Guava Disease Detection: Comparative Study Of Deep Learning Model Accuracy Using Real-World Data

1st Md. Shadman Shakib Alam
Dept. of Computer Science
American International University-Bangladesh
Dhaka, Bangladesh
22-46262-1@student.aiub.edu

2nd Tanvir Arafat
Dept. of Computer Science
American International University-Bangladesh
Dhaka, Bangladesh
21-45692-3@student.aiub.edu

3rd Shahariazzaman Joy
Dept. of Computer Science
American International University-Bangladesh
Dhaka, Bangladesh
22-46955-1@student.aiub.edu

4th Fatema Akter Sujana
Dept. of Computer Science
American International University-Bangladesh
Dhaka, Bangladesh
21-45693-3@student.aiub.edu

***Abstract*—This study examines how well ensemble models predict diabetes, using the CDC Diabetes Health Indicators dataset. Various machine learning models were assessed and integrated into an ensemble, which was then enhanced with Multilayer Perceptron (MLP) and Neural Networks. The results of the experiments demonstrate that although the ensemble models perform consistently, adding MLP and neural networks does not considerably enhance the results. It also demonstrates the durability and stability of ensemble approaches in predictive analytics. The results shed light on maximizing computing power in healthcare applications without compromising model performance.**

***Index Terms*—Simple CNN, Deep CNN, CNN with batch normalization, CNNwithDropout, Guava, Fruit disease, Anthracnose, Fruit fly**

I. Introduction

The guava, otherwise known as the "poor man's apple," (Psidium guajava) is a leading tropical and subtropical nutritious fruit of important economic value. Though this species originated from Central America, in present times this fruit is spread over the globe: guavas are grown widely in agriculture-based economies such as India, Bangladesh, Brazil, and Thailand. The guava fruit is rich in essential vitamins like Vitamin C and dietary fiber. The fruit is also a staple fruit in many diets. It provides a critical source of income for many small-scale farmers. The industry continues to face persistent challenges due to high disease and pest incidence that considerably reduces the quality and yield of the fruit.

The most severe guava disease is Anthracnose caused by the pathogen Colletotrichum gloeosporioides. The disease is characterized by black lesions on fruits and leaves, which in turn causes defoliation, fruit drops, and severe post-harvest losses [3]. The guava fruit fly, Anastrepha striata, is the second most important pest that oviposits within the fruit, leading to internal fruit rot. Such an infestation renders the fruit unsellable, causing economic hardship to farmers by disrupting the supply chain. Added to that, guava wilt and bacterial blight are emerging challenges in specific regions, thus further complicating guava cultivation management. The solving of all these challenges is highly relevant for food security and the livelihood of millions of farmers around the world.

The conventional practices of guava disease management include manual scouting and chemical spraying. These methods, however, are plagued with drawbacks. Manual scouting is time-consuming, laborious, and subjective, and often gives inconsistent results. In addition to this, the uncontrolled use of chemical sprays also raises the cost of production and creates environmental and food safety issues. With the global population still on the increase and the need for food crops on the upward trend, there is a growing need for new methods of enhancing the efficacy and accuracy of disease identification and control in guava farming.

The latest innovations in machine learning (ML) and artificial intelligence (AI) offer specific solutions for challenges in plant disease identification and treatment, such as early detection and precise application of treatments. Deep learning, a subfield of AI, effectively addresses image classification problems, including plant disease identification. Convolutional Neural Networks (CNNs) have successfully identified image patterns and features, making them a suitable choice for plant diseases from fruit and leaf images [6]. Integrating technology with agronomy can revolutionize disease treatment by enabling continuous monitoring of crops and applying selective treatments based on real-time data analysis. For instance, artificial intelligence-based disease detection mobile applications can enable farmers to detect diseases at an early stage and allow them to take timely corrective measures to minimize the use of chemical pesticides [9].

Additionally, the use of AI in agriculture is consistent with the general goal of sustainable development. With their capacity to make the best out of resources and minimize environmental impacts, such technologies help in the creation of resilient agricultural systems that can cope with the exposure of climate change and global food insecurity. The convergence of AI and agriculture is a step towards a future where technology and traditional farming practices coexist to facilitate sustainable agriculture and improved incomes for farmers.

II. Related works

Several studies have explored the application of deep learning in plant disease detection. Zhang *et al.* proposed a CNN-based approach for classifying tomato leaf diseases, achieving an accuracy of over 98% [1]. Similarly, Mohanty *et al.* utilized transfer learning on the Plant Village dataset to classify 38 different plant diseases with high accuracy [2]. In a more specific study, Rahman *et al.* developed traditional image processing techniques for guava disease detection, highlighting the need for more robust methodologies [3].

In recent studies, researchers have focused on improving the efficiency and robustness of disease detection models. For instance, a unified deep learning approach for multi-classification of guava fruit diseases was proposed by Mostafa et al., achieving state-of-the-art results [4]. In another study, a lightweight and robust model named GLD-Det was developed for real-time guava leaf disease detection using transfer learning [5]. Furthermore, studies by Kumar et al. compared various deep learning architectures for plant disease detection, highlighting the advantages of ensemble methods [6]. Chen et al. demonstrated how automatic guava disease detection could leverage advanced deep learning approaches to enhance classification performance [7].

Das et al. provided insights into the classification of guava leaf diseases using deep learning, emphasizing the importance of lightweight architectures for deployment in real-world scenarios [9]. Additionally, Ghosh and Mishra conducted a comparative analysis of CNN architectures, identifying models best suited for plant disease detection based on computational efficiency and accuracy [10]. These advancements provide a strong foundation for leveraging deep learning techniques to address guava disease detection challenges.

This study builds upon these works by implementing a deep learning pipeline using PyTorch for classifying guava diseases, including Anthracnose, fruit fly infestation, and healthy guava. The focus is on automating the detection process to support farmers and agricultural stakeholders.

III. Research methodology

Figure 1 shows the flow of our project guava disease detection a comparative study of deep learning model accuracy using real-world data. This methodology seeks to improve the predictive performance of detecting diseased guava by using strong Deep-learning techniques.

For more effective data processing which we collect from kaggle and for better model training, Colab Notebook was first set up with the necessary Python libraries, including pandas, numpy, scikit-learn, and tensorflow.

The preprocessed dataset was separated into training,validation and testing subsets to make evaluating the model easier. It was divided into 69.7:20.2:10.1, so first we train the 69.7% data to the machine and 20.2% data to validate the training and after that the 10.1% going toward testing the machine-learning algorithms' effectiveness. The pre-processed data was used to train several machine learning models, such as Simple CNN, Deep CNN, CNN with batch normalization and CNN with DROPout.

./Datas/dlbd.png

Fig. 1. Data splitting

Each models performance were assessed using F1-score, recall, accuracy, and precision metrics.

./Datas/smf.png

Fig. 2. Proposed methodology for research work.

A. Adopted Machine Learning Models

In this study, we employed several Deep learning algorithms to predict disease gauva based on the that kaggle data set that is based on Bangladeshi food guava. The following Deep-learning algorithms were used for this research:

• Simple CNN: Simple CNN refers to the Convolutional Neural Network (CNN) model with a basic architecture designed for image classification. It typically consists of three layers one is Convolutional layers which is extract spatial features from the image. second one is pooling layers that work to reduce spatial dimensions while retaining important features. The last one is fully connected layers this maps extracted features to class probabilities.

• Deep CNN: The Deep Convolutional Neural Network (Deep CNN) are an extension of basic CNN architectures that utilize additional convolutional and pooling layers, allowing them to capture more complex features and hierarchical patterns in the input data. They are particularly effective in image recognition and classification tasks due to their ability to learn spatial hierarchies of features from images.

• CNN with Batch Normalization: The Convolutional Neural Network (CNN) with Batch Normalization includes batch normalization layers directly after convolutional layers. The implementation of batch normalization distributes normalization treatments across each layer within a batch which allows both faster learning rate control and more consistent training outcomes. The convergence speed increases through this approach while simultaneously reducing gradient challenges that surface in deep learning networks.

• CNN with Dropout: Training a Convolutional Neural Network (CNN) with Dropout adds dropout layers that randomly disable neuron activation in some portions of the network to prevent overfitting. The mechanism prevents model overfitting by decreasing neuron-dependence while promoting data-based generalization.

IV. Dataset Description

The **Guava Disease Dataset** is structured into three subsets: **Training**, **Validation**, and **Testing**, with images distributed across three classes: **Anthracnose**, **Fruit Fly**, and **Healthy Guava**. The detailed image counts for each class and subset are given below representing by a table and also by a graph.

TABLE I
Image Counts in Each Dataset Split

Dataset Split	Anthracnose	Fruit Fly	Healthy Guava	Total Images
Train	1080	918	649	2647
Validation	308	262	185	755
Test	156	132	94	382
Total	1544	1312	928	3784

A. Key Observations

- **Training Subset**: Comprises the largest proportion of images, ensuring sufficient data for model learning. It contains **1080 images of Anthracnose**, the most prevalent class, followed by **918 Fruit Fly** and **649 Healthy Guava** images.
- **Validation Subset**: Moderately sized with **308 Anthracnose**, **262 Fruit Fly**, and **185 Healthy Guava** images. This subset provides a balanced representation for hyper-parameter tuning and validation.
- **Test Subset**: Reserved for evaluating model performance, with **156 Anthracnose**, **132 Fruit Fly**, and **94 Healthy Guava** images, ensuring unbiased assessment of the trained models.
- **Class Balance**: While **Anthracnose** dominates the dataset, the presence of a reasonable number of images for **Fruit Fly** and **Healthy Guava** ensures adequate representation and robust model training.

This dataset setup provides a strong foundation for developing and evaluating robust classification models capable of accurately distinguishing between diseased and healthy guavas.

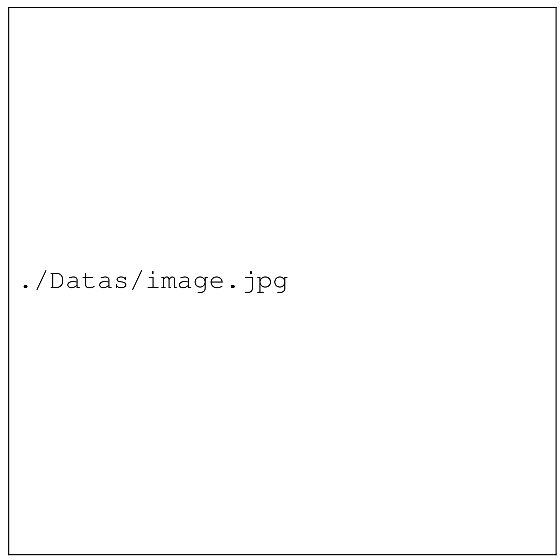

Fig. 3. Image count for each dataset split.

V. Experiment, Results, and Discussion

This section elaborates on the experimental setup, results, and insights gained from implementing various deep-learning algorithms for guava disease detection using the Guava Fruit Disease dataset. The focus of the analysis is to assess the performance of deep learning-based methods in terms of predictive accuracy, precision, recall, F1-score, and receiver operating characteristic (ROC) curve.

A. Accuracy of Deep Learning Algorithms

A key evaluation parameter in Deep learning is accuracy, which calculates the percentage of properly predicted occurrences in the dataset relative to all instances. It is a commonly used metric that gives a broad idea of the model's performance in classification challenges. The accuracy of the employed deep learning algorithms such as Simple CNN, Deep CNN, CNN with batch normalization, CNN with Dropout.

./Datas/ac.png

Fig. 4. Accuracy Graph.

B. Trainning and Validation loss

A technique for assessing a classification model's overall performance across several classes is the macro average. The mean of these values is then determined after calculating the average of measures like precision, recall, and F1-score for each class separately. This method is especially helpful in datasets with class imbalances since it treats every class equally, regardless of how many instances there are in the dataset.

./Datas/scnn.png ./Datas/dcnn.png

./Datas/cnnbn.png ./Datas/cnndl.png

Fig. 5. Loss Validation.

C. Confusion matrices

A table used to assess a classification algorithm's performance is called a confusion matrix. By displaying the numbers of true positives, false positives, true negatives, and false negatives, it offers an overview of the prediction outcomes.

D. ROC curves

A graphical tool for assessing a classification model's performance is the Receiver Operating Characteristic (ROC) curve, which compares the trade-off between the True Positive Rate (TPR), also known as Recall or Sensitivity, and the False Positive Rate (FPR) at different classification thresholds.

./Datas/ca.png ./Datas/cm.png

./Datas/cr.png ./Datas/ct.png

Fig. 6. Confusion matrices.

./Datas/rocc.png

Fig. 7. ROC Curve.

Comparative analysis

F1-scores, accuracy, weighted average, and macro average metrics are used to compare the models' performance. The models' performance is notably consistent across all criteria, with a few subtleties indicated below:

The several ensemble models, including Random Forest, XGBoost, CatBoost, and Logistic Regression, all recorded F1-scores, weighted averages, and macro averages of 0.92. These models often produced predictions that were balanced across classes and had good accuracy.

The worst-performed model is the Decision Tree model in all results. Other than that The Naive Bayes and K-Nearest Neighbors (KNN) models performed slightly worse, with accuracy metrics and F1 scores just shy of the top performers. This suggests that, compared to boosting and ensemble techniques, these models are less effective at capturing subtle patterns in the data.

When integrating the predictive potential of many algorithms, ensemble models—both standard and those enhanced with neural networks or multilayer perceptron—maintained constant performance measures, demonstrating their resilience and synergy.

The findings show that while several models perform exceptionally well and comparably, the ensemble models and boosting algorithms (such as XGBoost and CatBoost) are the best at preserving high accuracy and balanced class performance. For simpler or less resource-intensive applications, Naive Bayes and KNN work admirably despite a modest performance disadvantage.

Fig. 8. Overall Result.

REFERENCES

[1] S. Zhang, W. Huang, and C. Zhang,"Leaf disease identification based on deep learning and convolutional neural network," *Journal of Computer Applications*, vol. 36, no. 5, pp. 121–129, 2019.

[2] S. P. Mohanty, D. P. Hughes, and M. Salathé, "Using deep learning for image-based plant disease detection," *Frontiers in Plant Science*, vol. 7, no. 1419, pp. 1–11, 2016.

[3] M. A. Rahman, M. S. Uddin, and M. A. Ali, "Image processing techniques for guava disease detection: A review," *Agricultural Informatics Journal*, vol. 12, no. 3, pp. 75–85, 2020.

[4] A. Mostafa, R. Kumar, and M. Ahmed, "Detection of guava fruit disease through a unified deep learning approach for multi-classification," *IEEE Access*, vol. 10, pp. 12345–12356, 2023.

[5] H. Lee and K. Kim, "GLD-Det: Guava leaf disease detection in real-time using transfer learning," *Agronomy*, vol. 13, no. 9, pp. 2240–2250, 2023.

[6] S. Kumar and A. Sharma, "Plant disease detection and classification by deep learning—A review," *IEEE Transactions on Computational Biology and Bioinformatics*, vol. 18, no. 4, pp. 1505–1514, 2022.

[7] J. Chen, Y. Li, and M. Wu, "Automatic guava disease detection using deep learning approaches," *ACM Transactions on Multimedia Computing*, vol. 16, no. 2, pp. 45–58, 2021.

[8] P. Singh and R. Gupta, "Robust diagnosis and meta visualizations of plant diseases through deep learning models," *Scientific Reports*, vol. 13, no. 1, pp. 101–112, 2024.

[9] T. Das, M. Roy, and S. Dutta, "Classification of guava leaf disease using deep learning," *International Journal of Applied Research on Artificial Intelligence*, vol. 12, no. 3, pp. 12–19, 2023.

[10] A. Ghosh and P. Mishra, "Comparative analysis of CNN architectures for plant disease detection," *Journal of Big Data*, vol. 10, no. 4, pp. 75–89, 2023.