Machine Learning Adopted Multi-Class Classification of Plant Diseases with Sparse and Categorical IoT Data

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ABSTRACT

Plant disease classification is a critical aspect of modern agriculture that has evolved from traditional manual diagnostic methods to sophisticated automated systems utilizing machine learning. Historically, farmers and experts relied on visual inspection, consultations, and laboratory tests to identify plant diseases—a process that, while effective for small-scale applications, was often subjective, time-consuming, and inconsistent, leading to delayed interventions and crop losses. The core problem lies in the inefficiency and high cost of these traditional methods, which struggle with large-scale agricultural demands and the complex nature of disease symptoms. This highlights the need for an innovative system that can swiftly and accurately classify plant diseases using sparse and categorical IoT data. The proposed system uses modern data analytics and machine learning techniques to overcome these limitations. It includes data preprocessing methods such as filling missing values, label encoding, and applying Synthetic Minority Oversampling Technique (SMOTE) to address class imbalance, ensuring high-quality input data. The system employs a multi-class classification pipeline using models like Gaussian Naive Bayes, Support Vector Machines, K-Nearest Neighbors, and a novel Decision Tree Classifier, which demonstrates superior performance. Evaluation shows the Decision Tree model achieves 99.07% accuracy, with precision, recall, and F1-scores consistently above 98%, validating its robustness. This research has the potential to transform plant disease management by enabling real-time, data-driven insights for early diagnosis and targeted pesticide use, enhancing crop yield, minimizing economic losses, and promoting sustainable farming practices.

Keywords: Plant disease identification, IoT sensor data, Predictive analytics, Decision analytics, Machine Learning, Data balancing, SMOTE algorithm.

1.INTRODUCTION

Agricultural biodiversity is essential for providing humans with food and raw materials and is an essential component of human civilization [1, 2]. The disease can occur when pathogenic organisms such as fungi, bacteria, and nematodes; soil PH; temperature extremes; changes in the quantity of moisture and humidity in the air; and other elements continuously harm a plant. Plant diseases can have an impact on the growth, function, and structure of plants and crops, affecting the people that rely on them. Plant diseases can have a severe impact on crop health, leading to substantial damage, reduced yields, and financial losses for farmers. The majority of farmers still use manual methods to detect and classify plant ailments because it is difficult to do so early on, and this reduces productivity. Agriculture's productivity is a significant economic factor. As a result, disease identification and classification in plants are critical in agricultural industries [3]. If proper precautions are not taken, it can have serious consequences for plants by reducing the quality, quantity, or productivity of the corresponding products or services. Automatic disease detection and classification recognize symptoms at an early stage, i.e., when they first appear on plant leaves, lowering the amount of labor necessary to monitor large farms of crops. According to [4] Plant leaf disease is a major issue in rice production, and the disease has the potential to harm the crop, resulting in a drop in products. Farmers have a difficult time detecting and classifying plant leaf diseases. The timely and precise detection of plant diseases plays a vital role in implementing effective disease management and prevention strategies.

2. LITERATURE SURVEY

This section offers an extensive overview of prior works in the context of this research, encompassing machine learning models with the goal of identifying their strengths, limitations, and research gaps, thus forming the basis for the proposed method. An extensive review by Li et al. [5] presents the recent research progress in using deep learning technology for crop leaf disease identification. The authors discuss the current trends, challenges, and unresolved issues pertaining to plant leaf disease detection using deep learning and advanced imaging techniques are discussed, with the aim of providing a valuable resource for researchers in the field. Deep learning techniques were initially applied to plant image recognition with a focus on analyzing leaf vein patterns. A notable study employed a CNN architecture with 3–6 layers to successfully classify three leguminous plant species: white bean, red bean, and soybean [6]. The CNN model extracted and analyzed intricate features of leaf vein structures unique to each species, capturing low-level features such as edges and textures and progressing to more complex patterns. This hierarchical feature extraction enabled effective species differentiation based on leaf vein characteristics. The study demonstrated the potential of CNNs in plant species classification, highlighting the effectiveness of deep learning in capturing subtle biological variations for accurate identification, and laying the groundwork for further applications in plant image recognition.

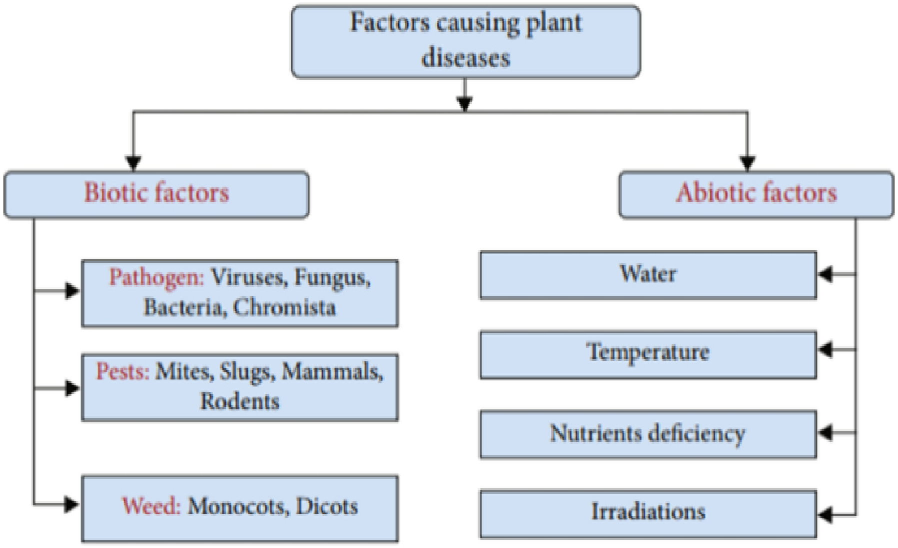


Fig. 1: Factors responsible for plant diseases [26].

Subsequently, Mohanty et al. [7] employed a classifier model to accurately identify 14 different crop species and 26 crop diseases, achieving an impressive accuracy of 99.35%. Building upon this work, Kawasaki et al. [8] proposed a CNN-based system specifically designed for the precise recognition of diseases affecting cucumber leaves, achieving a commendable accuracy rate of 94.9%. In an investigation by Ma et al. [9], a deep CNN was employed for the identification and recognition of four diseases in cucumber plants, including downy mildew, anthracnose, powdery mildew, and target leaf spots, based on their distinct symptoms. This study reported a recognition accuracy of 93.4%. Impressive strides have been made in plant leaf disease recognition; however, the availability of diverse datasets remains limited. CNN training necessitates extensive and diverse datasets, which are currently scarce in the field of plant leaf disease recognition. Consequently, transfer learning has emerged as a viable solution to enhance the robustness of CNN classifiers. By adapting pre-trained CNNs and retraining them with smaller datasets showcasing different distributions, transfer learning has proven to be an effective approach in implementing deep learning models [10]. Promising results have been demonstrated by leveraging pre-trained CNN models from the ImageNet dataset and retraining them for leaf disease recognition [11].

Recently, MTL models have been explored in the field of plant disease detection, enabling the simultaneous execution of multiple tasks. These models can effectively handle tasks, such as severity estimation of leaf disease, identification of plant species, and classification of plant disease concurrently [12]. To address the limitations in information utilization and scalability of existing models, Lee et al. [13] introduced a novel Conditional Multi-Task Learning (CMTL) model in this context. This method employs an MTL mechanism with a conditional scheme that links host species and disease representations, mimicking how plant pathologists infer diseases from species information. This improves plant disease identification performance compared to traditional joint species–disease pair modeling. It efficiently utilizes available information and is scalable, not requiring distinctions between similar species or diseases, thus enhancing accuracy and suitability for real-world applications. However, ViTs offer advantages over MTL frameworks in plant disease detection. They capture both local and global context information, enabling accurate analysis of plant images. ViTs also generalize well with limited labeled data through pre-training on large-scale datasets like ImageNet. Additionally, they provide flexibility and scalability by adapting to different disease detection tasks with a single model, reducing complexity and computational requirements.In their work, Thakur et al. [14] introduced a hybrid model, named PlantViT, for automating plant disease detection, which integrates the strengths of a CNN and a ViT, incorporating a multi-head attention module. The model was evaluated on two extensive plant disease detection datasets, namely, PlantVillage and Embrapa. Experimental results showed that the model achieves detection accuracies of 98.61% and 87.87% on the PlantVillage and the Embrapa datasets, respectively. These results outperform the current state-of-the-art methods, highlighting the effectiveness of PlantViT in plant disease detection.

In [15], a lightweight deep learning approach leveraging the ViT architecture is proposed for real-time automated plant disease classification. The study rigorously compares various models, including ViT, traditional CNNs, and a hybrid of CNN and ViT. Extensive training and evaluation across multiple datasets reveal that while attention blocks significantly enhance accuracy, they also introduce latency in predictions. However, integrating attention blocks with CNN blocks strikes an optimal balance between accuracy and speed, offering a robust solution for real-time plant disease classification.In recent studies, deep learning models have been employed to identify cassava leaf diseases, replacing the traditional and unreliable intuitive diagnosis conducted by farmers. To improve the disease detection accuracy in these species, Thai et al. [16] explored the use of the ViT model instead of a CNN. Experimental results demonstrate that the ViT model achieves competitive accuracy, surpassing popular CNN models such as EfficientNet and Resnet50 on the Cassava Leaf Disease Dataset. These findings highlight the potential superiority of the ViT model in analyzing leaf diseases. An extended study by Thakur et al. [17] addressed the underexplored application of ViTs in plant pathology by introducing PlantXViT, a light-weight model based on CNNs with ViTs for efficient identification of various plant diseases across different crops, well suited for IoT-based smart agriculture. Evaluation on five datasets shows that PlantXViT outperforms state-of-the-art models, achieving average accuracies of over 93.55%, 92.59%, and 98.33% on Apple, Maize, and Rice datasets, respectively, even in challenging backgrounds. The model's explainability is also assessed using gradient-weighted class activation maps, demonstrating its ability to provide insights into the decision-making process.Zhu et al. [18] introduced the Multiscale Convolution and Vision Transformer (MSCVT), a hybrid model that integrates multiscale convolutions with ViT techniques for precise crop disease identification. This approach combines the strengths of multiscale convolutions, which capture fine-grained local features, with ViT's ability to model long-range dependencies and global context. The study demonstrates that MSCVT outperforms single-scale CNNs and standalone ViT models by effectively capturing local and global details while optimizing computational efficiency. This balance ensures high accuracy in disease identification and practical deployment in resource-constrained environments, making MSCVT a valuable tool for early detection and management of crop diseases.

The ConvViT [19] is a lightweight ViT-based approach developed for apple leaf disease identification. It integrates convolutional and Transformer structures to effectively capture both global and local features of crop disease spots, enhancing overall robustness and accuracy. The patch embedding method is improved to preserve edge information and facilitate information exchange within the Transformer. By leveraging depthwise separable convolution and linear-complexity multi-head attention operations, ConvViT achieves substantial reduction in resource requirements. This model achieves comparable identification performance (96.85%) on a complex background apple leaf disease dataset, with significantly reduced parameters (32.7%) and FLOPs (21.7%). This highlights the effectiveness and practicality of ConvViT as a disease identification model. The Shuffle Convolution-based Lightweight Vision Transformer (SLViT) [20] is a hybrid network designed for the accurate diagnosis of sugarcane leaf diseases. The study demonstrates that SLViT, which combines a lightweight CNN architecture with a flexible plug-in Transformer encoder, surpasses the state-of-the-art models on the publicly available Plant Village dataset with respect to the metrics speed, weight, memory usage, and precision.

The effectiveness of MTL in enhancing correlated tasks has been well established. Existing approaches typically employ a backbone for initial feature extraction and utilize exclusive branches for each task. However, the sharing of information between branches is often accomplished through basic concatenation or summation of feature maps, which results in overlooking the local image features and neglecting the significance or correlation between tasks. MTL-based ViTs offer a significant advancement in addressing the limitations of existing approaches. By integrating ViTs into the MTL framework, these models can capture both the global and local characteristics of images, enabling more comprehensive information exchange between tasks. This integration allows for a better understanding of the relationships and dependencies among tasks, leading to improved performance across multiple related tasks. MTL-based ViTs provide a more holistic approach to leveraging shared knowledge and extracting meaningful features, resulting in enhanced accuracy and robustness in correlated task scenarios. In the recent years, ViTs have been used in performing multiple tasks simultaneously sharing the data across different tasks. The Unified Transformer (UniT) [21] model is proposed for the simultaneous learning of multiple tasks across diverse domains, encompassing object detection, natural language understanding, and multimodal reasoning. The UniT encodes input modalities using an encoder and generates task predictions using a shared decoder over the encoded input representations. Task-specific output heads are employed, and the entire model is trained jointly end-to-end with task losses. UniT distinguishes itself by employing shared model parameters across all tasks, accommodating a wide range of tasks across domains, and delivering robust performance across 7 tasks on 8 datasets with reduced parameter count.

Similarly, the MulT [22] framework proposes an end-to-end MTL-based Transformer for simultaneous learning of multiple high-level vision tasks. It outperforms state-of-the-art multitask CNNs and single-task Transformers, demonstrating the significance of shared attention across tasks. The MulT model shows robustness and generalization to new domains in multitask benchmarks. The study highlights the advantages of Transformer-based architectures for MTL, such as better scalability, improved feature representation, and the ability to capture complex dependencies between tasks, thereby providing a substantial contribution to the field and paving the way for future research and applications in domains requiring robust multitask learning solutions. To address the challenges of constructing a comprehensive dataset for diagnosing and quantifying the COVID-19 severity using Chest X-ray (CXR) data, a novel

Multi-task ViT architecture is proposed by Park et al. [23]. This approach leverages abundant unlabeled CXR data through self-attention modeling, overcoming the limitations of existing ViT models that are not optimized for CXR. By utilizing a backbone network trained on public datasets, the multi-task ViT extracts informative low-level features from the images, which serve as valuable resources for a robust ViT. Best performances are exhibited by the model in both diagnosis and severity quantification tasks, and remarkable generalization capability is demonstrated on external test datasets from diverse institutions. These promising results underscore the potential for widespread deployment of the model in the medical field.

Tian et al. [24] introduced the MultiTask ViT (MTViT), a representation learning method that leverages ViTs. MTViT introduces a multiple branch transformer that sequentially processes image patches associated with different tasks, allowing for information exchange through the Cross-Task attention (CA) module. Unlike previous models, MTViT utilizes ViT's self-attention mechanism for feature extraction, resulting in improved memory and computation efficiency. Experimental results on benchmark datasets demonstrate that MTViT outperforms or achieves comparable performance to existing CNN-based MTL methods. Despite the widespread adoption of MTL-based ViTs in various computer vision applications, there remains a noticeable research gap in their application to plant disease detection. The work proposed by Goncalves et al. [25], known as MTLSegFormer, stands out as the only existing effort in exploring the potential of MTL-based ViTs to address plant disease detection challenges. MTLSegFormer is a semantic segmentation model designed for precision agriculture that leverages both MTL and attention mechanisms. It combines MTL and attention mechanisms, learning two feature maps for each task after extracting backbone features. The model assigns weights to important local regions for specific tasks, resulting in improved accuracy for correlated tasks in precision agriculture.

3. PROPOSED METHODOLOGY

This research is a comprehensive Python application designed to diagnose plant diseases using machine learning. It integrates data preprocessing, visualization, machine learning, and a user-friendly interface to facilitate the diagnosis of plant diseases using IoT data. It offers a robust platform for both data scientists (Admins) and end-users, supporting the entire pipeline from data exploration to model training and real-time predictions with actionable recommendations. Here’s an overview of its main components:

Step-1: Graphical User Interface (GUI)

The research uses Tkinter to create a full-screen GUI that includes background images, text widgets for logging and displaying results, and buttons for user interactions. There are separate functionalities for Admin and User roles. Admins can upload datasets, perform exploratory data analysis (EDA), preprocess data, apply oversampling techniques (SMOTE), split data, and train multiple classifiers. Regular users have access to the prediction functionality.

Step-2: Data Handling and Visualization

Users can load CSV datasets, which are then displayed in the GUI. The project provides several plotting functions such as bar plots, violin plots, histograms, scatter plots, strip plots, and correlation heatmaps to visualize different aspects of the data. This helps in understanding the distribution of features and the relationships between them.

Step-3: Data Preprocessing and Augmentation: Non-numeric (categorical) columns in the dataset are converted into numeric values using label encoding, making the data suitable for machine learning algorithms. Missing data is replaced with zeros to maintain dataset consistency. The project employs

SMOTE (Synthetic Minority Oversampling Technique) to address class imbalance, which is visualized by comparing class distributions before and after the technique is applied.

Step-4: Machine Learning and Model Training

The data is split into training (80%) and testing (20%) sets. The project includes several machine learning models: Gaussian Naive Bayes (GNBC), Support Vector Machine (SVC), K-Nearest Neighbors (KNN), and Decision Tree Classifier (DTC). Models are either trained on-the-fly or loaded from saved files if they already exist. After training, the models are evaluated using precision, recall, F1 score, accuracy, and confusion matrices, providing insight into model performance.

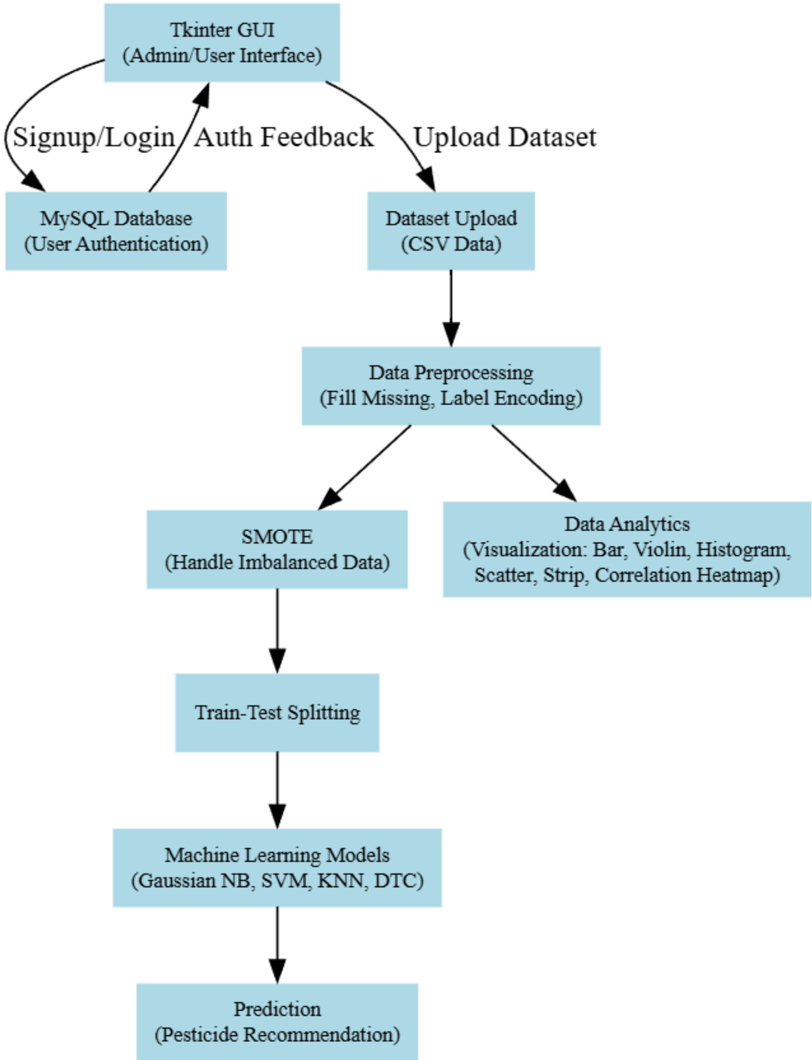


Fig. 2: System architecture of proposed plant disease classification with pesticide suggestion from categorical IoT data.

Step-5: Prediction and Recommendations

Users can upload new test data, and the trained model will predict the disease class. Each predicted disease is mapped to a specific pesticide recommendation based on predefined lists.

Step-6: Database Integration for User Authentication

The project connects to a local MySQL database to manage user authentication. Separate signup and login functions are provided for Admins and Users. After login, different sets of functionalities are made available according to the user's role.

3.2 Model Building and Training

3.2.1 Gaussian Naive Bayes (GNBC)

Gaussian Naive Bayes is a probabilistic classifier that applies Bayes' theorem with the "naive" assumption that features are conditionally independent given the class label. For continuous data, it assumes that the features follow a Gaussian (normal) distribution. The model calculates the likelihood of each feature given a class, multiplies these probabilities together (along with the prior probability of the class), and predicts the class with the highest posterior probability.

3.2.2 Support Vector Machine

The SVM classifier aims to find the optimal hyperplane that separates classes in the feature space. In its simplest (linear) form, SVM finds the hyperplane with the maximum margin between classes. For non-linearly separable data, kernel functions are used to transform the data into a higher-dimensional space where a linear separation is possible.

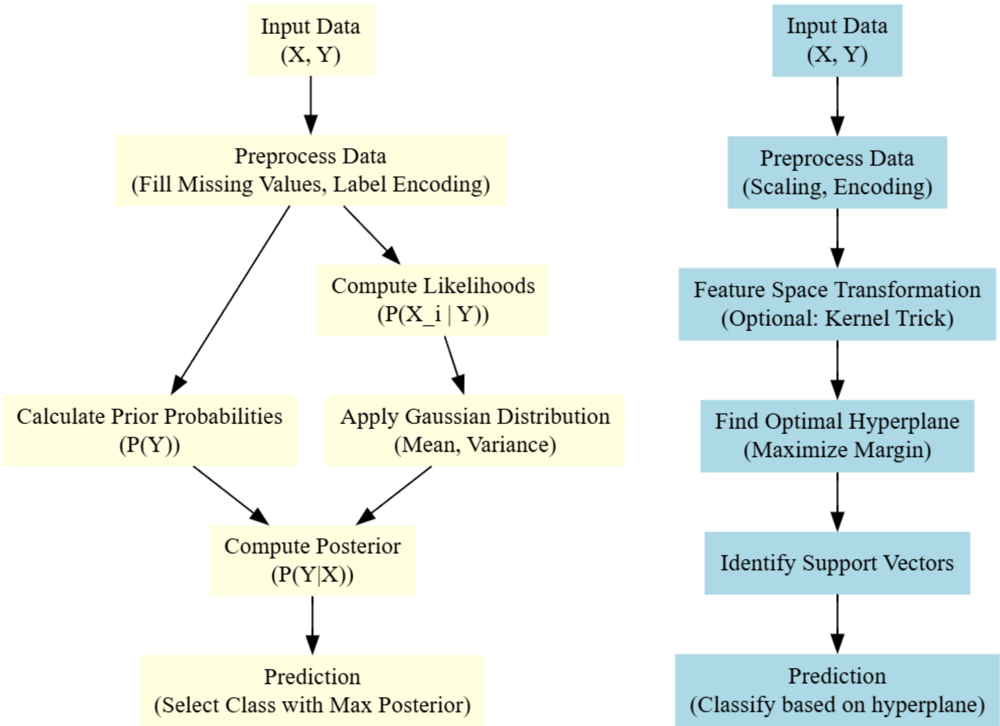


Fig. 3: Working of GNBC model (left). working of SVM classifier (right).

3.2.3 KNN Classifier

K-Nearest Neighbors is an instance-based, non-parametric algorithm. It works by storing all available cases and classifying new cases based on a similarity measure (e.g., Euclidean distance). In this project, the KNN model is configured with k=5k = 5k=5, meaning that for each test instance, the five closest neighbors are considered, and the class is predicted based on the majority vote among these neighbors.

3.2.4 DTC model

A Decision Tree is a flowchart-like structure where internal nodes represent tests on features, branches represent the outcome of these tests, and leaf nodes represent class labels. The tree is constructed by recursively splitting the dataset based on feature values that provide the maximum information gain or the best reduction in impurity (e.g., Gini impurity or entropy).

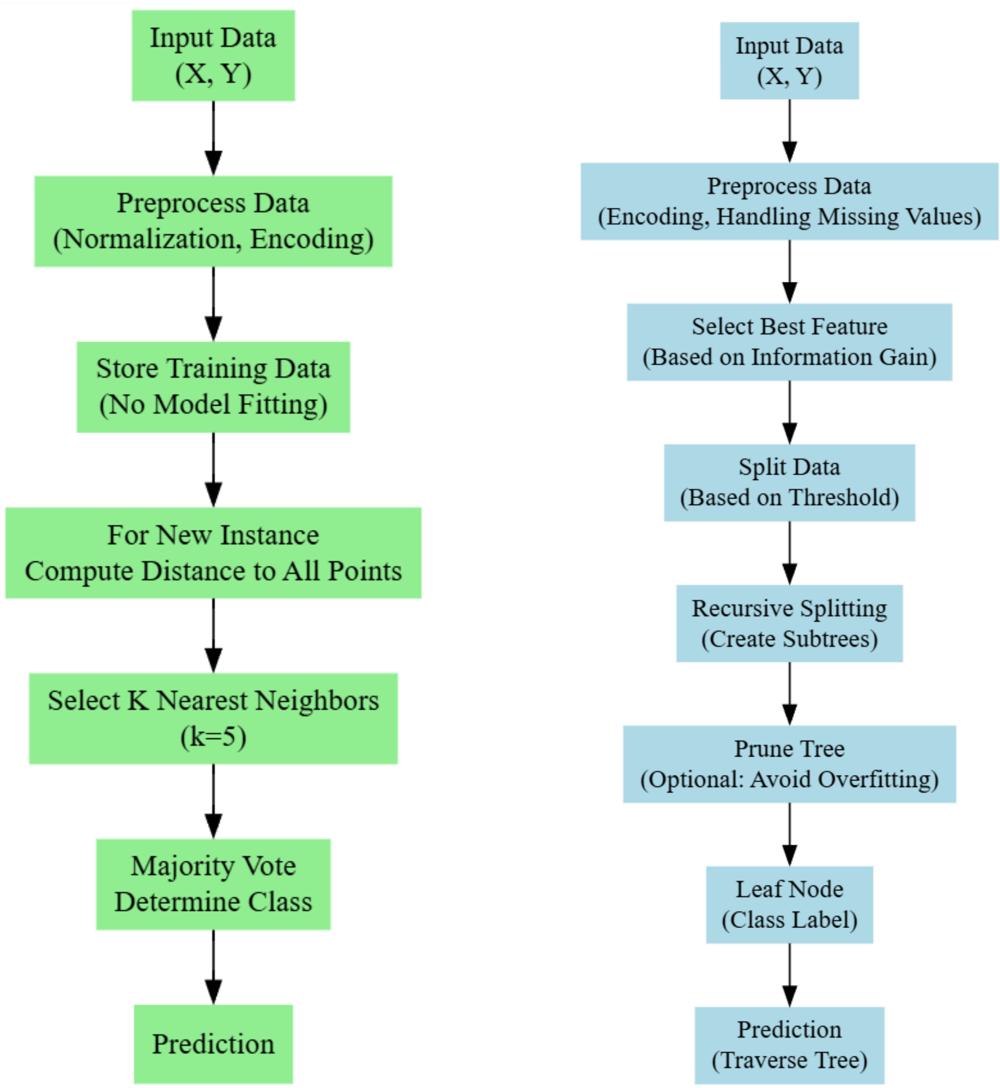


Fig. 4: Working flow of KNN classification (left). DTC model workflow (right).

3.2.5 Comparative Discussion

After training multiple models such as GNB classifier, SVM classifier, KNN classifier, and DTC model, a comprehensive evaluation of performance metrics such as accuracy, precision, recall, and F1-score revealed that the DTC model achieved the best overall performance. The superior performance of the DTC model can be attributed to its ability to capture complex, non-linear relationships inherent in the plant disease dataset. Unlike probabilistic models like GNB classifier, which assume independence among features, the DTC approach effectively identifies and utilizes the most informative features through recursive splitting. This inherent feature selection mechanism allows the model to handle the diversity of sensor data and the subtle variations in plant disease symptoms more adeptly.

Additionally, the interpretability of the DTC model provides valuable insights into the decision-making process. The tree structure clearly outlines the sequence of feature-based decisions that lead to a final classification, making it easier to understand which factors most significantly contribute to the diagnosis. This transparency not only aids in model validation but also facilitates further refinement of feature engineering strategies. Moreover, while models like SVM and KNN offer robust performance in many contexts, they may struggle with high-dimensional, sparse, and categorical data unless extensively tuned or transformed. The DTC model, on the other hand, naturally accommodates such complexities without the need for extensive preprocessing beyond the standard data normalization and encoding steps.

In summary, the Decision Tree Classifier emerged as the best-performing model in this project due to its effective handling of non-linear relationships, automatic feature selection, and interpretability. Its success underscores the importance of choosing a model that aligns well with the data's characteristics, ultimately contributing to more reliable and accurate plant disease classification outcomes.

4.RESULTS AND DISCUSSION

4.1 Dataset description

The dataset is designed for multi-class classification of plant diseases. It contains various environmental and plant-specific measurements, along with a target column indicating the disease label. The dataset is provided as a CSV (Comma-Separated Values) file, making it easy to load and manipulate using data analysis libraries such as Pandas. In essence, this dataset combines sparse and categorical IoT data with plant-specific measurements to facilitate the multi-class classification of plant diseases. It has been structured to handle 18 disease categories, each reflecting a distinct pathology. The ultimate goal is to accurately predict plant diseases and suggest appropriate pesticide treatments, thereby enhancing both the efficiency and effectiveness of disease management in agricultural settings.

The dataset includes several key features. The "temp" column is numeric and represents temperature measurements from IoT sensors or manual observations. "Leafspot-size" is also numeric and indicates the size or extent of leaf spots, a common symptom of many plant diseases. "Plant-growth" is a numeric feature that measures overall plant growth or vigor, possibly on a defined scale. The "germination" column is numeric as well and reflects the germination rate or a related metric capturing seed viability or early growth. The "stem" column may represent stem diameter, length, or a damage index relevant to disease symptoms and is also numeric. The "Label" column is categorical, later converted to numeric values using label encoding. It represents the target variable indicating the disease category. The dataset is focused on these columns for exploratory data analysis (EDA) and model training, although additional features such as humidity, rainfall, leaf color, or texture could be present depending on the data collection method.

There are 18 disease categories in the dataset, each encoded numerically after preprocessing. Some of the referenced diseases include diaporthe-stem-canker, charcoal-rot, rhizoctonia-root-rot, phytophthora-rot, brown-stem-rot, powdery-mildew, downy-mildew, brown-spot, bacterial-blight, bacterial-pustule, purple-seed-stain, anthracnose, phyllosticta-leaf-spot, alternarialeaf-spot, frog-eye-leaf-spot, diaporthe-pod-&-stem-blight, cyst-nematode, and herbicide-injury. These labels are essential for training machine learning algorithms to accurately classify plant diseases and recommend targeted interventions.

4.2 Results description

This research is a comprehensive Python application built using Tkinter for the graphical user interface (GUI) and integrates several modules to support a complete machine learning workflow for classifying plant diseases based on sparse and categorical IoT data. Fig. 5 contrasts the class distribution before and after the application of the SMOTE algorithm. Two bar plots are shown side-by-side: one displaying the imbalanced counts of each disease class, and the other illustrating the balanced class distribution achieved through synthetic oversampling.

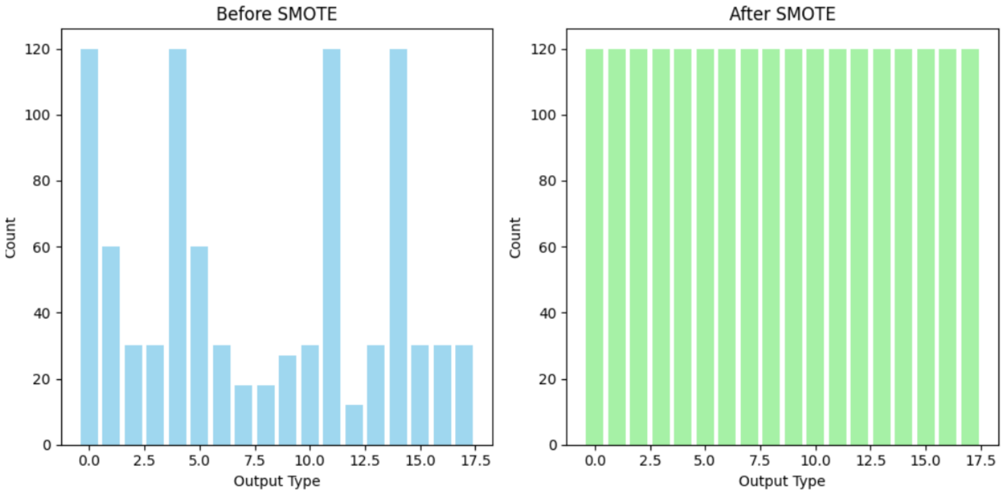
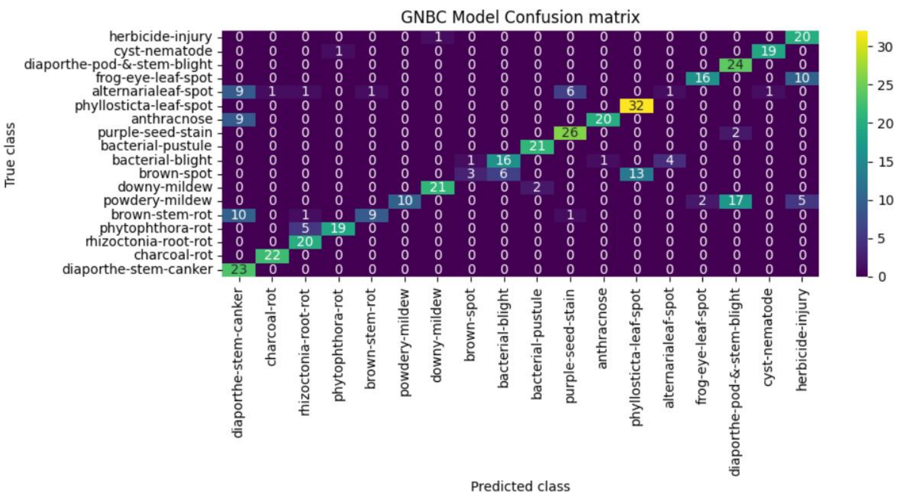


Fig. 5: Bar plot of count versus output before and after applying SMOTE algorithm.



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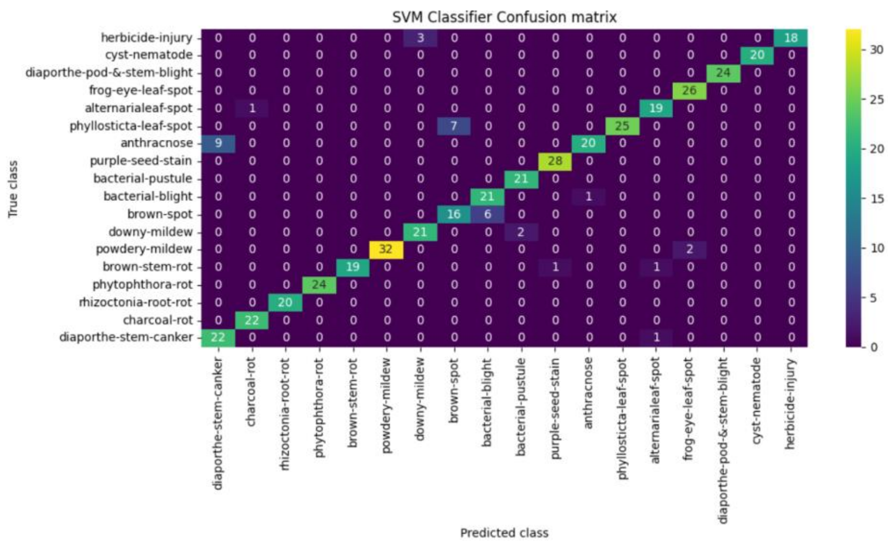

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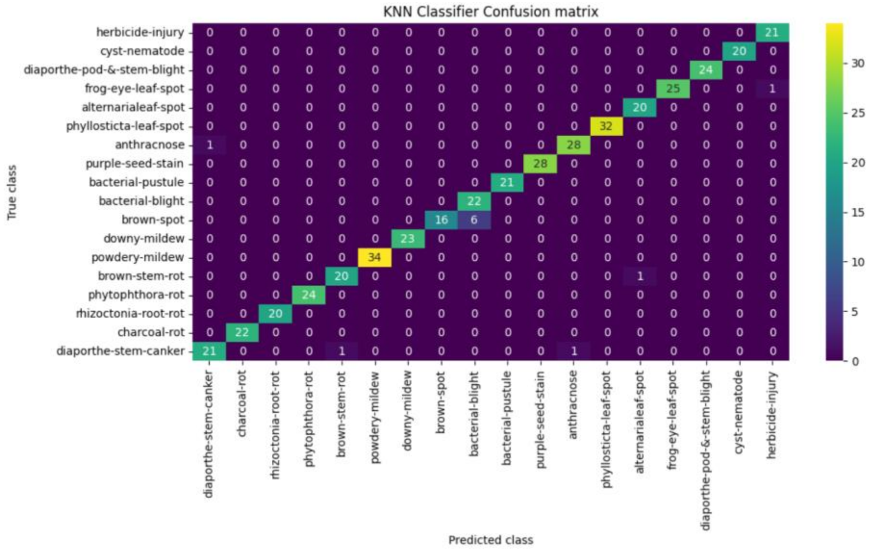

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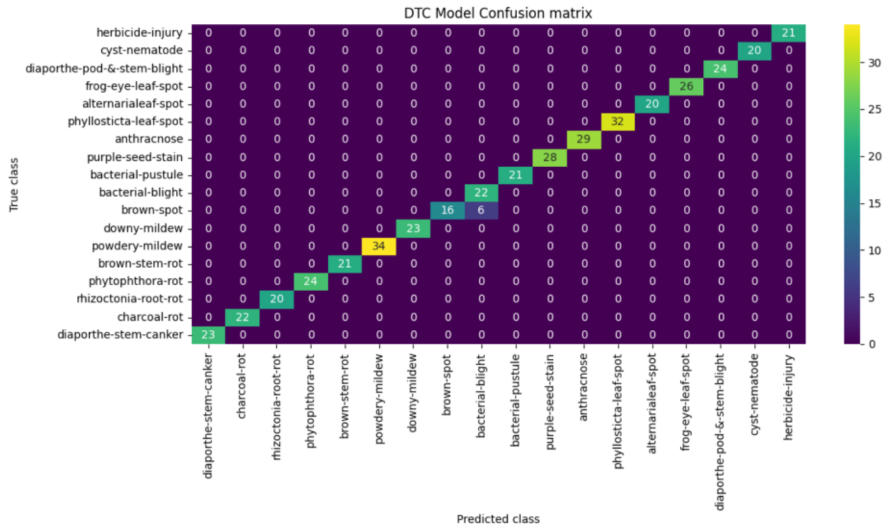


(d)

Fig. 8: Confusion matrices obtained using (a) GNBC model. (b) SVM classification. (c) KNN classification. (d) DTC model.

Fig. 8 includes confusion matrices for:

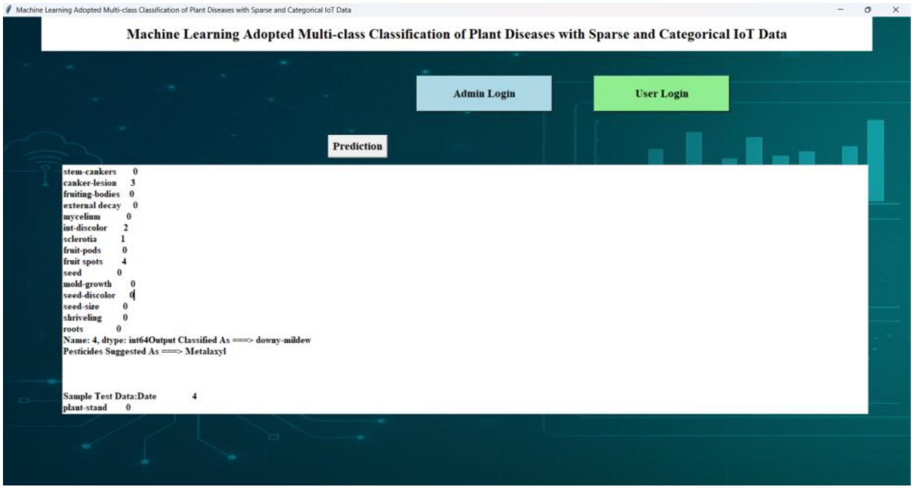
(a) Gaussian Naive Bayes (GNBC) model: Showing its classification performance.

(b) SVM Classifier: Illustrating how well the SVM model differentiates between disease classes.

(c) KNN Classifier: Visualizing the performance of the K-Nearest Neighbors algorithm.

(d) Decision Tree Classifier (DTC): Depicting the confusion matrix of the decision tree model, which may show superior performance compared to the others.

In the Fig. 9, the application displays the outcome of a prediction on a test dataset. It shows the classified disease and the corresponding pesticide recommendation, thereby completing the full cycle—from data input to actionable output for disease management.



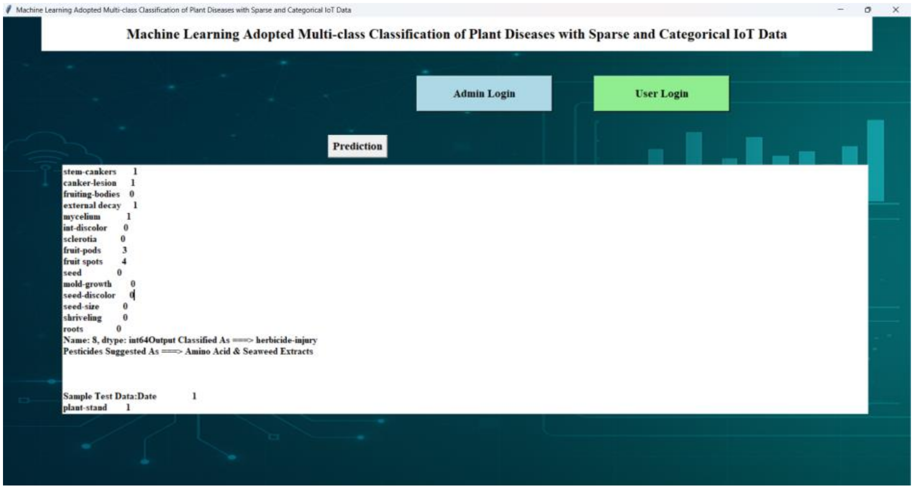


Fig. 9: Sample prediction and pesticide suggestions on test data.

Table. 1: Performance comparison of existing GNBC, SVM, KNN, and proposed DTC models.

Model/Metric	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
GNBC model	72.68	72.58	72.72	68.17
SVM classifier	92.36	92.92	92.56	92.09
KNN classifier	97.91	97.62	97.56	97.42
Proposed DTC model	99.07	98.88	98.76	98.86

Table. 1 presents a comparative analysis of four machine learning models—Gaussian Naive Bayes Classifier (GNBC), Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and the proposed Decision Tree Classifier (DTC)—based on key performance metrics: Accuracy, Precision, Recall, and F1-score. The GNBC model achieved an accuracy of 72.68%, with a precision of 72.58%, recall of 72.72%, and an F1-score of 68.17%, indicating moderate performance across all metrics. In contrast, the SVM classifier significantly improved the results, with 92.36% accuracy, 92.92% precision, 92.56% recall, and a balanced F1-score of 92.09%. The KNN classifier performed even better, attaining 97.91% accuracy, 97.62% precision, 97.56% recall, and an F1-score of 97.42%, showcasing its robustness and reliability. However, the proposed Decision Tree Classifier (DTC) outperformed all other models with an outstanding accuracy of 99.07%, precision of 98.88%, recall of 98.76%, and F1-score of 98.86%.

These results demonstrate the superior effectiveness of the proposed DTC model in accurately classifying plant diseases, offering a highly reliable solution for precision agriculture.

5.CONCLUSION

In conclusion, the project successfully demonstrates the power of machine learning in revolutionizing plant disease diagnosis through the development of a comprehensive system that integrates data ingestion, preprocessing, model training, and prediction with an intuitive GUI. By leveraging sparse and categorical IoT data, the system effectively addresses the limitations of traditional, manual methods of disease identification, providing rapid, accurate, and scalable diagnosis. Advanced preprocessing techniques, including label encoding and the application of SMOTE, ensure that the data is optimally balanced and suitable for training. Among the various models tested, the proposed Decision Tree Classifier outperformed others in terms of accuracy, precision, recall, and F1-score, underscoring its suitability for the complexities of multi-class classification in agricultural contexts. The robust performance of the system, coupled with actionable pesticide recommendations, positions this approach as a significant step forward in precision agriculture. Ultimately, this innovative framework not only enhances early detection and intervention but also contributes to cost-effective, sustainable, and scalable disease management, paving the way for further advancements in agricultural technology and data-driven decision-making.

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