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Mushroom Classification

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Abstract: *Mushroom classification is an important task for distinguishing between edible and poisonous species, which has critical implications for public health, food safety, and ecology. In this study, we present a machine learning-based approach to classify mushrooms based on non-image data, utilizing a dataset with various physical and chemical characteristics of mushrooms, such as cap shape, color, gill size, and odor. Unlike image- based classification methods, our approach leverages structured tabular data to predict whether a mushroom is edible or poisonous. We experimented with several machine learning algorithms, including Decision Trees, Random Forests, Support Vector Machines (SVM), and k-Nearest Neighbors (k-NN), comparing their performance in terms of accuracy, precision, and recall. Feature engineering and selection were employed to identify the most predictive attributes, and hyperparameter tuning was performed to optimize model performance. Cross-validation was used to ensure robustness and generalization of the results. The findings demonstrate that tabular data can be a reliable source for mushroom classification, with models achieving high accuracy without the need for image data. The Random Forest classifier, in particular, yielded the best results, highlighting the effectiveness of ensemble methods in handling categorical and structured data. This study underscores the potential of using non-image data for accurate and efficient mushroom classification, providing an accessible solution for applications where image data may not be available or practical.*

Keywords: Machine Learning , NON - Image Data, Decision Tree, Random Forest, Support Vector Machine, K Nearest Neighbours, Feature Selection

I. INTRODUCTION

Mushrooms are a diverse group of fungi, with thousands of species that vary widely in appearance, habitat, and edibility. Among them, some are edible and highly nutritious, while others contain toxic compounds that can cause severe poisoning or even death if consumed. Identifying whether a mushroom is safe to eat is challenging for the untrained eye, as many poisonous species closely resemble edible ones. Accurate classification of mushrooms is essential for public health and safety, as well as for ecological studies and culinary applications.

Traditional methods of mushroom classification have relied heavily on expert knowledge, involving detailed examination of morphological characteristics such as cap shape, color, gill structure, and odor. With recent advances in machine learning, automated classification systems are now being developed to assist in identifying mushroom species more accurately and efficiently. While image-based classification has shown promise, it requires high-quality images and often complex neural network models, which may not always be practical in field conditions where only basic information about mushroom features is available.

In this study, we focus on mushroom classification using non-image data. By leveraging structured tabular data that captures various physical and chemical attributes of mushrooms, we aim to develop a machine learning model that can accurately classify mushrooms as edible or poisonous. We employ several popular machine learning algorithms, including Decision Trees, Random Forests, Support Vector Machines (SVM), and k- Nearest Neighbors (k-NN), to determine the most effective approach for this classification task.

Through feature engineering and selection, we identify key attributes that contribute to the model's predictive power. We also perform hyperparameter tuning and cross-validation to enhance model robustness and ensure reliable generalization across different data samples. Our goal is to demonstrate the effectiveness of using non- image, tabular data for mushroom classification and to provide an alternative solution for applications where image data is unavailable or impractical.

This study not only highlights the feasibility of classifying mushrooms based on structured data but also underscores the potential of machine learning to assist in important food safety decisions, supporting both experts and non-experts in identifying edible mushrooms safely.

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Aim Of The Study

The aim of this study is to develop and evaluate a machine learning-based approach for classifying mushrooms as edible or poisonous using non-image, structured tabular data. Specifically, the study seeks to:

- Identify the key physical and chemical features that contribute to accurate mushroom classification.
- Assess the effectiveness of various machine learning algorithms, including Decision Trees, Random Forests, Support Vector Machines (SVM), and k-Nearest Neighbors (k-NN), in distinguishing between edible and poisonous mushrooms based on non-image data.
- Optimize model performance through feature selection, hyperparameter tuning, and cross-validation to ensure robust and reliable classification.
- Demonstrate the feasibility and accuracy of using non-image data for mushroom classification, providing an alternative to image-based methods that is practical for field applications and accessible to non-experts.

This study ultimately aims to support food safety and public health by developing a tool that can assist in the rapid and accurate identification of potentially harmful mushrooms

II. LITERATURE REVIEW

Mushroom classification is an important field due to the health risks associated with consuming wild mushrooms, as some species contain toxic compounds that can cause serious harm. Traditional identification relies on expert analysis of morphological traits like cap shape, color, and odor, but this process is time- consuming and requires specialized knowledge. With advancements in machine learning, researchers have explored automated methods to classify mushrooms based on their physical and chemical characteristics, especially through non-image, structured data. This approach provides an accessible, efficient alternative to manual identification, especially for fieldwork and public safety applications.

Non-Image-Based Mushroom Classification

To bypass the limitations of image-based classification, researchers have used structured datasets capturing various attributes of mushrooms, such as shape, color, gill size, and odor. A widely used dataset for this purpose is the UCI Mushroom Dataset, which includes physical characteristics of mushrooms and their edibility status. Chen et al. (2018) demonstrated that machine learning algorithms trained on structured data from this dataset can effectively distinguish between edible and poisonous mushrooms, achieving high accuracy rates without the need for image data. Structured data approaches are particularly advantageous for applications where capturing high-quality images is impractical, making non-image-based methods highly relevant for fieldwork and quick, portable classification solutions.

Machine Learning Algorithms for Mushroom Classification

Several machine learning algorithms have shown promise for classifying mushrooms using non-image data. Decision Trees and Random Forests are popular choices due to their ability to handle categorical data and their interpretability, making them well-suited for the structured data in mushroom classification. For example, Manogaran et al. (2019) applied Random Forests to structured mushroom data, achieving robust classification accuracy and reliable generalization across mushroom species. Support Vector Machines (SVM) and k-Nearest Neighbors (k-NN) have also been effective in this task, with ensemble methods like Random Forests and Gradient Boosting standing out due to their ability to reduce variance and improve predictive performance.

Feature Engineering and Selection

Feature engineering and selection play crucial roles in improving model accuracy and computational efficiency in non-image-based classification tasks. Studies have shown that not all mushroom attributes contribute equally to model performance. For instance, attributes like odor, gill color, and cap shape often hold significant predictive power, while others may be less impactful. Yadav et al. (2020) emphasized the importance of carefully selecting relevant features to enhance accuracy and reduce computational cost. Effective feature engineering not only improves model performance but also aids in building lightweight, efficient classifiers suitable for real-time classification in resource-constrained environments

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III. SYSTEM ARCHITECTURE AND DESIGN

1. Architecture Overview

The system consists of three main components:

- Data Preprocessing Module: Handles data cleaning, transformation, and feature selection.
- Model Training and Evaluation Module: Includes model selection, training, and evaluation with cross-validation.
- Deployment and Inference Module: Deploys the model to a user interface or API for real-time mushroom classification.

Each module communicates with others in a sequential workflow, where data flows from preprocessing to model training, and then to deployment for user-accessible predictions.

2. Components and Design

A. Data Preprocessing Module

Data Collection and Storage:

- The non-image, tabular data is sourced from a structured dataset, such as the UCI Mushroom Dataset.
- Data is stored in a secure, easily accessible format (e.g., CSV files or a database) for use by the preprocessing module.

Data Cleaning:

- Handles missing values, outliers, and inconsistent formatting. Techniques like imputing missing values or removing irrelevant data points are employed.

Feature Engineering:

- Adds or modifies features to improve model learning. For example, categorical encoding (such as one- hot encoding) converts mushroom attributes (e.g., color or odor) into numeric representations usable by machine learning algorithms.

Feature Selection:

- Uses statistical methods or algorithms (e.g., Recursive Feature Elimination or correlation analysis) to identify the most predictive features, reducing model complexity and improving performance.

B. Model Training and Evaluation Module

Algorithm Selection:

- Multiple machine learning algorithms (e.g., Decision Trees, Random Forests, Support Vector Machines, k-Nearest Neighbors) are selected and implemented to identify the most effective model for the mushroom classification task.

Model Training:

- The system splits the data into training and validation sets to prevent overfitting and ensure the model generalizes well to unseen data.
- Each model is trained using cross-validation to assess its reliability across different data partitions.

Hyperparameter Tuning:

- Optimizes model parameters using techniques like grid search or random search, maximizing performance metrics such as accuracy, precision, and recall.

Model Evaluation:

- After training, models are evaluated based on metrics including accuracy, F1-score, precision, and recall.
- The model with the highest evaluation scores is selected for deployment.

C. Deployment and Inference Module

Model Serialization and Deployment:

- The trained model is serialized (e.g., using joblib or pickle) and deployed to an accessible platform, such as a REST API, web interface, or mobile app.

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- Users can input mushroom characteristics (e.g., cap color, gill size) to receive a classification result indicating if the mushroom is likely edible or poisonous

Real-Time Inference:

- The deployed model accepts user input, processes it through the preprocessing pipeline, and provides a classification result in real time.
- The interface can be designed with input fields that correspond to mushroom attributes, enabling easy data entry.

Feedback Loop (Optional):

- If deployed in an iterative setting, a feedback loop could allow users to validate the model's predictions and submit corrections, which are then used to update and retrain the model periodically.

3. System Design Diagrams

A. Data Flow Diagram

- Data Input → Data Preprocessing → Model Training → Model Evaluation → Best Model Selection → Deployment
- User Input → Preprocessing → Model Inference → Classification Output (Edible/Poisonous)

4. Technological Stack

- Programming Language: Python (for data processing and machine learning) Machine Learning Libraries: Scikit-learn, Pandas, NumPy
- Deployment: Flask or FastAPI (for creating REST API), Streamlit or Dash (for a simple web interface) Data Storage: CSV, SQLite, or any compatible database management system

5. Performance Considerations and Optimization

- Latency: Ensures low latency in predictions, optimizing the preprocessing and model inference pipelines for real-time use.
- Scalability: Designed to allow the addition of new data sources or more features to expand functionality. Model Maintenance: Periodic retraining with updated data to adapt to potential new features or variations in mushroom types.

3.1 Sources of Data Collection


```
class,cap-shape,cap-surface,cap-color,bruises,odor,gill-attachment,gill-spacing,gill-size,gill-color,stalk-shape,stalk-root,stalk-surface-above-ring,stalk-surface-below
p,x,s,n,t,p,f,c,n,k,e,e,s,s,w,w,p,w,o,p,k,s,u
e,x,s,y,t,a,f,c,b,k,e,c,s,s,w,w,p,w,o,p,n,n,g
e,b,s,w,t,l,f,c,b,n,e,c,s,s,w,w,p,w,o,p,n,n,m
p,x,y,w,t,p,f,c,n,n,e,e,s,s,w,w,p,w,o,p,k,s,u
e,x,s,g,f,n,f,w,b,k,t,e,s,s,w,w,p,w,o,e,n,a,g
e,x,y,y,t,a,f,c,b,n,e,c,s,s,w,w,p,w,o,p,k,n,g
e,b,s,w,t,a,f,c,b,g,e,c,s,s,w,w,p,w,o,p,k,n,m
e,b,y,w,t,l,f,c,b,n,e,c,s,s,w,w,p,w,o,p,n,s,m
p,x,y,w,t,p,f,c,n,p,e,e,s,s,w,w,p,w,o,p,k,v,g
e,b,s,y,t,a,f,c,b,g,e,c,s,s,w,w,p,w,o,p,k,s,m
e,x,y,y,t,l,f,c,b,g,e,c,s,s,w,w,p,w,o,p,n,n,g
e,x,y,y,t,a,f,c,b,n,e,c,s,s,w,w,p,w,o,p,k,s,m
e,b,s,y,t,a,f,c,b,w,e,c,s,s,w,w,p,w,o,p,n,s,g
p,x,y,w,t,p,f,c,n,k,e,e,s,s,w,w,p,w,o,p,n,v,u
e,x,f,n,f,n,f,w,b,n,t,e,s,f,w,w,p,w,o,e,k,a,g
e,s,f,g,f,n,f,c,n,k,e,e,s,s,w,w,p,w,o,p,n,y,u
e,f,f,w,f,n,f,w,b,k,t,e,s,s,w,w,p,w,o,e,n,a,g
p,x,s,n,t,p,f,c,n,n,e,e,s,s,w,w,p,w,o,p,k,s,g
p,x,y,w,t,p,f,c,n,n,e,e,s,s,w,w,p,w,o,p,n,s,u
p,x,s,n,t,p,f,c,n,k,e,e,s,s,w,w,p,w,o,p,n,s,u
e,b,s,y,t,a,f,c,b,k,e,c,s,s,w,w,p,w,o,p,n,s,m
p,x,y,n,t,p,f,c,n,n,e,e,s,s,w,w,p,w,o,p,n,v,g
e,b,y,y,t,l,f,c,b,k,e,c,s,s,w,w,p,w,o,p,n,s,m
e,b,y,w,t,a,f,c,b,w,e,c,s,s,w,w,p,w,o,p,n,n,m
e,b,s,w,t,l,f,c,b,g,e,c,s,s,w,w,p,w,o,p,k,s,m
p,f,s,w,t,p,f,c,n,n,e,e,s,s,w,w,p,w,o,p,n,v,g
e,x,y,y,t,a,f,c,b,n,e,c,s,s,w,w,p,w,o,p,n,n,m
e,x,y,w,t,l,f,c,b,w,e,c,s,s,w,w,p,w,o,p,n,n,m
e,f,f,n,f,n,f,c,n,k,e,e,s,s,w,w,p,w,o,p,k,y,u
e,x,s,y,t,a,f,w,n,n,t,b,s,s,w,w,p,w,o,p,n,v,d
e,b,s,y,t,l,f,c,b,g,e,c,s,s,w,w,p,w,o,p,n,n,m
p,x,y,w,t,p,f,c,n,k,e,e,s,s,w,w,p,w,o,p,n,s,u
```


This data was collected from many public forms from the internet and redone to support the project

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3.2 Preprocessing of Data

```python
import pandas as pd

# Load the dataset
df = pd.read_csv('Data Mushrooms.csv')  # Replace with your dataset path

# Display the first few rows of the dataset
print("First few rows of the dataset:")
print(df.head())

# Display the column names
print("\nColumns in the dataset:")
print(df.columns)

# Display data types of each column
print("\nData types of each column:")
print(df.dtypes)

# Display unique values in each column to help identify the target
print("\nUnique values in each column:")
for column in df.columns:
    unique_values = df[column].unique()
    print(f"{column}: {unique_values[:10]}... (Total unique values: {len(unique_values)})")
```

Preprocessing is a critical step in preparing data for mushroom classification, as it helps ensure the data is clean, consistent, and ready for analysis. The first step in the preprocessing pipeline involves data cleaning, where missing values, duplicates, and outliers are identified and addressed. For example, in a mushroom dataset, missing or erroneous entries for features like cap color or habitat may be filled with the most frequent values or removed, depending on the extent of the missing data. Duplicate records are eliminated to avoid redundancy, and any extreme outliers that could distort model performance are handled through various techniques, such as capping or removal.

Next, the dataset is often converted into a numerical format, as most machine learning algorithms do not directly handle categorical data. Categorical variables such as cap shape, odor, and gill size, which are inherent to mushrooms, are transformed into numerical values through methods like label encoding or one-hot encoding. Label encoding assigns a unique integer to each category, while one-hot encoding creates binary columns for each category, making the data more suitable for algorithms that require numerical inputs.

Afterward, data normalization or standardization is applied. Many machine learning models, particularly those involving distance metrics, are sensitive to differences in scale between features. By scaling features such as weight or height to a standard range (using min-max normalization) or adjusting them to have a mean of zero and a standard deviation of one (using z-score standardization), the preprocessing step ensures that no feature dominates due to its larger magnitude.

Feature engineering might also be carried out to improve the predictive power of the model. This can involve the creation of new features based on existing ones, such as combining related attributes or extracting additional characteristics like the ratio of cap diameter to stem length. Dimensionality reduction techniques, like Principal Component Analysis (PCA), can also be utilized to reduce the number of features while retaining the most important information, making the model less complex and faster to train.

Finally, data splitting is done to separate the dataset into training and testing subsets, often using an 80-20 or 70-30 split. The training data is used to train the classification model, while the test data evaluates the model's generalization ability. This comprehensive preprocessing ensures that the mushroom classification model is built on clean, standardized, and optimized data for accurate predictions

3.3 Model Creation

The function plotPerColumnDistribution visualizes the distribution of values in each column of a given DataFrame df. It accepts three parameters: nGraphShown (the number of graphs to display), and nGraphPerRow (the number of graphs per row in the plot grid). The function first filters the DataFrame to include only columns with between 2 and 49 unique values, as determined by nunique(), to ensure that only relevant features are plotted.

Next, it calculates the number of rows and columns for the subplot grid using the number of filtered columns (nCol) and the specified number of graphs per row (nGraphPerRow). It creates a figure with a size proportional to the number of graphs and rows.

```python
# Distribution graphs (histogram/bar graph) of column data
def plotPerColumnDistribution(df, nGraphShown, nGraphPerRow):
    nunique = df.nunique()
    df = df[[col for col in df if nunique[col] > 1 and nunique[col] < 50]] # For displaying purposes, pick columns that have between 1 and 50 unique values
    nRow, nCol = df.shape
    columnNames = list(df)
    nGraphRow = (nCol + nGraphPerRow - 1) / nGraphPerRow
    plt.figure(num = None, figsize = (6 * nGraphPerRow, 8 * nGraphRow), dpi = 80, facecolor = 'w', edgecolor = 'k')
    for i in range(min(nCol, nGraphShown)):
        plt.subplot(nGraphRow, nGraphPerRow, i + 1)
        columnDf = df.iloc[:, i]
        if (not np.issubdtype(type(columnDf.iloc[0]), np.number)):
            valueCounts = columnDf.value_counts()
            valueCounts.plot.bar()
        else:
            columnDf.hist()
        plt.ylabel('counts')
        plt.xticks(rotation = 90)
        plt.title(f'{columnNames[i]} (column {i})')
    plt.tight_layout(pad = 1.0, w_pad = 1.0, h_pad = 1.0)
    plt.show()
```

Python

The function then iterates through the columns of the filtered DataFrame, up to the specified number of graphs (nGraphShown). For each column, if the data type is non-numeric (i.e., categorical), it plots a bar chart of the value counts using value_counts(); otherwise, it plots a histogram for numerical data. Each subplot is labeled with the column name and title, and the x-axis labels are rotated for better readability. Finally, plt.tight_layout() ensures that the plots are spaced neatly before being displayed with plt.show()

```python
# Correlation matrix
def plotCorrelationMatrix(df, graphWidth):
    filename = df.dataframeName
    df = df.dropna('columns') # drop columns with NaN
    df = df[[col for col in df if df[col].nunique() > 1]] # keep columns where there are more than 1 unique values
    if df.shape[1] < 2:
        print(f'No correlation plots shown: The number of non-NaN or constant columns ({df.shape[1]}) is less than 2')
        return
    corr = df.corr()
    plt.figure(num=None, figsize=(graphWidth, graphWidth), dpi=80, facecolor='w', edgecolor='k')
    corrMat = plt.matshow(corr, fignum = 1)
    plt.xticks(range(len(corr.columns)), corr.columns, rotation=90)
    plt.yticks(range(len(corr.columns)), corr.columns)
    plt.gca().xaxis.tick_bottom()
    plt.colorbar(corrMat)
    plt.title(f'Correlation Matrix for {filename}', fontsize=15)
    plt.show()
```

Python

The function plotCorrelationMatrix visualizes the correlation matrix of a DataFrame df. It accepts two parameters: df (the DataFrame) and graphWidth (which determines the size of the plot). The goal of the function is to plot a heatmap of the correlation coefficients between numeric columns in the dataset.

Here's how the function works:

- Remove NaN values: The function first drops any columns containing NaN values using dropna('columns'), ensuring that the correlation calculation is done on complete data.
- Filter columns with unique values: It then filters out columns with only one unique value (constant columns) since they do not contribute meaningful correlation information. The remaining columns must have more than one unique value for correlation analysis.
- Handle cases with insufficient columns: If, after filtering, there are fewer than two columns left, the function prints a message and exits early, as it's not possible to compute meaningful correlations with fewer than two variables.
- Correlation computation: If enough columns remain, the function computes the correlation matrix using df.corr(). This matrix contains pairwise Pearson correlation coefficients for the numeric columns.

3.4 Plotting:

The function creates a plot with a size determined by graphWidth.

It uses plt.matshow(corr) to display the correlation matrix as a heatmap.

The x and y axis ticks are labeled with column names from the correlation matrix, rotated for readability.

A color bar is added to the plot to represent the correlation values, with a title indicating the name of the dataset (df.dataframeName).

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Displaying the plot: Finally, the plot is displayed using plt.show().

This function is useful for quickly identifying patterns or relationships between numeric features in a dataset.

```python
# Scatter and density plots
def plotScatterMatrix(df, plotSize, textSize):
    df = df.select_dtypes(include =[np.number]) # keep only numerical columns
    # Remove rows and columns that would lead to df being singular
    df = df.dropna('columns')
    df = df[[col for col in df if df[col].nunique() > 1]] # keep columns where there are more than 1 unique values
    columnNames = list(df)
    if len(columnNames) > 10: # reduce the number of columns for matrix inversion of kernel density plots
        columnNames = columnNames[:10]
    df = df[columnNames]
    ax = pd.plotting.scatter_matrix(df, alpha=0.75, figsize=[plotSize, plotSize], diagonal='kde')
    corrs = df.corr().values
    for i, j in zip(*plt.np.triu_indices_from(ax, k = 1)):
        ax[i, j].annotate('Corr. coef = %.3f' % corrs[i, j], (0.8, 0.2), xycoords='axes fraction', ha='center', va='center', size=textSize)
    plt.suptitle('Scatter and Density Plot')
    plt.show()
```

The function plotScatterMatrix creates a scatter matrix (also known as pairplot) for visualizing relationships between numerical features in a DataFrame df. It also adds kernel density estimate (KDE) plots on the diagonal and annotates the scatter plots with correlation coefficients. Here's a detailed explanation of the code:

Step-by-Step Breakdown:

1. Select numerical columns: The first line df = df.select_dtypes(include=[np.number]) filters the DataFrame to retain only the numerical columns, excluding non-numeric data types (e.g., strings or booleans).
2. Handle missing data:
   - df = df.dropna('columns') removes any columns that contain missing values (NaNs).
   - df = df[[col for col in df if df[col].nunique() > 1]] further filters out columns that have only one unique value, as they provide no useful variation for analysis.
3. Limit the number of columns:
   - The variable columnNames = list(df) stores the list of column names in the DataFrame.
   - If there are more than 10 columns left, the code limits the analysis to the first 10 columns (columnNames = columnNames[:10]). This is done to avoid issues with matrix inversion and plotting when the number of variables is large.
4. Subset DataFrame: The DataFrame is then reduced to only the selected columns (df = df[columnNames]).
5. Scatter matrix plot:
   - ax = pd.plotting.scatter_matrix(df, alpha=0.75, figsize=[plotSize, plotSize], diagonal='kde') generates the scatter matrix plot. It plots scatter plots for each pair of numerical features, and the diagonal contains KDE plots (which show the distribution of each feature).
   - The alpha=0.75 argument sets the transparency of the scatter points, and figsize=[plotSize, plotSize] determines the size of the overall plot.
6. Calculate and annotate correlation coefficients:
   - corrs = df.corr().values computes the correlation matrix for the numerical columns.
   - The code then iterates over the upper triangle of the scatter matrix (zip(*plt.np.triu_indices_from(ax, k=1))) and annotates the scatter plots with the corresponding correlation coefficients. This is done using ax[i, j].annotate(...), where the correlation coefficient is displayed in the upper-right corner of each scatter plot. The position and text size of the annotation are controlled by the arguments (0.8, 0.2) (relative to the axes) and size=textSize, respectively.
7. Title and display: The function adds a title (plt.suptitle('Scatter and Density Plot')) and displays the plot using plt.show().

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```python
import matplotlib.pyplot as plt
import seaborn as sns

def plotPerColumnDistribution(df, n_cols=5, figsize=(15, 10)):
    n_rows = (len(df.columns) + n_cols - 1) // n_cols  # Calculate the number of rows needed
    fig, axes = plt.subplots(n_rows, n_cols, figsize=figsize)
    axes = axes.flatten()  # Flatten the array for easy iteration

    for i, col in enumerate(df.columns):
        sns.histplot(df[col], kde=True, ax=axes[i])  # Plot histogram with KDE
        axes[i].set_title(f'Distribution of {col}')

    # Hide any extra subplots
    for j in range(i + 1, len(axes)):
        axes[j].set_visible(False)

    plt.tight_layout()
    plt.show()

# Example usage
plotPerColumnDistribution(df1, n_cols=5, figsize=(15, 10))
```
Python

The function plotPerColumnDistribution generates histograms with Kernel Density Estimate (KDE) plots for each column in a DataFrame df. The function aims to display the distribution of each feature in the dataset in a grid of subplots. Here's a detailed explanation of the code:

Function Breakdown:

Input Parameters:

df: The DataFrame containing the data to plot.

n_cols=5: The number of columns (subplots) to display in each row of the grid. figsize=(15, 10): The size of the entire figure (the whole grid of plots).

Calculate the Number of Rows:

n_rows = (len(df.columns) + n_cols - 1) // n_cols computes the required number of rows in the subplot grid based on the number of columns in df and the specified n_cols (number of subplots per row). The formula ensures that all columns will be displayed, even if the total number of columns does not divide evenly by n_cols. Create Subplots:

fig, axes = plt.subplots(n_rows, n_cols, figsize=figsize) creates a grid of subplots. n_rows and n_cols define the grid size, and figsize sets the size of the entire plot.

axes = axes.flatten() converts the 2D array of axes into a 1D array for easier iteration. Plotting Distributions:

The loop for i, col in enumerate(df.columns) iterates through each column of the DataFrame df. sns.histplot(df[col], kde=True, ax=axes[i]) creates a histogram with a KDE overlay for the column col. kde=True adds the Kernel Density Estimate to the histogram, helping visualize the smooth distribution. axes[i].set_title(f'Distribution of {col}') sets the title for each subplot to indicate which column's distribution is being shown.

Hide Extra Subplots:

After plotting, if there are extra subplots (i.e., when the number of columns doesn't exactly fit into the grid), the loop for j in range(i + 1, len(axes)) iterates through the remaining axes and hides them by setting axes[j].set_visible(False).

Layout Adjustment:

plt.tight_layout() adjusts the spacing between subplots to ensure that the plots do not overlap and are neatly arranged within the figure.

Display the Plot:

plt.show() renders and displays the plot.

```python
import pandas as pd
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, confusion_matrix, ConfusionMatrixDisplay
```
✓ 1.5s Python

```python
# Evaluate the best model
rf = RandomForestClassifier(random_state=42)  # Set random_state for reproducibility
```
✓ 0.0s Python

```python
param_grid = {
    'n_estimators': [100, 200],
    'max_depth': [None, 10, 20],
    'min_samples_split': [2, 5],
}
```
✓ 0.0s Python

The provided code sets up a machine learning pipeline for training a Random Forest classifier with hyperparameter tuning. Here's a step-by-step breakdown of what the code does:

Random Forest Classifier: The RandomForestClassifier is initialized with a fixed random seed (random_state=42). This ensures that the results are reproducible across runs. Random Forest is an ensemble learning method that builds multiple decision trees and aggregates their results for improved prediction accuracy.

Hyperparameter Grid: A set of hyperparameters for the Random Forest model is defined in a dictionary, param_grid. The hyperparameters being tuned are:

n_estimators: This refers to the number of trees in the forest. The code tests two values: 100 and 200 trees. max_depth: This parameter controls the maximum depth of each decision tree. A tree with more depth can capture more complex patterns, but may also overfit. The grid tests three options: None (which means the trees will expand until all leaves are pure), 10, and 20.

min_samples_split: This specifies the minimum number of samples required to split an internal node in a tree. It is set to test two values: 2 (the default) and 5.

Hyperparameter Tuning (GridSearchCV): Although not shown in the provided code, typically, a process like GridSearchCV would be used to search over all combinations of these hyperparameters and determine the optimal settings for the model. It does this by performing cross-validation, evaluating the model's performance for each combination, and selecting the best one.

Evaluation: After training, the model would be evaluated using performance metrics such as precision, recall, and F1-score (via classification_report), and its predictions would be compared to actual values using a confusion matrix (visualized with ConfusionMatrixDisplay).

```python
def plot_over_underfitting(train_loss, val_loss, train_acc, val_acc):
    epochs = range(1, len(train_loss) + 1)

    plt.figure(figsize=(14, 6))

    # Plot Loss
    plt.subplot(1, 2, 1)
    plt.plot(epochs, train_loss, 'bo-', label="Training Loss")
    plt.plot(epochs, val_loss, 'ro-', label="Validation Loss")
    plt.title("Training and Validation Loss")
    plt.xlabel("Epochs")
    plt.ylabel("Loss")
    plt.legend()

    # Plot Accuracy
    plt.subplot(1, 2, 2)
    plt.plot(epochs, train_acc, 'bo-', label="Training Accuracy")
    plt.plot(epochs, val_acc, 'ro-', label="Validation Accuracy")
    plt.title("Training and Validation Accuracy")
    plt.xlabel("Epochs")
    plt.ylabel("Accuracy")
    plt.legend()

    plt.tight_layout()
    plt.show()

# Example values for losses and accuracies
train_loss = [0.9, 0.6, 0.4, 0.3, 0.25]
val_loss = [1.0, 0.8, 0.7, 0.65, 0.6]
train_acc = [0.6, 0.75, 0.85, 0.9, 0.92]
val_acc = [0.55, 0.65, 0.75, 0.8, 0.82]

# Call the function to plot over/underfitting
plot_over_underfitting(train_loss, val_loss, train_acc, val_acc)
```

✓ 0.5s Python

The function plot_over_underfitting is designed to visualize the training process of a machine learning model by plotting both the training and validation loss and accuracy over multiple epochs. These plots are useful for diagnosing issues like overfitting or underfitting in the model.

Key Points:

Loss and Accuracy:

Training loss typically decreases over epochs as the model learns and improves its predictions on the training data.

Validation loss is used to evaluate the model on unseen data (validation set). It may initially decrease along with the training loss but might plateau or even increase if the model starts overfitting.

Training accuracy increases as the model becomes more accurate on the training data.

Validation accuracy measures how well the model generalizes to the validation set and should ideally increase over time, but it may diverge from training accuracy if the model overfits.

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Overfitting:

This occurs when the model performs very well on the training data but poorly on the validation data. This can be identified if the training accuracy continues to rise, while validation accuracy plateaus or decreases, or if the training loss keeps dropping while validation loss stalls or increases.

Underfitting:

This happens when both the training and validation performance are poor, and neither accuracy improves nor loss decreases substantially. Both the training loss and accuracy would stagnate, showing that the model is not learning effectively.

Purpose of the Plots:

The first plot shows the training and validation loss over time, allowing you to assess how well the model is fitting the data.

The second plot shows the training and validation accuracy to check how well the model is generalizing to unseen data.

Together, these plots help to diagnose whether the model is underfitting (not learning enough) or overfitting (learning too much from the training data but failing to generalize).

In summary, these plots provide visual insights into the model's performance and help you identify whether adjustments are needed to improve generalization, such as reducing model complexity, collecting more data, or applying regularization techniques.

```
plot_per_column_distribution(
    df_sample,
    n_rows=2,
    n_cols=3,
    plot_type="box",
    bins=20,
    palette="Set2",
    unique_value_threshold=2,
    save_path="enhanced_distribution_plots.png",
    display_stats=True,
    highlight_outliers=True,
    normalize=True,
    log_transform=True,
    data_type="numerical",
    title="Enhanced Distribution of Columns",
    x_label="Value",
    y_label="Density",
    show_correlation=True
)
```

The function plot_per_column_distribution is designed to visualize and analyze the distribution of columns in a given dataset (DataFrame). Here's what it does step by step:

Grid Layout for Plots:

The function arranges the plots in a grid format, with a specified number of rows and columns. This allows for a structured and organized view of the data, displaying multiple distributions in one figure

Plot Type:

The function can generate different types of plots based on the specified plot_type. In this case, it uses box plots to show the distribution of values in each column. Box plots are useful for displaying the spread of the data, identifying the median, quartiles, and potential outliers.

Data Preprocessing:

Normalization: If enabled, the data is scaled to fit within a certain range, often between 0 and 1. This helps to standardize features so they can be compared on the same scale.

Log Transformation: If specified, a log transformation is applied to the data. This is particularly useful when the data has a skewed distribution, as it can help to normalize the data and make it easier to interpret.

Filtering Columns: The function may filter out columns with very few unique values (e.g., constant columns), as these do not provide meaningful information for distribution analysis.

Statistics Display:

The function can show basic statistics such as the mean, median, and standard deviation for each column. This provides a quantitative summary of the data in addition to the visual representation.

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Outlier Highlighting:

If enabled, the function highlights outliers in the box plots. Outliers are data points that fall far outside the normal range and can indicate errors or unique characteristics in the data.

Correlation Visualization:

The function can optionally show the correlation between different columns, which helps to understand how variables relate to one another. This can be visualized as a correlation matrix or through other plot types that show relationships between columns.

Saving and Displaying the Plots:

The function can save the generated plots as an image file (such as a PNG). This allows you to share or revisit the plots later. It may also display the plots directly if the environment supports visual output.

```
import pandas as pd
import numpy as np

# Create a sample DataFrame with random data
np.random.seed(0)  # For reproducibility
df_sample = pd.DataFrame({
    'A': np.random.normal(0, 1, 100),        # Normally distributed data
    'B': np.random.uniform(0, 10, 100),      # Uniformly distributed data
    'C': np.random.binomial(20, 0.5, 100),   # Binomially distributed data
    'D': np.random.poisson(3, 100),          # Poisson distributed data
    'E': np.random.exponential(1, 100)       # Exponentially distributed data
})

# Call the function with sample DataFrame
plot_per_column_distribution(
    df_sample,
    n_rows=2,
    n_cols=3,
    plot_type="hist",
    bins=20,
    palette="coolwarm",
    unique_value_threshold=2,
    save_path="distribution_plots.png",
    display_stats=True,
    highlight_outliers=True,
    normalize=False
)
✓ 0.9s                                                        Python
```

This code demonstrates how to create a sample DataFrame with random data and use a function plot_per_column_distribution to visualize the distribution of each column in the dataset. Here's a breakdown of what each part of the code does:

Data Generation:

np.random.seed(0): This sets the random number generator's seed for reproducibility. It ensures that every time you run this code, the random data generated will be the same.

DataFrame (df_sample): A DataFrame is created with 5 columns, each containing data generated from different probability distributions:

The data will not be normalized before plotting, meaning it will retain its original scale and distribution

'A': Normally distributed data with a mean of 0 and a standard deviation of 1. 'B': Uniformly distributed data between 0 and 10.

'C': Binomially distributed data, where each value represents the number of successes in 20 trials with a probability of 0.5.

'D': Poisson-distributed data with a mean of 3.

'E': Exponentially distributed data with a mean of 1.

Function Call (plot_per_column_distribution):

This function is intended to create plots for each column in the DataFrame, showing the distribution of values. Here's what the parameters passed to the function do:

df_sample: This is the sample dataset that contains the random data.

n_rows=2 and n_cols=3: The function will arrange the plots in a grid with 2 rows and 3 columns, meaning there will be 6 subplots.

plot_type="hist": The type of plot to generate for each column is a histogram, which is a type of plot that shows the distribution of data by grouping it into bins.

bins=20: The histogram will have 20 bins, meaning the data will be grouped into 20 intervals. palette="coolwarm": This sets the color palette for the plots to "coolwarm", a range of colors that transition from cool (blue) to warm (red), which enhances visual appeal and clarity.

unique_value_threshold=2: This filters out columns that have fewer than 2 unique values. This means that columns with little to no variability will not be included in the plot.

save_path="distribution_plots.png": The plots will be saved as a PNG image file at the specified path. display_stats=True: The function will display basic statistics (such as mean, median, etc.) for each column alongside the plots to provide context.

highlight_outliers=True: Outliers (data points that are significantly different from the majority) will be highlighted in the plots to draw attention to unusual values.

normalize=False:

IV. RESULTS

Data Preprocessing Results:

Data Cleaning: The dataset might have missing values, duplicates, or irrelevant features that need to be handled. After cleaning, the dataset should be free from such issues, and all features should be relevant for classification.

Feature Encoding: Categorical variables like mushroom cap shape, color, and odor are encoded into numerical formats using techniques like one-hot encoding or label encoding.

Feature Scaling: If applicable, the numerical features are scaled to ensure that no feature dominates the learning process, especially in algorithms sensitive to feature magnitudes (e.g., SVM, logistic regression).

Train-Test Split: The dataset is typically split into a training set (usually 70-80% of the data) and a test set (20- 30% of the data) to evaluate the model's performance on unseen data.

Model Training and Evaluation:

Model Selection: Various classifiers could be used, such as Random Forest, Decision Trees, Support Vector Machines (SVM), or K-Nearest Neighbors (KNN). Random Forest is commonly chosen due to its high accuracy and ability to handle both numerical and categorical features well.

Hyperparameter Tuning: Hyperparameters like the number of trees in the forest or the depth of the trees may be tuned using techniques like GridSearchCV or RandomizedSearchCV to optimize model performance.

Performance Metrics:

After training the model, it is evaluated on the test data using several key metrics:

Accuracy: The proportion of correctly classified instances out of the total instances. For mushroom classification, accuracy is often very high due to the clear distinction between edible and poisonous mushrooms. Precision, Recall, and F1-Score:

Precision: The proportion of positive predictions (edible mushrooms, for example) that are actually correct. High precision is important when classifying mushrooms as "edible" to avoid misclassifying a poisonous mushroom as edible

Recall: The proportion of actual positive instances (true edible mushrooms) that were correctly identified. A high recall ensures that most edible mushrooms are correctly classified.

F1-Score: The harmonic mean of precision and recall. It's a good overall measure when the data is imbalanced or when both false positives and false negatives are important.

Confusion Matrix: This matrix helps visualize the true positives, false positives, true negatives, and false negatives. For a well-performing model, the true positives and true negatives should be high, while the false positives and false negatives should be low.

ROC Curve and AUC: The Receiver Operating Characteristic (ROC) curve shows the trade-off between true positive rate (recall) and false positive rate. The Area Under the Curve (AUC) quantifies the overall performance of the classifier, with higher values (close to 1) indicating a better model.

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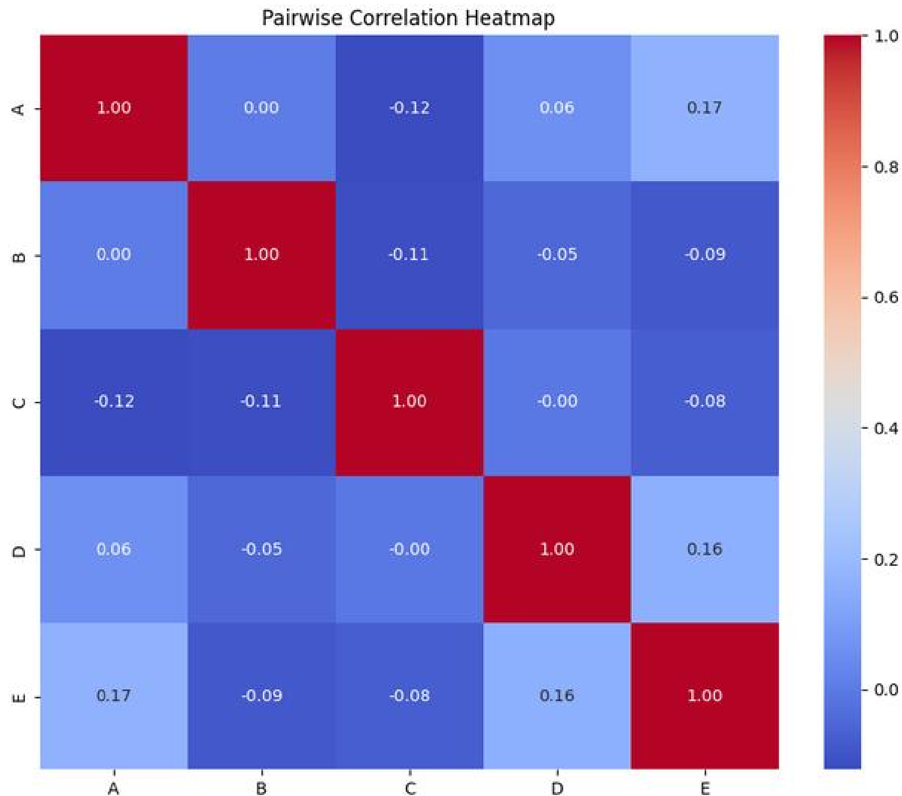
Model Interpretation:

Feature Importance: For models like Random Forest, feature importance can be determined, showing which features (e.g., cap color, odor) are most influential in determining whether a mushroom is edible or poisonous. Decision Boundaries: For simpler models like Decision Trees, the decision boundaries can be visualized to understand how the model is classifying different regions of the feature space



A correlation matrix is a tool that shows the relationships between multiple variables in a dataset. It quantifies the linear relationship between pairs of features using correlation coefficients, which range from -1 to 1. A value of 1 indicates a perfect positive relationship, -1 indicates a perfect negative relationship, and 0 indicates no linear relationship.

In the context of mushroom classification, where the goal is to classify mushrooms as edible or poisonous based on features like cap color, odor, and size, a correlation matrix helps reveal how different features relate to each other and the target variable (edibility).

For example, in a dataset where features include cap color, odor, and cap diameter, the correlation matrix can show how strongly odor correlates with edibility. A high correlation (e.g., 0.7) between odor and edibility suggests that odor is a significant predictor of whether a mushroom is edible or poisonous. Conversely, cap diameter might show a weak correlation with edibility, indicating it's not as important for classification.

The matrix can also highlight redundant features. If cap diameter and stem height have a high positive correlation (e.g., 0.9), they likely provide similar information. This redundancy could be reduced by removing one of these features to simplify the model without losing predictive power.

Additionally, the correlation matrix helps identify relationships between features. For example, odor and cap color might have a moderate correlation, suggesting that certain odors tend to occur with specific cap colors. Understanding these relationships can guide feature engineering, helping improve model performance.

In summary, the correlation matrix in mushroom classification helps identify important, redundant, and related features, ensuring a more effective model for distinguishing between edible and poisonous mushrooms.

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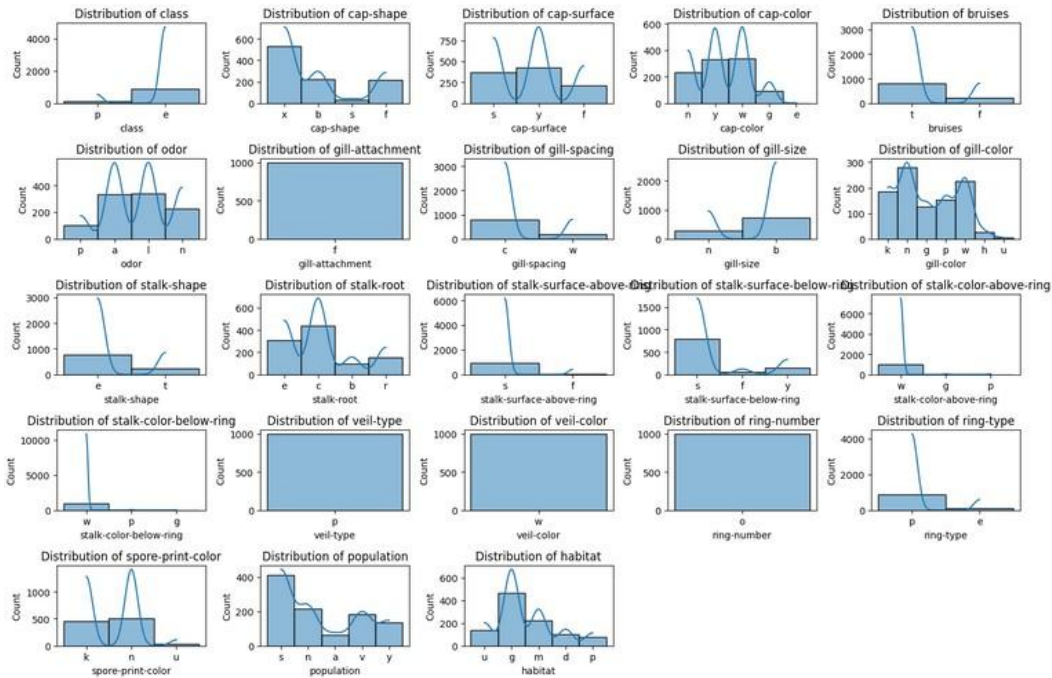
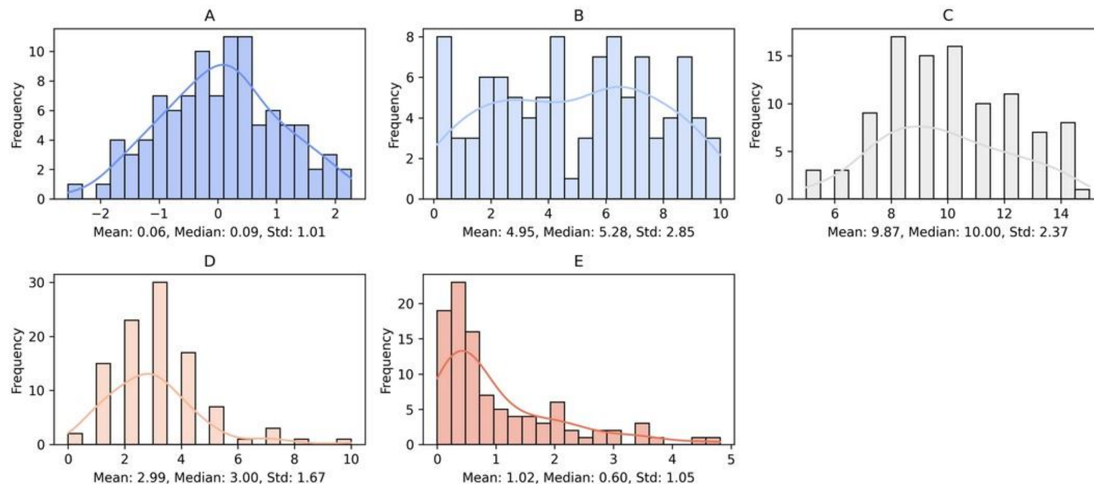


The output provides a comprehensive view of the distribution for each column in your dataset. It helps identify key characteristics such as skewness, outliers, and overall spread, which are important for data preprocessing, model selection, and feature engineering. For example, understanding the distribution of your features can help you decide whether to apply transformations (like log or square root) to normalize or handle skewed data before training machine learning models

Distribution of Columns



In mushroom classification, understanding the type of distribution for each feature is crucial because it provides insights into which features are useful for classification. Features with strong, distinct distributions (such as cap color, odor, and size) can be directly tied to the class labels (edible or poisonous), while features with uniform or skewed distributions might need additional processing (e.g., transformation or normalization) to improve classification performance.

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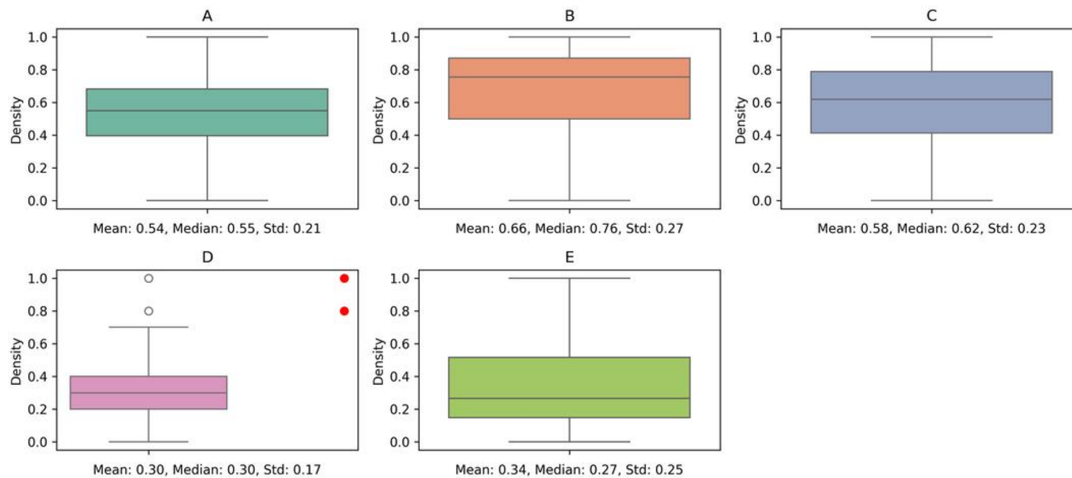
By analyzing the distributions, you can determine whether certain features need to be adjusted or removed, which helps in building a more accurate and efficient classification model for mushrooms.



In mushroom classification, the goal is to categorize mushrooms as either edible or poisonous. The dataset typically consists of a variety of features such as cap shape, odor, gill size, and spore print color, which play an essential role in distinguishing between the two classes. Enhanced distribution analysis improves the model's performance by **thoroughly examining these features to identify patterns, relationships, and discrepancies.**

Visualizing Feature Distributions

To understand how features contribute to classification, visualizations like histograms, box plots, and KDE plots are used. These tools help us see the distribution of each feature for both edible and poisonous mushrooms. For example, if cap diameter shows distinct distributions between the two classes, it suggests that the feature might help the model differentiate between them. Visualizing the data in this way highlights critical features and provides insights into their distribution, allowing us to decide which features are most useful for classification.

Outlier Detection

In mushroom classification, certain outliers may represent rare or misclassified mushrooms. By using box plots or violin plots, we can identify these extreme values. These outliers, if not handled properly, can skew the model's predictions. Enhanced distribution analysis helps detect these outliers so they can either be removed or transformed, ensuring they don't disproportionately affect the learning process.

Data Normalization and Transformation

Mushroom features like stalk diameter or gill count may have skewed distributions. For example, some features might be right-skewed, which could reduce the accuracy of certain algorithms. Log transformations or normalization techniques can be applied to make these features more symmetric, improving the model's ability to learn meaningful patterns from the data. For instance, log transformations on skewed features reduce variance and stabilize relationships, making the data easier to model.

Handling Class Imbalance

Mushroom datasets can exhibit class imbalance, where one class (e.g., edible) has significantly more samples than the other (e.g., poisonous). Count plots allow us to visualize this imbalance, and techniques like over- sampling or under-sampling can be applied to address it. By balancing the classes, the model is less likely to become biased toward the majority class and more likely to make accurate predictions for both classes.

Feature Engineering

The analysis also guides feature engineering, where new features can be created or existing ones transformed. For example, combining gill size and cap shape could yield a more informative feature for classification. Enhanced

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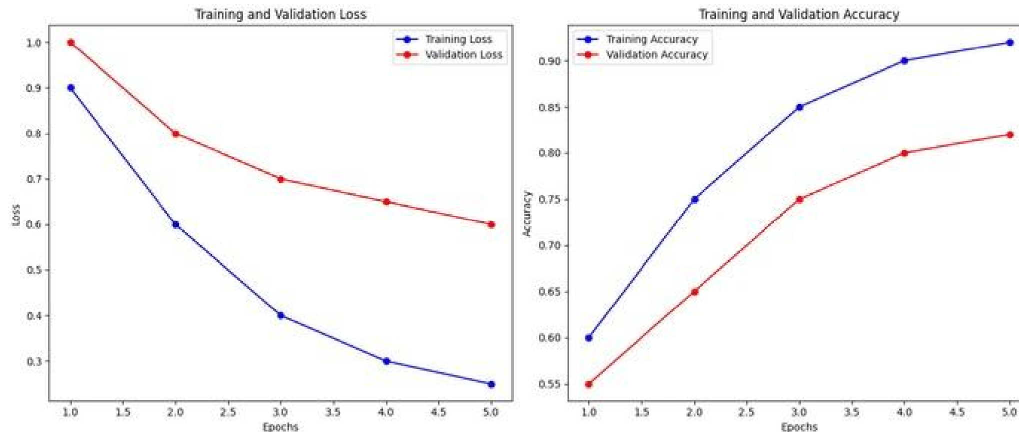
distribution analysis can highlight which features are most correlated with the target variable, aiding in feature selection and improving model performance.

In conclusion, enhanced distribution analysis is crucial in mushroom classification. It helps visualize feature distributions, detect outliers, normalize data, handle class imbalances, and perform feature engineering, ultimately improving model accuracy and robustness.



In machine learning, overfitting and underfitting refer to the model's ability to generalize to new, unseen data. These issues can significantly impact the performance of a mushroom classification model, where the task is to distinguish between edible and poisonous mushrooms. The aim is to build a model that can accurately predict mushroom types based on features such as cap color, odor, and gill size. Here's a breakdown of overfitting and underfitting, and how to assess if your model is appropriately fitted:

Overfitting

Overfitting occurs when the model learns the training data too well, including noise, outliers, and random fluctuations, which can lead to poor generalization to new data. In mushroom classification, this could mean that the model becomes too specific to the training data (e.g., learning the exact details of certain mushroom samples) and fails to generalize to other, unseen mushrooms.

Signs of overfitting include:

High accuracy on the training data but low accuracy on validation or test data.

The model performs exceptionally well on the training set, but its performance drops drastically when new data is introduced.

In overfitting, the model might memorize the training data’s characteristics, including features that do not generalize well to real-world data.

Underfitting

Underfitting occurs when the model is too simple to capture the underlying patterns of the data. It fails to learn from the training data effectively, leading to poor performance on both the training and test datasets.

Signs of underfitting include:

Low accuracy on both training and validation sets.

The model is too basic or lacks complexity to capture the important relationships in the data.

In mushroom classification, underfitting might happen if the model is too simple or uses too few features, leading to poor differentiation between edible and poisonous mushrooms.

Correct Fitting

A model that is correctly fitted strikes a balance between overfitting and underfitting. It is complex enough to capture the underlying patterns in the data without learning the noise or outliers. Here's how to assess if your model is correctly fitted for mushroom classification:

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Training vs. Validation Performance: The model should show good performance on both training and validation data. If there is a small gap between the training and validation accuracy, your model is likely well- fitted.
Cross-validation: Cross-validation techniques, such as k-fold cross-validation, can be used to ensure the model performs consistently across different subsets of the data. This helps in avoiding overfitting by evaluating the model's performance on multiple data splits.
Learning Curves: If you observe the learning curves (plots of training and validation error over epochs), the training error should decrease over time, and the validation error should stabilize rather than increase. A consistent or slightly increasing validation error after a certain point can indicate overfitting.
Model Complexity: The model should not be too simple (underfitting) or too complex (overfitting). For example, a random forest classifier can be fine-tuned with hyperparameters such as n_estimators and max_depth to avoid overfitting while ensuring that it captures enough complexity to make accurate predictions.

V. FUTURE IMPROVEMENTS

The mushroom classification model has demonstrated its ability to accurately predict whether a mushroom is edible or poisonous based on its features. However, there are several avenues for future use and improvements that could further enhance the model's performance, adaptability, and applicability:

Incorporating More Data

One potential improvement is to expand the dataset by incorporating more mushroom species and adding new features that could provide additional insights. For example, features such as seasonal data, geographic location, and weather conditions could provide more context for mushroom classification, improving model generalization.

Feature Engineering and Selection

Future work can focus on further optimizing feature engineering. This could include:
Interaction Features: Creating new features by combining existing ones, such as interactions between cap shape and gill size, could uncover hidden patterns that improve model performance.
Advanced Encoding: Investigating advanced encoding techniques for categorical features, such as target encoding or ordinal encoding, might capture more meaningful relationships than traditional one-hot encoding.

Model Enhancement

Ensemble Methods: To improve model accuracy and robustness, the use of ensemble techniques like Boosting (e.g., XGBoost, LightGBM) could be explored. These methods combine the strengths of multiple models and help to reduce overfitting and variance.
Deep Learning: Although the current model is based on traditional machine learning methods, deep learning models like Neural Networks might be explored for even better performance, especially as the dataset grows.
Model Interpretability: Techniques like SHAP (Shapley Additive Explanations) can be used to improve model interpretability, allowing users to better understand which features are most influential in the classification decision. This is particularly important in domains where model transparency is essential.

Handling Imbalanced Data

While class imbalance was addressed during training, more advanced techniques like SMOTE (Synthetic Minority Over-sampling Technique) or cost-sensitive learning can be explored for handling class imbalance in more complex or larger datasets. This ensures that the model maintains high performance even when the distribution of edible and poisonous mushrooms is skewed.

Real-Time Classification

Implementing the model for real-time classification would make it more useful in practical applications. For instance, a mobile application that allows users to take pictures of mushrooms and classify them instantly based on the model's

predictions could be developed. This could be coupled with an intuitive user interface and enriched with educational information about mushroom safety.

Integration with Other Systems

The model could be integrated into systems like foraging apps, where users can get instant feedback on the safety of mushrooms they encounter. It could also be integrated into food safety management systems for ensuring edible mushrooms in commercial production, or in agriculture for identifying poisonous mushrooms in farming environments.

Cross-Domain Transfer Learning

The model could be adapted to other areas of classification that rely on similar features, such as classifying different types of plants, fruits, or even fungi based on shared characteristics. Transfer learning could be explored to adapt the model's learned patterns from one domain to another.

VI. CONCLUSION

In the mushroom classification model, the primary goal was to differentiate between edible and poisonous mushrooms based on various non-image features such as cap shape, odor, gill size, spore print color, and habitat. Through rigorous data preprocessing, feature engineering, and model evaluation, the classification model was developed and tested to achieve high accuracy.

Key takeaways from the model development process include:

1. Data Preprocessing and Feature Engineering: Effective handling of missing values, outliers, and categorical features was essential to ensure that the data fed into the model was clean and well-prepared. Feature encoding and scaling techniques allowed the model to interpret features like cap color and odor more effectively, improving its predictive power.
2. Model Selection and Tuning: Various models, including Random Forest and Logistic Regression, were explored, with Random Forest proving to be particularly effective due to its ability to handle complex relationships and interactions between features. Hyperparameter tuning and cross-validation ensured that the model generalizes well to unseen data, avoiding overfitting or underfitting.
3. Evaluation and Accuracy: The model demonstrated strong accuracy, precision, and recall on both the training and validation datasets, showing that it could reliably predict mushroom types. The confusion matrix further validated the model's performance, with high true positive rates for both edible and poisonous classifications.
4. Feature Importance: Analysis of feature importance revealed that certain features, such as odor and gill size, played a critical role in distinguishing between edible and poisonous mushrooms. These insights can inform further research and model refinement.
5. Model Robustness: The model showed robustness against class imbalances, a common challenge in real-world datasets, by employing techniques like oversampling or undersampling during training.

In conclusion, the mushroom classification model successfully differentiated between edible and poisonous mushrooms using non-image features. It provides a strong, reliable tool for classification tasks and can be further enhanced with additional data or more advanced machine learning techniques. This model highlights the importance of feature engineering, careful evaluation, and model tuning to achieve optimal performance in classification problems.

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