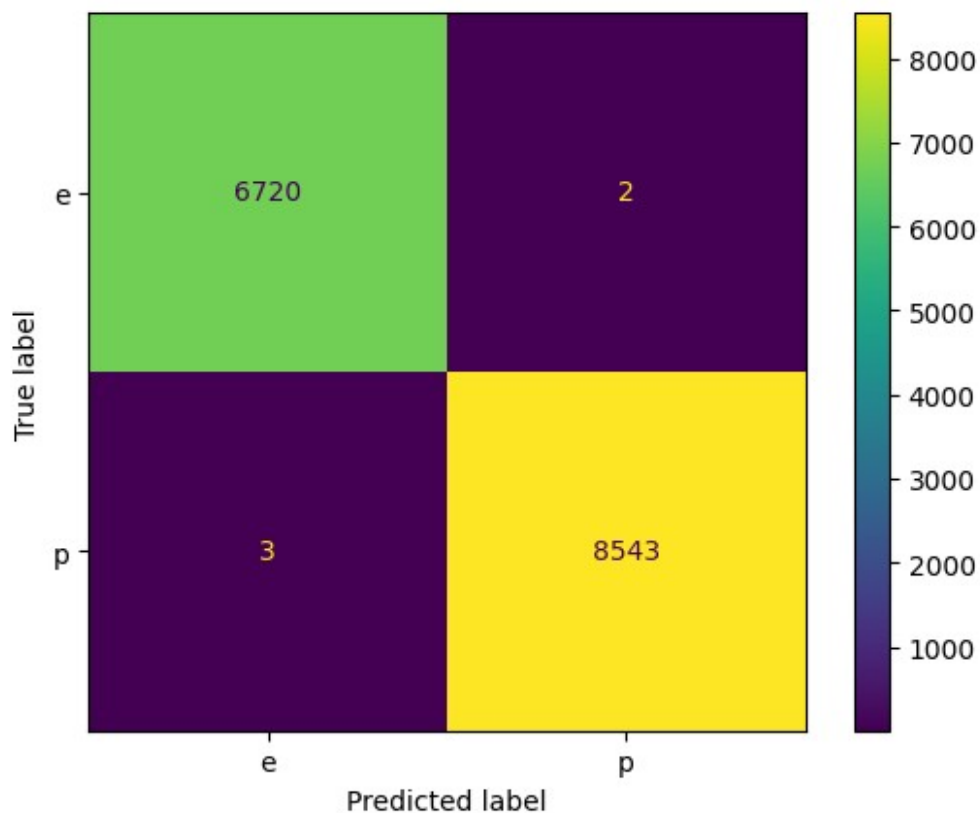


#Random Forest

```
s = time.perf_counter()
rf_model = RandomForestClassifier(n_jobs=-1).fit(X_le_train,
y_le_train.iloc[:, 0])
log_training_time('Random Forest', s, time.perf_counter())

rf_pred = rf_model.predict(X_le_test)
evaluate_performance(rf_pred, 'Random Forest')
evaluate_features(rf_model)
```

Random Forest

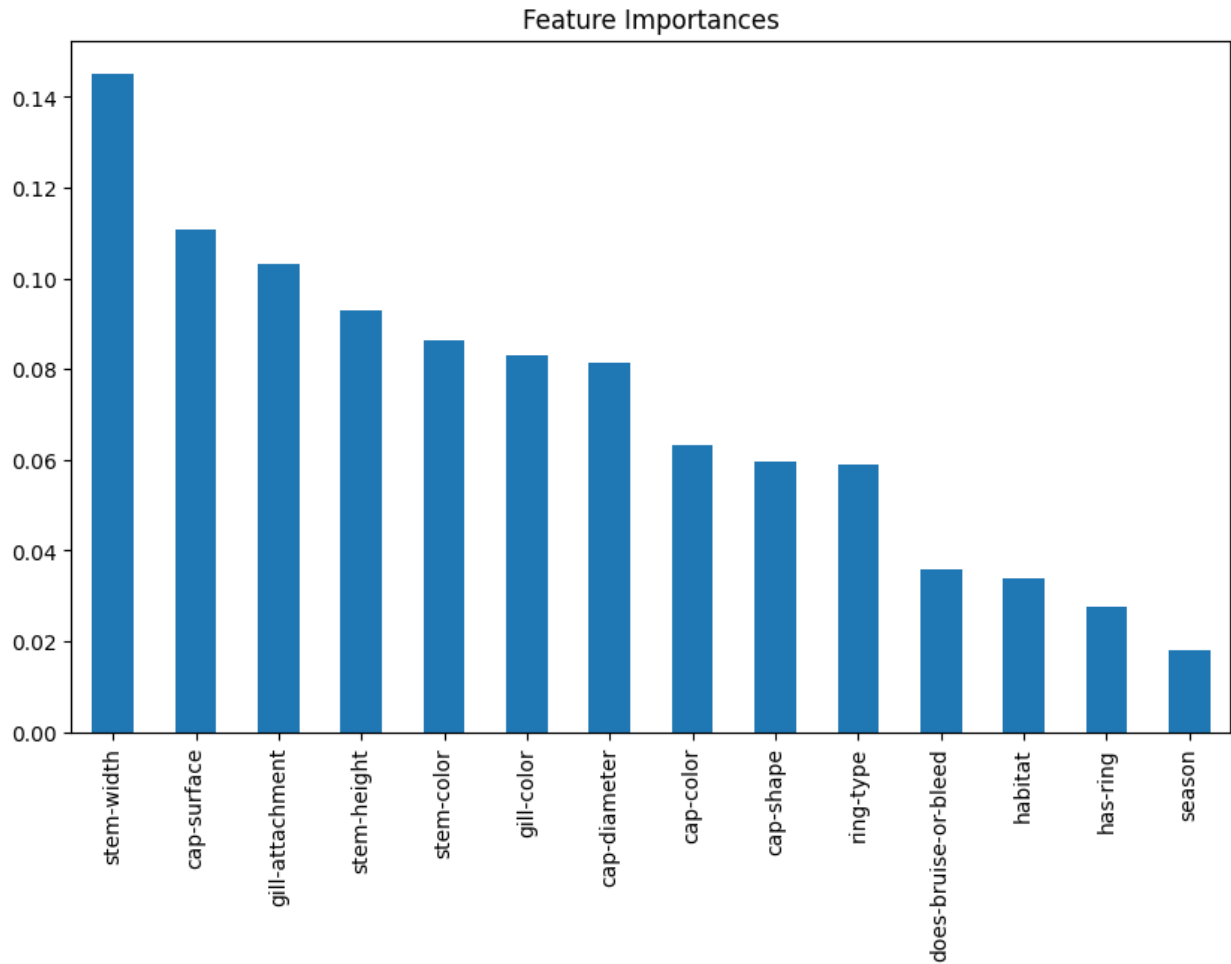


Accuracy: 0.9996725

Training Time: 778

Classification Report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	6722
1	1.00	1.00	1.00	8546
accuracy			1.00	15268
macro avg	1.00	1.00	1.00	15268
weighted avg	1.00	1.00	1.00	15268

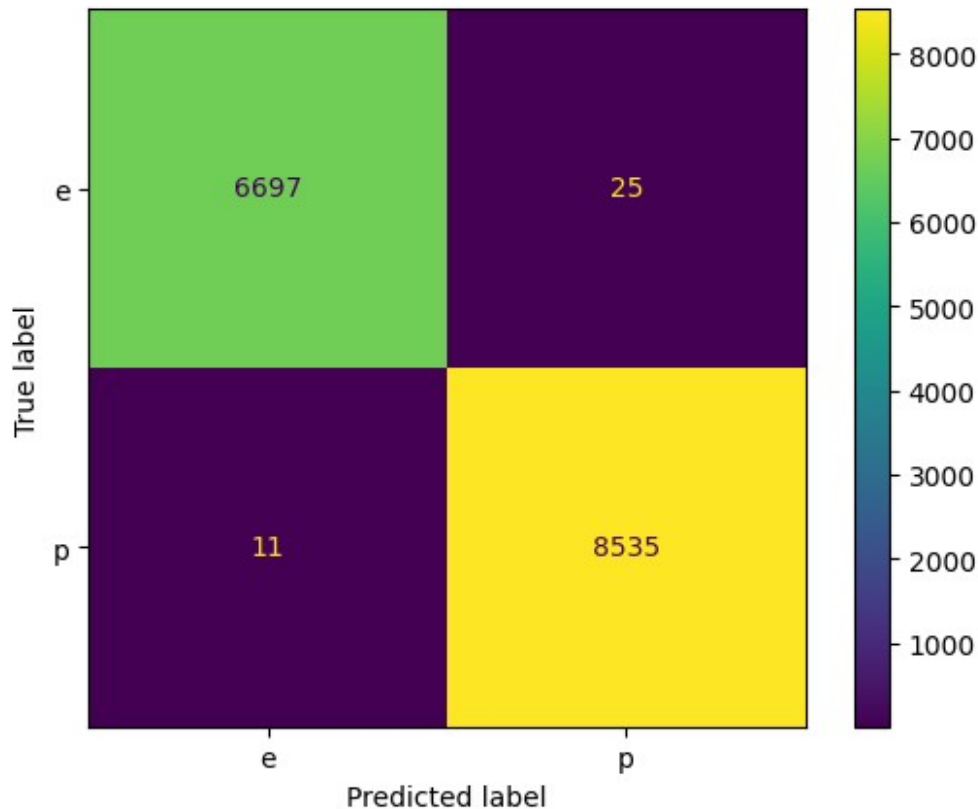


```
#MLPClassifier (Neural Network)
# (not covered in class)

s = time.perf_counter()
mlp_model = MLPClassifier().fit(X_le_train, y_le_train.iloc[:, 0])
log_training_time('MLP Classifier', s, time.perf_counter())

mlp_pred = mlp_model.predict(X_le_test)
evaluate_performance(mlp_pred, 'MLP Classifier')

MLP Classifier
```



Accuracy: 0.9976421
Training Time: 23316

Classification Report:

	precision	recall	f1-score	support
0	1.00	1.00	1.00	6722
1	1.00	1.00	1.00	8546
accuracy			1.00	15268
macro avg	1.00	1.00	1.00	15268
weighted avg	1.00	1.00	1.00	15268

...

Results and Analysis

For the task of classifying mushrooms as edible versus poisonous, the consequences of labeling a poisonous mushroom as edible are potentially deadly. Therefore, a high precision score is crucial for minimizing false positives, i.e., labeling a poisonous mushroom as edible. Mislabeling edible mushrooms as poisonous is not nearly as consequential. However, for the sake of developing a good model, I aimed to achieve a high recall score as well, and ultimately a high F1-score since it is derived from both precision and recall.

Generally, the models performed with such high precision, recall, and F1-scores that there wasn't enough granularity to distinguish between them meaningfully. For my model comparisons, I plotted two graphs: one showing the accuracy scores and the other illustrating the training times of the models.

Three models attained near-perfect accuracy scores: the hyperparameter-tuned gradient boosting classifier, the random forest classifier, and the MLP classifier. However, the random forest classifier was exceptionally faster to train and did not require any advanced training techniques to achieve such a high accuracy score.

```
...
None #Disable cell output

models = list(training_times.keys())
times = list(training_times.values())

plt.figure(figsize=(10, 6))
plt.bar(models, times, color='skyblue')
plt.xlabel("Models")
plt.ylabel("Training Time (ms)")
plt.title("Model Training Times")
plt.xticks(rotation=45, ha="right")
plt.show()

models = list(accuracy_scores.keys())
times = list(accuracy_scores.values())

plt.figure(figsize=(10, 6))
plt.bar(models, times, color='skyblue')
plt.xlabel("Models")
plt.ylabel("Accuracy Score")
plt.title("Model Accuracy Scores")
plt.xticks(rotation=45, ha="right")
plt.show()
```

