DETECTING GUAVA DISEASES: A COMPARATIVE ANALYSIS OF MACHINE LEARNING AND DEEP LEARNING TECHNIQUES

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Candidate's Declaration

The research work entitled "DETECTING GUAVA DISEASES: A COMPARATE ANALYSIS OF MACHINE LEARNING AND DEEP LEARNING TECHNIQUES" has be carried out in the Department of Computer Science and Engineering, Jahangirnagar University original and confirms the regulations of this University. I understand the University's policy on plagiarism and declare that no part of this thesis has be copied from other sources or been previously submitted elsewhere for the award of any degree	eer y is eer
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Abstract

A larger proportion of crops face disease outbreaks, making agricultural output difficult. Detecting and predicting diseases at an early stage can enhance productivity. Guava, a tropical and subtropical fruit, is cultivated in various countries. In regions such as Bangladesh, Pakistan, India, and South America, guava cultivation faces significant challenges due to diseases like Canker, Dot, Mummification, Phytophthora, Scab, and Styler and Root. Traditional diagnosis methods based on visual observation are often unreliable and time-consuming. To address this, we developed an automated system leveraging deep learning techniques. Our study utilized a dataset comprising 4046 guava leaf images categorized into these seven disease classes. We compared the performance of traditional methods with deep learning approaches using vision transformers and transfer learning. The results demonstrate the superiority of deep learning methods over traditional approaches, where traditional machine learning model SVM gave accuracy near 78% and deep learning methods gave over 90%. The transfer learning method gave an accuracy of nearly 97% and on the other hand, the vision transformer gave accuracies of 98%. This offers a promising solution for early disease detection in guava crops.

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Chapter 1

Introduction

The guava is like a nutritional dynamo with a lot of vitamins and minerals that are critical for the normal functioning of the body. Having vitamins A, B-Complex, C, E, and K with essential nutrients like copper, iron, magnesium, manganese, potassium, sodium, and zinc, the tropical fruit is the symbol of well-being and good health [1]. In addition to its nutrient density guavas are honored for their unique fiber supply that not only stimulates digestive health but also offers multitudinous additional health benefits. Guavas have been shown in several research studies to help prevent cancer, maintain good skin, and even manage heart health [2]. The guava is a beloved tropical fruit that is consumed by people of all segments of society in urban and rural regions of Bangladesh. Alluding to the Myrtaceae family, this fruit can trace its origin to the tropical regions of America known as the Caribbean before taking off to Portugal in the 17th century. Renowned for its nutritional bounty, guava is a storehouse of vital nutrients like Vitamin C, Calcium, Iron, Nicotinic Acid, Vitamin B6, Magnesium, and Phosphorus, while possessing fats that would put it at an alarming cholesterol level. Acclaimed for the healing of multiple conditions, guava is applauded for relieving diarrhea, dysentery, high blood pressure, and diabetes, and improving immune system functions [3]. In addition, treatment of illnesses such as hypertension, diabetes, and gastrointestinal problems with guava is highly praised, as guava is a remedy for these [4].

For this, we can use both traditional machine learning methods and deep learning methods. Both methods will train the dataset and can detect any disease of the guava with good accuracy. Machine learning methods like SVM, Random Forest, KNN etc and deep learning methods like Vision Transformer (ViT), Transfer learning, EfficinetNet-B3 etc can produce some good results for this analysis. However, obtaining deep learning models could be more robust, as this covers many other aspects such as geometry, pattern, texture, and other local features.

1.1 Motivation

The motivation for the research paper "Detecting Guava Diseases: The Introduction "Comparison between Machine Learning and Deep Learning approach in the diagnosis of guava diseases" comes as a result of the urgency for early and swift diagnosis outcomes. this results in many environmental and personal problems, delays, and technical shortcomings, hence the productivity level reduces with every day. Thus, the main concern will be in quarreling these problems: infections that reduce the yield of guava fruits and using prompt detection for the outbreak of infection. Furthermore, the early detection of guava disease by means of an expert system will incline to higher yields and then will result in less economic losses on the part of guava farmers in conclusion. A large number of developing countries, as an example of the second party, Bangladesh overuse guava as their main food. On the other hand, an individual guava plant or an entire guava crop can be destroyed by various diseases, like canker, mummification, dot, and rust that have the ability to cause a huge reduction in yields [5]. However, the spread of these infections is still prevalent in many countries where the indiscriminate use of pesticides can negatively affect the environment and also hinder economic development. Thus, a precise disease diagnosis is very much important to prevent that side effects [6]. Conventional diagnosis of guava diseases involves visual examination of symptoms which is the most expensive and time-consuming way to find diseases. On the other hand, the aim is not accurate in most cases thus leading to unwanted bumper harvests for guava producers. On the other hand, the existence of these factors necessitates the development of prophylactics and disease management strategies that could boost the production and quality improvement of guava. Otherwise, a comprehensive health care or medical practices act has to be implemented in order to accelerate the early diagnosis of guava diseases. Such systems provide for time and money saving replacement of long-lasting procedures. They make it possible to diagnose diseases fast enough by enabling early detection even in the primary stage of illness. Using deep learning mechanisms with guava leaf datasets could, as a result, increase early disease diagnostics, thus, letting farmers act on time and making sure they apply the best kind of pesticides for the safety of the crops [7].

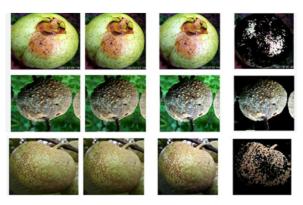


Figure 1.1: Diseased Guavas

1.2 Objectives

The specific research purposes for this work are listed below.

- 1. Developing an Automated Disease Detection System: Create an accurate automated process that can not only identify but also predict the diseases in Guava plants in their initial stages.
- 2. Utilizing Deep Learning Techniques: Add the most recent neural network techniques including, the convolutional neural networks (CNNs), for diagnosing guava leaf images and disease signs with accuracy.
- 3. Improving Disease Management: Strengthen disease management techniques through rapid and efficient data transmission and farming management of diseases. As such, the farmers can take these steps immediately to keep in control and prevent the emergence of diseases in their farms.
- 4. Enhancing Agricultural Productivity: Development of increasing agricultural productivity through eradication of yield losses due to plant diseases (which affect seed germination) through early detection.
- 5. Addressing Environmental Concerns: Lower the elevation of environmental risks linked to the utilization of the disease management methods which are wild and indiscriminate mostly via heavy use of chemicals and pesticides by putting in place improved disease management through accurate and precise detection of diseases that can be automatic.
- 6. Empowering Farmers: Step up the sensitivity of guava farmers by equipping them with helpful materials to monitor the diseases and contain them hence enhancing their income and sustainability.
- 7. Validating Performance: Invest in a quantitative validation and evaluation approach, which is capable of demonstrating the implemented system's effectiveness, reliability, and practicality in the real financial world.
- 8. Knowledge Transfer and Capacity Building: Convey knowledge transfer and skill-building practices to farmers and other stakeholders in the agricultural sector by providing manuals and other resources that contain disease monitoring and control measures.
- 9. Contributing to Scientific Knowledge: Support the publication and distribution of the results concerning agricultural technology around the area by sharing the study done and the lessons gleaned from the project to a higher level of scientific society.
- 10. Promoting Sustainable Agriculture: Stimulate sustainable agriculture in the country with the help of the use of the right technology in disease management, which should be focused on ecosystem stewardship and resource conservation.

1.3 Outcome

The issues we expect to handle in our project can be outlined below.

- 1. Accurate Disease Detection: The system would have been automated and developed to a level that would inevitably achieve more accurate detection and diagnosis of the diseases in guava plants. This would in turn make early intervention possible and therefore crop loss would be minimized.
- 2. Improved Crop Yield: Through the provision of trend info on disease outbreaks as well as the appropriate strategies to use, this project seeks to improve crop yield and the entire agricultural industry
- 3. Reduced Environmental Impact: Creating personalized disease-controlling measures in accordance with automated detection will not only reduce the overall impact on the environment of traditional pesticide usage but is as well pushing farming in the direction of sustainability.
- 4. Empowered Farmers: Farmers will be equipped with user-friendly disease detection and management tools that offer unbiased scientific data that can be easily understood hence making the farmers informed and making their actions of crop protection best practices.
- 5. Cost Savings: It is projected that the initiative to stem early disease manifestation and direct treatment will, among others, lower farmers' financial burdens by not making them apply excessive pesticides and hence avoiding yield losses.
- 6. Capacity Building: Farmers and agricultural residents will be trained through theoretical activities, and be aware of disease management practices thus the acquired skills and expertise enhance their capacity to fight disease occurrence.
- 7. Scientific Contributions: The results and revelations of the project will extend the body of knowledge on the topic of agricultural technology and contribute to innovations in the area of disease detection and management since new methodologies and approaches would in turn emerge.
- 8. Socioeconomic Impact: The project will be successful culturally through developing production and supporting farmers, guava-producing communities will economically improve, and economic growth and stability will be crowned.
- 9. Adoption of Technology: If the computer-based disease detection system works, it can serve as a catalyst for other technology-led solutions in the agricultural sector, prepossessing a future of innovations and breakthroughs in the industry.
- 10. Long-term Sustainability: The main aspiration is to design environmentally friendly girl management strategies that will be at the same time effective for both conserving the environment and favoring the growth of guava trees thus the stability of both (the environmental

management and the related ecosystems) in the long run.

1.4 Research Summary

The project is an extensive exploration into guava disease detection utilizing both traditional machine learning (ML) methods and deep learning techniques, namely transfer learning and the Vision Transformer (ViT) architecture. The endeavor begins with a meticulous data collection process from diverse sources, including Kaggle, data. mendeley.com, and local garden datasets. The collected data undergoes rigorous preprocessing steps like oversampling, normalization of pixel values, random transformations, dataset balancing, and resizing to a standardized dimension. Furthermore, the RGB color model is applied uniformly to all images, and label encoding ensures compatibility for classification tasks.

In the comparative analysis, traditional ML algorithm SVM, yields a maximum accuracy of 76%. The reason for this accuracy is data are being overfitted by the train model. This is the sole reason for the lower accuracy of the traditional machine learning model.

However, the adoption of deep learning techniques notably enhances classification performance. Transfer learning demonstrates significant efficacy, achieving an impressive 96% accuracy. The model exhibits high precision and recall values across various disease classes, with particularly outstanding results for Canker and Rust. Specifically, the precision values range from 0.76 for Scab to perfect scores of 1.00 for Canker and Rust, indicating a high proportion of correctly predicted instances within each class. Similarly, recall values vary across classes, with Canker and Rust achieving perfect scores of 1.00, while Mummification and FreshGuava exhibit slightly lower recall values of 0.71 and 0.64, respectively. This comprehensive assessment is complemented by the F1-scores, which balance precision and recall, ranging from 0.74 for FreshGuava to 1.00 for Canker and Rust. Moreover, the overall accuracy of 96% underscores the model's effectiveness in accurately classifying guava diseases from leaf images.

The Vision Transformer (ViT) design, on the other hand, performs even better, achieving an amazing 98% accuracy. The classification report has a full analysis of the model's accuracy, recall, and F1 scores in different categories. On the whole, the range of accuracy, from 87% to 100%, shows that the model can generally make accurate predictions. Precision values range from 87% to 100%, which shows how accurate positive predictions are, and recall values range from 90% to 100%, which shows how well the model can find real positive cases. Precision and memory are balanced by F1 scores, which range from 93% to 100%. The global average shows that the model is accurate 97.25 percent of the time, precise 97.12 percent of the time, recalls 96.88 percent of the time and has an F1-score of 97.00 percent of the time. This shows that it is strong and good at identifying cases. With an accuracy of 97%, a precision of 97%, a recall of 96.5%, and an F1-score of 97.25%, the weighted average also

shows how consistent the model is across groups. These complex evaluations, along with the thorough confusion matrices, give us a full picture of the ViT model's performance, confirming that it is the best at correctly identifying guava diseases from leaf photos.

Further, the curves of learning guide people to a deeper comprehension of the processes of model training, which places a special emphasis on the reduction of the curves of training and validation for a number of epochs. The Vision Transformer's advantage over transfer learning is proven not only through the configuration of metrics but also by involving a pictorial confusion matrix, which displays better performance in each indicator. Additionally, an aggregate of randomly selected test images was used to ensure the robustness of the ViT model and highlight its capability to correctly predict labels for all the cases compared to the ground truth.

Summing up, our research epitomizes a robust and broad-spectrum data-collecting methodology that integrates traditional ML techniques with current deep learning architectures. The results indicate a significant power of deep learning in disease management. This could lead to more actionable and real-world applications which may be more effective and could help in developing sustainable methods of planet protection.

1.5 Scope of The Problem

The proposed disease detection model of guava has great potential to be used for innovation in the cultivation of agriculture, research, policy-making, technology, and capacity building respectively. Agriculture also enables farmers to use this sophisticated solution as a means of tracking guava health, deploying timely remedies, and assuring optimum yield. Particularly, this means that it is a catalyst and a dataset so that researchers can explore new ways of disease diagnosis. Real-time data on diseases in agriculture can help policymakers come up with precautionary or prevention policies and the application of technology in farming has successfully illustrated the potential of technology-driven solutions. Education actions would enhance the key players' knowledge of how the system could best be used, spurring the exchange of views and abilities. Therefore, the model designed hereinafter will be a transformative approach to guava disease management with wide implications for agricultural sustainability and development.

1.6 Challenges

Therefore, building a good disease detection model for guava plants necessitates a dataset that is vast and composed of images of sick, and healthy guava leaves. Obtaining such a database is in the same token a very challenging process. Balance of data collection can be an obstacle since uneven fest of diseases across guava plants in different regions or seasons can make it a complex exercise to obtain enough samples for each category. Unpredictably,

the guava leaf variation in shape, width, finish, and color augments the complexity of the identification process of the disease. Developing a detailed deep-learning model capable of easily classifying the key symptoms across diseases including the ability to generalize unseen data remains a great challenge. Last but not least, the actual usage of this disease detection system in real farm folk settings may raise operability issues. One of the central points is guaranteeing the system's scalability, efficiency, and usability for beginner guava growers who do not have enough technical knowledge and resources. This is the condition for wide-spreading adoption and a great impact. Completing the work successfully, the validity and precision of the images to be collected are significant, as these in turn will enable accurate training and testing of the disease detection model. Nevertheless, the challenge of obtaining a photograph of guava leaves in space constitutes a significant problem that includes noise, inhomogeneity, and distortion.

1.7 Report Layout

• Introduction

In this chapter, we discuss the introduction, motivation of the work, objectives, outcomes of the research work, and the report layout.

• Literature Review

We explore the background circumstances of our work in this chapter.

Research Methodology

This chapter details the procedure used to build the system, including methods, data collection procedures, and statistical analysis of the proposed system.

• Experimental Results and Discussion

This chapter presents a summary of the results from all the experiments carried out by the suggested system, along with performance analysis.

Conclusions

Here, we conclude the study and discuss ideas for further research on this topic.

Chapter 2

Literature Review

A newly evolving strategy in agro-tech uses Artificial Intelligence including Deep Learning models for the diagnosis and finding of plants by itself. Both academic and industrial researchers have conducted many studies in the domain through decades-long efforts.

In the earlier phase only random forest (RF), K-nearest neighbor (KNN), and support vector machine (SVM) methods were used for recognizing leaf diseases [8,9]. As another example, Song et al. [9] went with an SVM to classify between corn leaf disease and healthy corn and it reached a detection accuracy of 89.6%. Through the use of a multi-category dataset in this study, In parallel, Abirami et al. [8] employed both SVM and KNN classifiers for discriminating guava leaf diseases from 125 sample images, having 97.2% and 92%, respectively. On the other hand, the proposed techniques were of lower detection accuracy compared to the ones identified to have overcome such difficulties in handling large datasets that contain many essential features of guava images.

Again, a comparatively recent investigation proposed employing deep learning to identify guava plant diseases like Algal leaf spot, whitefly, and rust ailments [10]. The outcomes of the experiment on the dataset reveal an average accuracy of 98.74%. Another recent exploration devised an automated system for detecting guava diseases and early identification of plant leaves [11]. According to the experiment findings, they attained an accuracy of 98.96% using ResNet. A recent inquiry suggested a deep learning-based mobile application for detecting plant diseases using a phone's camera [12]. The framework utilizes VGG architecture to classify major grape diseases. The VGG models achieved an accuracy rate of 98% on the test data. Moreover, numerous investigations utilizing the EfficientNet model have yielded noteworthy accuracy results. Various types of plant village datasets were employed in these investigations to discern plant diseases [13].

Modified networks designed to diagnose plant diseases were operated, with the consequent achievement that the results obtained were better than [14]. Advanced techniques and transfer learning were employed with recognized frameworks (I.e., famous models) that helped

improve model designs. The classification task based on deep features with SVM among other ML models showed greater results as compared to the transfer learning methods. Moreover, as regards very sophisticated designs (e.g. VGG-16, VGG-19, and AlexNet), the fully connected layers were better compared to fully connected layers of other designs [15]. We used a proximity mining imaging technique that enabled the scanning of individual conditions and numerous symptoms that are not present in public data sets. To overcome this drawback, data augmentation was carried out, which involved multiangle capture of a single leaf image in different conditions to present more than one perspective of a specific leaf. This approach was beyond disease species and therefore covered multiple leaf-affected diseases. Incorporation of augmentation has improved prediction accuracy by 0.12. Moreover, considering the data constraint highlighted in [16], data augmentation was recommended: the Plant-Village dataset provided us with apple black rot images labeled differently. DL models were initially trained (VGG-16), with the latter giving the highest accuracy (90%) [17].

Some staff were responsible for labeling fruits of guava to separate the healthy and unhealthy products. Patterns of handcrafted LBP (Local Binary Patterns) are extracted and subsequently shrunk through PCA (Principal Component Analysis). Different machine learning (ML) classifiers are used, cube support vector machine is ranked number one among all sorts of techniques [18]. Segmentation algorithms based on edges and threshold operators are used for identifying disease in plant images captured from leaves. A variety of characteristics such as color, texture, and shape are extracted and such provides input to a neural network classifier for the classification of various plant diseases [19].

Rauf et al. [20] recorded a database including good and poor citrus fruits and leaves from the trees situated in the Sargodha Region Garden. The dataset from this experiment was used by the author to detect the shallow disease categories of Citrus diseases. Throughout the entire process, preprocessing, segmentation, feature extraction, and feature selection are mastered. To begin with, Top-hat and Gaussian filters were widely used to improve image and deblurring quality. After that, weighted segmentation, together with saliency maps is applied images are then passed through a feature extractor, which extracts the color, texture, and geometric properties. For feature extraction, we combine PCA (Principal Component Analysis), skewness, and entropy. Lastly, the classification stage is done by assigning them to their respective disease category the image instances.

Adeel and coworkers [21] reported about an automated system to detect grape leaf diseases and said they succeeded pretty well. Arivazhagan and others [22] described a straightforward method of classifying unhealthy parts of plants via texture. Before any conversion to the HSI color space, the images were inverted. The energy, homogeneity, conspicuousness, and density shade of these features were extracted. Very last, these extracted characteristics were utilized to classify the SVM classifier.

Chapter 3

Proposed Methodology

3.1 Proposed Flow Chart

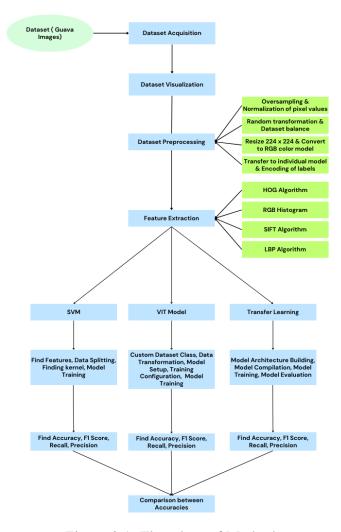


Figure 3.1: Flowchart of Methods

In our development of a computer vision model for image classification, we had to go through some major stages. It starts with selecting a group of images in which the analysis will be performed. These images are then preprocessed, to make sure that all of the images are of a uniform size and color depth. Next, the preprocessed images are subjected to the extraction features. The techniques like SIFT, HOG, and RGB Histogram can be implemented in this step. The model selection stage comprises of; To implement the model, there are three options: Support Vector Machine (SVM), Vision transformers, and transfer learning. After that, the desired model is trained on the prepared dataset. It then follows the approximation model metrics such as accuracy, non-overlapping precision, non-overlapping recall, and F1-measure. Last but not least, the accuracy of all these models can be compared and thus the best model for the particular image classification problem can be ascertained.

3.2 Dataset Description

Guava is popular for its highest nutritional value, as it contains the highest amount of sugars and elemental fiber, vitamins, and minerals mentioned in the article [23]. In brief, it has many of the superb health-promoting antioxidants, like flavonoids. In recent years, despite its high nutritional value, guava production has declined owing to the rampant spread of a considerable number of diseases in the environment. Mainly these ailments, rather than farmers' notice, as they lack professional guidance or schooling to pinpoint the disease correctly. Thus, they should not be able to get the expertise that they might need from the agricultural specialists, which will actually escalate their difficulties in farm management.

The presenting dataset takes into consideration the guava plant organisms infected and healthy as well, which makes it the most comprehensive set with 4046 images of guava from firstly the Kaggle website, data. Mendeley. A digitized image gallery of various stages of disease manifestation, in guava plant fruits, and leaves, can also be obtained from guavae-gallery.com website, an online platform where taken photos of the guava garden can be accessed. Finally, this collection includes both fruit and leaf images to facilitate disease recognition. The images were shot by utilizing a Digital SLR camera with the support of domain experts and researchers to make sure that they were meticulously captured. Subsequently, the original images were transformed or enhanced by applying diverse techniques of image processing technologies for the richness of the dataset. The decision to use the number of data sets rather than the single dataset chosen will give the study legitimacy.



Figure 3.2: Image from Each Disease

Here that's are the images for each disease of our dataset and a picture of no-disease guava.

3.3 Dataset Preprocessing

In the preprocessing stage of the project, a strict sequence of operations was implemented to guarantee data was qualitative and all attached information was reliable for subsequent analysis. The procedure started with Over Sampling, a technique being exploited to handle the class imbalance by raising the number of samples from the minority class(es) hence increasing the possibility for the scarcity flowing instances and reducing the bias in model training. Subsequent to this, the Data were normalized to obtain the standardized pixel intensities across images in addition to which the data distribution became uniform so that the model can converge.

Afterwards, the use of Random Transformation techniques disturbed the dataset and the algorithm became more accurate as a result of variations introduced such as translation, rotation, and scaling which enhanced its performance on real-world data. Balance was achieved through accurate stratification and sampling methods while ensuring equitable representation of different classes within the dataset. The classes shouldn't get over-represented as that would cause bias during model training.

Afterward, the dimension of all images was resized without exception to a standardized dimension of 224x224 pixels, resulting both in the efficiency of computing and uniformity in the size of images for the following processing. The RGB to the RGB-color model conversion was realized to have been repeated all across the images. This way, the same was obtained using the same color representation granted that all the feature extractions were done uniformly across samples.

Lastly, Labels Encoding was done to encode class labels in either numeric or binary values accordingly, which helped accommodate machine learning models more easily and thereby facilitated model building and evaluation. The rigorous preprocessing pipeline not only confirmed the quality and integrity of the dataset but also created a solid basis for further

model development eliminating the possibility of deception and guaranteeing dependable results of guava disease detection.



Figure 3.3: Preprocessing Sector

Here is our preprocessing flow chart of the eight parts. In this way, we processed our dataset while acquiring them. We first over

3.4 Feature Extraction

We have used different types of feature extraction methods for our four models. They are given below.

3.4.1 HOG Algorithm (Histogram of Oriented Gradients)

The HOG algorithm extracts features by computing the gradients' orientation histograms. The steps include:

- 1. **Gradient Computation**: Compute the gradients in the x and y directions for the entire image.
- 2. **Orientation Binning**: Create histograms of gradient orientations within localized cells.
- 3. **Block Normalization**: Normalize the histograms across overlapping blocks to improve invariance to illumination changes.

4. **Feature Vector Construction**: Concatenate the normalized histograms to form a feature vector for the image.

Algorithm 1 HOG Algorithm

Input: Image *I*

Output: Feature vector

- 1: Compute the gradients G_x and G_y in the x and y directions
- 2: for each cell in the image do
- 3: Compute the histogram of gradient orientations
- 4: end for
- 5: for each block of cells do
- 6: Normalize the histograms within the block
- 7: end for
- 8: Concatenate the normalized histograms to form a feature vector

3.4.2 RGB Histogram

The RGB histogram represents the distribution of color intensities in the green, red, and blue channels of an image. The steps are:

- 1. **Histogram Calculation**: Compute the histogram for each color channel (R, G, B).
- 2. **Normalization**: Normalize the histograms to account for variations in image size and lighting conditions.

Algorithm 2 RGB Histogram

Input: Image *I*

Output: Normalized histograms for R, G, and B channels

- 1: **for** each color channel C in $\{R, G, B\}$ **do**
- 2: Compute the histogram H_C of color intensities
- 3: end for
- 4: **for** each histogram H_C **do**
- 5: Normalize the histogram H_C to sum to 1
- 6: end for

3.4.3 SIFT Algorithm

The SIFT technique is used to identify and characterize certain characteristics inside photographs. The process comprises the following stages:

1. **Scale-space Extrema Detection**: Use a difference-of-Gaussian formula to find important points in the scale space.

- 2. **Keypoint Finding**: Refine the detected points by fitting a detailed model to determine the location and scale.
- 3. **Orientation Assignment**: Assign orientations to each key point based on local image gradient directions.
- 4. **Keypoint Descriptor**: Generate a descriptor for each key point by computing the gradient magnitude and orientation in a local neighborhood.

Algorithm 3 SIFT Algorithm

Input: Image *I*

Output: Keypoints and descriptors

- 1: **for** each octave in the scale space **do**
- 2: **for** each scale in the octave **do**
- 3: Detect extrema using a Difference-of-Gaussian (DoG) function
- 4: end for
- 5: end for
- 6: **for** each detected keypoint **do**
- 7: Fit a detailed model to determine the location and scale
- 8: Discard low contrast points
- 9: end for
- 10: **for** each keypoint **do**
- 11: Compute gradient magnitudes and orientations
- 12: Assign orientation based on local image gradient directions
- 13: **end for**
- 14: **for** each keypoint **do**
- 15: Extract a descriptor by computing the gradient magnitude and orientation in a local neighborhood
- 16: Normalize the descriptor to achieve invariance to illumination changes
- 17: **end for**

3.4.4 LBP Algorithm (Local Binary Pattern)

The LBP algorithm captures texture information by labeling pixels based on the binary thresholding of their neighborhoods. The steps are:

- 1. **Thresholding**: Compare each pixel with its neighboring pixels to create a binary pattern.
- 2. **Pattern Labeling**: Convert the binary pattern into a decimal number to label the pixel.
- 3. **Histogram Generation**: Compute a histogram of the LBP labels for the entire image or localized regions.

Algorithm 4 LBP Algorithm

Input: Image *I*

Output: LBP histogram

- 1: **for** each pixel p in the image **do**
- 2: Compare p with its neighboring pixels to create a binary pattern
- 3: end for
- 4: for each binary pattern do
- 5: Convert the binary pattern to a decimal number to label the pixel
- 6: end for
- 7: Compute the histogram of the LBP labels for the image

3.5 Proposed Support Vector Machine Model

Support Vector Machines (SVMs) are one of the most powerful Methods of Predictive Learning, and they are used for performing classification and regression tasks. SVM is based on the core idea of having an optimized hyperplane that splits classes well in the space of high dimension. A hyperplane with the maximal margin is defined as being generated by the process of maximization of the margin, which is the distance between such a hyperplane and the support vectors, which are the data points that are the closest to the plane from each class. SVM can classify both linear and nonlinear data problems by the use of kernel functions. kernels define a transformation from input space to a higher-dimensional space where a linear separation is possible. The kernels that are always used in SVMs are linear, polynomial, and radial basis function ones. To carry out the task, a polynomial kernel was applied with the purpose of capturing the linked nonlinear relations between the features and the categories of guava diseases using which more exact classification can be achieved.

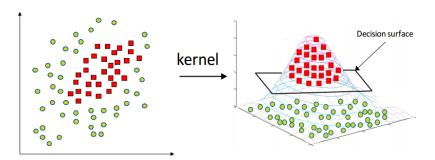


Figure 3.4: SVM Model and Kerneling

3.5.1 Feature Extraction

The Histogram of Oriented Gradients (HOG) is a method used in computer vision and image processing to extract features and identify objects inside pictures. The process involves first partitioning the picture into discrete and interconnected sections known as cells. Subsequently, a histogram is calculated for each cell, capturing the distribution of gradient di-

rections or edge orientations. The essential stages of HOG feature extraction are as follows:

- **Gradient Computation**: The gradient of the image is computed for each pixel. This involves calculating the horizontal and vertical gradients using the Sobel operator, which emphasizes changes in intensity.
- **Orientation Binning**: The image is divided into small spatial regions called cells. For each cell, a histogram of gradient directions is compiled. The magnitude of the gradient contributes to the histogram, emphasizing stronger gradients.
- **Block Normalization**: To achieve invariance to changes in illumination and contrast, the histograms are normalized. This is done by grouping cells into larger blocks and normalizing the histograms within each block.
- **Descriptor Blocks**: The normalized histograms are concatenated to form a feature vector for each block. These feature vectors are then used as the input for machine learning algorithms.

HOG is particularly effective for object detection as it captures edge information and the distribution of local intensity gradients, which are robust to variations in lighting and pose.

3.5.2 Data Splitting

The preprocessed dataset was partitioned into training, validation, and test sets to assess the models' performance. At first, the data was divided into 80% for training and 20% for testing. Afterward, the testing data was divided equally to create validation and test sets, guaranteeing an equal distribution of samples for evaluating the model. To be more precise:

- **Training Set**: 80% of the total dataset was used to train the model. This set helps the model learn the underlying patterns in the data.
- Validation Set: 10% of the total dataset, obtained from the initial 20% split, was used to tune hyperparameters and validate the model during training.
- **Test Set**: The remaining 10% of the data was used to evaluate the final performance of the trained model.

3.5.3 Model Training

Support Vector Machines (SVM) are supervised learning models used for classification tasks. In this project, a polynomial kernel was used with the SVM to capture the nonlinear relationships between the features and the target classes. The polynomial kernel transforms

the input features into a higher-dimensional space, allowing the SVM to find an optimal hyperplane for classification. The steps for training the SVM with a polynomial kernel are as follows:

- **Kernel Selection**: The polynomial kernel was chosen for its ability to handle complex data distributions. The degree of the polynomial kernel determines the flexibility of the decision boundary.
- **Model Training**: The SVM model was trained on the training set using the polynomial kernel. During training, the SVM algorithm optimizes the hyperplane that best separates the different classes by maximizing the margin between the support vectors.
- **Hyperparameter Tuning**: Hyperparameters such as the regularization parameter (C) and the degree of the polynomial kernel were tuned using the validation set to prevent overfitting and improve generalization.
- Model Evaluation: The trained SVM model was evaluated on the test set to assess its performance. Metrics such as accuracy, precision, recall, and F1-score were calculated to measure the effectiveness of the model in classifying guava diseases.

By using HOG for feature extraction and an SVM with a polynomial kernel, the methodology aims to effectively classify guava diseases, leveraging both robust feature representation and powerful classification techniques.

3.6 Proposed Vision Transformer Model

The Vision Transformer (ViT) model, originally designed for natural language processing tasks, has been adapted for image classification tasks. The following steps outline the processes and steps that will be implemented in the code for setting up and training the ViT model for guava disease detection.

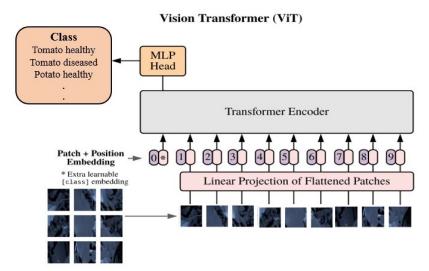


Figure 3.5: ViT Model

3.6.1 Custom Dataset Class

A custom dataset class will be created to handle the loading, transformation, and label encoding of images. This class will read images from specified directories, apply necessary transformations, and return image-label pairs for training and evaluation. Specifically, the dataset class will:

- Scan through the directories containing images.
- · Assign labels based on directory names.
- Store file paths and corresponding labels.

This setup will ensure that the data is organized and ready for model training.

3.6.2 Data Transformations

To prepare the images for input into the ViT model, several transformations will be applied:

- **Resize**: All images will be resized to 224x224 pixels to match the input requirements of the ViT model. This resizing ensures a consistent input size, which is crucial for maintaining the system's performance.
- **Normalization**: The values of the pixels of the images will be normalized to have a mean of 0.5 and a standard deviation of 0.5 across the RGB channels. This normalization helps in standardizing the input data, improving the convergence of the model during training.

3.6.3 Model Setup

In this work, we will initialize the Vision Transformer model with the pre-trained weights from model 'google/vit-base-patch16-224'. The model is an image transformer variant that works on image patches, and given it is a transformer under the hood, it can easily capture the global dependencies of provided images. For our task, we will re-initialize the classification head of the model to be able to predict the output for a set of eight types of guava diseases.

3.6.4 Training Configuration

The training setup will involve several key configurations:

- **Device Setup**: The model will be configured to utilize GPU acceleration if available, significantly speeding up the training process.
- Loss Function: Cross-entropy loss will be used as the criterion for training, suitable for multi-class classification problems.
- **Optimizer**: The AdamW optimizer will be employed, with different learning rates for the transformer layers and the classification head to fine-tune the model effectively. Initially, the transformer layers will be frozen to stabilize the training process, focusing on training the newly added classification head. Midway through the training, some transformer layers will be unfrozen to allow for fine-tuning.
- Training and Validation Loop: The model will be trained over 20 epochs, with a loop iterating through the training and validation datasets. Following each epoch, the training and validation losses will be documented to assess the model's performance and verify its effective learning without overfitting.

3.7 Proposed Transfer Learning Model

The transfer learning approach leverages pre-trained models, adapting them for specific tasks with smaller datasets. The following steps outline the processes and steps that will be implemented in the code for setting up and training the transfer learning model using MobileNetV2 for guava disease detection.

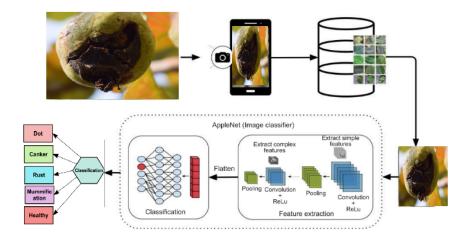


Figure 3.6: Transfer Learning Model

3.7.1 Model Architecture

The model will use MobileNetV2, a compact and effective deep learning model that has been pre-trained on the ImageNet dataset. This pre-trained model acts as the foundation, with strong feature extraction capabilities:

- **Base Model**: MobileNetV2 is initialized with pre-trained weights from ImageNet. The top layer is excluded to allow customization for the specific task.
- **Freezing Layers**: The base model layers are frozen to retain the learned features and prevent them from being updated during initial training.
- **New Layers**: New layers are added on top of the base model to adapt it to the guava disease classification task:
 - A GlobalAveragePooling2D layer to reduce the dimensions of the feature maps and prepare for the dense layer.
 - A Dense layer with 128 units and ReLU activation to introduce non-linearity.
 - A Dense layer with a number of units equal to the number of classes and softmax activation to output class probabilities.

3.7.2 Model Compilation and Training

The model is compiled and trained with the following configurations:

- **Optimizer**: Adam optimizer is used for its efficiency and adaptability.
- Loss Function: The loss function is used, which is appropriate for solving multi-class classification problems.

- Metrics: Accuracy is tracked during training and evaluation to monitor performance.
- **Training**: The model undergoes training using the training set, while the validation data is used to monitor and prevent overfitting, as well as make necessary adjustments to the model throughout the training process.

The training is conducted over 10 epochs with a batch size of 32, ensuring that the model has sufficient exposure to the data to learn effectively without overfitting.

3.7.3 Evaluate Model

The performance of the model is assessed on the test set to verify that it can effectively generalize to data that it has not been trained on. The assessment criteria encompass:

- **Test Loss**: The categorical cross-entropy loss on the test set.
- **Test Accuracy**: The proportion of correctly classified instances in the test set.

Chapter 4

Experimental Results

4.1 Dataset after Preprocessings

Following the completion of all of the various types of preprocessing, we were able to get our dataset, which was 224 by 224 pixels in size displayed RGB values, and was normalized. The data that we have is likewise subjected to random transformation, and we have also balanced the dataset.















Figure 4.1: Preprocessed Data

4.2 Evaluation Measure

True positive (TP), false positive (FP), true negative (TN), and false negative (FN) are the four sorts of prediction instances that are largely taken into consideration in the development of the assessment measures that were discussed earlier in this report. The following provides a more in-depth explanation of them.

Accuracy

With regard to classification problems, the most common metric that is used in the machine learning and deep learning domains is accuracy. It is possible to describe it in a concise manner as the percentage of occurrences that were properly predicted out of the total number of instances, which includes both accurate and inaccurate forecasts. Regarding the four previously described prediction situations, the equation for accuracy may be formulated as follows:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

Precision

Precision is an important parameter in classification tasks, particularly when the goal is to minimize false positive predictions. The percentage of genuine positive predictions and overall positive predictions that the model makes is what is meant to be understood by this proportion. The precision equation is written as follows in terms of the four prediction cases previously mentioned:

$$Precision = \frac{TP}{TP + FP}$$

Recall

Alternatively referred to as sensitivity or true positive rate, recall is an essential metric in classification endeavors, especially when it is critical to accurately identify every positive instance. Its definition is the ratio of real positive cases in the dataset to the genuine positive forecasts. In terms of the four prediction instances mentioned earlier, the equation for recall can be expressed as follows:

$$Recall = \frac{TP}{TP + FN}$$

F1 Score

The F1 score is a composite metric that integrates accuracy and recall, yielding a harmonized number that strikes a compromise between these two crucial criteria. It is especially beneficial in situations when there is an imbalanced distribution of classes or where both false positives and false negatives have significant consequences.

The F1 score is computed by taking the harmonic mean of accuracy and recall. The formula for calculating the F1 score is as follows:

$$F1 \text{ Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

4.3 Transfer Learning

Transfer learning is a method in machine learning that involves using a model learned on one task to enhance the learning and performance of another related activity. Transfer learning enables us to analyze the classification report, which provides detailed performance indicators for a deep-learning model that was built on a dataset exclusively dedicated to guava ailments. The model demonstrates exceptional accuracy values for the majority of disease classes, with Dot and Phytophthora achieving flawless precision ratings of 1.00. Nevertheless, classes like Scab (0.85) have lower recall values. Recall values also fluctuate across

classes; for instance, Styler and Root, Mummification, Dot, Phytophthora, and Rust all receive perfect recall ratings of 1.00, whereas Scab shows a lower recall rate of 0.85. The F1-score, which combines precision and recall, varies between 0.89 for Scab and 1.00 for Dot and Phytophthora. The model achieves an overall accuracy of 97%, indicating its effectiveness in classifying guava illnesses from leaf photos.

	precision	recall	f1-score	support
Styler and Root	0.95	1.00	0.98	20
Mummification	0.91	1.00	0.95	20
Dot	1.00	1.00	1.00	20
Scab	0.94	0.85	0.89	20
FreshGuava	1.00	0.95	0.97	20
Canker	1.00	0.95	0.97	20
Phytopthora	1.00	1.00	1.00	20
Rust	0.95	1.00	0.98	20
accuracy			0.97	160
macro avg	0.97	0.97	0.97	160
weighted avg	0.97	0.97	0.97	160

Figure 4.2: Classification Report of Transfer Learning

The model's accuracy, precision, recall, and F1 scores are as follows: Accuracy: 0.97, Precision: 0.97 (macro average), 0.97 (weighted average), Recall: 0.97 (macro average), 0.97 (weighted average), and F1-score: 0.97 (macro average), 0.97 (weighted average).

Metric	Value
Accuracy	0.97
Macro average of Precision	0.97
Weighted average of Precision	0.97
Macro average of Recall	0.97
Weighted average of Recall	0.97
Macro average of F1-score	0.97
Weighted average of F1-score	0.97

Table 4.1: Classification Metrics of Transfer Learning

So, the classification report gave us this. Now it's time for the confusion matrix of the transfer learning model.

A learning curve is a visual representation that illustrates the correlation between a model's performance, such as accuracy or error, and the quantity of training data or training iterations it has undergone. Learning curves are commonly used in machine learning to assess how well a model is learning from the training data and whether it is overfitting or underfitting.



Figure 4.3: Confusion Matrix of Transfer Learning

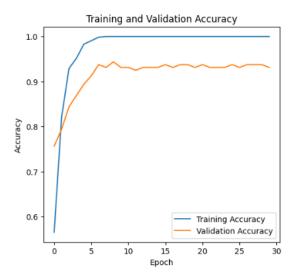


Figure 4.4: Training and Validation Results of Transfer Learning

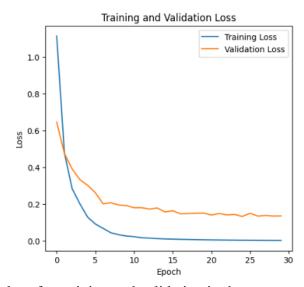


Figure 4.5: Loss values for training and validation in the context of Transfer Learning.

Transfer learning is a machine learning approach that involves reusing or adapting a model learned on one job as the starting point for a model on a second related task. Rather than beginning the learning process again, you use the information acquired from the source job to enhance learning on the target work. This is especially advantageous when dealing with a limited dataset for a specific objective or when the process of training a model from the beginning is computationally burdensome. Image detection benefits greatly from its high accuracy rate of 97% for our model.

4.4 Vision Transformer

The Vision Transformer (ViT) is a deep learning framework that utilizes the transformer architecture, first developed for natural language processing (NLP), for computer vision applications. ViT, in contrast to conventional CNNs, utilizes tokenized image patches instead of convolutions to analyze pictures. It treats images as sequences of patches rather than grids of pixels.

The classification report provides a comprehensive evaluation of the model's performance in several classes, including valuable information on its accuracy, precision, recall, and F1-score metrics. The accuracy of the model varies from 98% to 100% over the whole range, demonstrating its general capability to produce accurate predictions. The precision, which measures the correctness of positive predictions, ranges from 95% to 100%, while the recall, which measures the model's ability to correctly identify real positive cases, also ranges from 95% to 100%. The F1-score, which balances accuracy and recall, falls within the range of 97% to 100%. The macro average, which assigns equal weight to each class, demonstrates an accuracy, precision, recall, and F1-score of 98%. In addition, the weighted average, taking into account the support of each class, shows a 98% accuracy, 98% precision,

98% recall, and 98% F1-score. The detailed assessments reveal the model's strength and efficiency in categorizing examples, offering practical ideas for future improvement and use.

	precision	recall	f1-score	support
Carles	0.05	1 00	0.00	20
Canker	0.95	1.00	0.98	20
Dot	1.00	1.00	1.00	20
FreshGuava	1.00	1.00	1.00	20
Mummification	0.95	0.95	0.95	20
Phytopthora	1.00	0.95	0.97	20
Rust	1.00	0.95	0.97	20
Scab	1.00	1.00	1.00	20
Styler and Root	0.95	1.00	0.98	20
accuracy			0.98	160
macro avg	0.98	0.98	0.98	160
weighted avg	0.98	0.98	0.98	160

Figure 4.6: Classification Report of Vision Transformer

Thus, the model's F1 scores, recall, accuracy, and precision are The results show that the accuracy was 0.98, the precision was 0.98 (weighted average), the recall was 0.98 (weighted average), the macro average was 0.98, and the F1-score was 0.98 (weighted average).

Metric	Value
Accuracy	0.98
Macro average of Precision	0.98
Weighted average of Precision	0.98
Macro average of Recall	0.98
Weighted average of Recall	0.98
Macro average of F1-score	0.98
Weighted average of F1-score	0.98

Table 4.2: Classification Metrics of Vision Transformer

So, the classification report gave us this. Now it's time for the confusion matrix of the vision transformer model. In the vision transformer, we got better results than the transfer learning method in every case like values for recall, accuracy, precision, f1 score, and support. So, the confusion matrix of the model is given below.

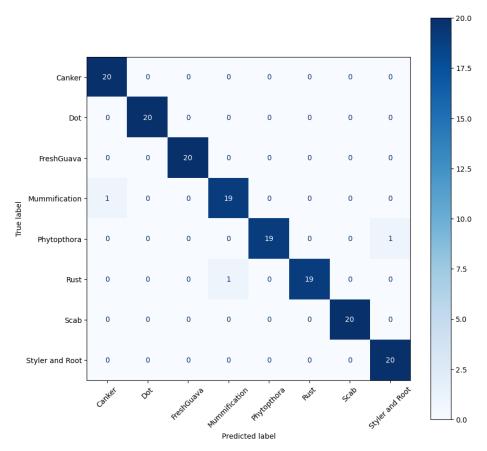


Figure 4.7: Confusion Matrix of Vision Transformer

Now, the learning curve of our vision transformer model is given below where we show the number of data loss over epochs and the accuracy over epochs in the training set, and the validation loss and accuracy too.

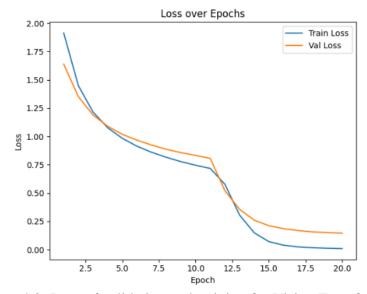


Figure 4.8: Loss of validation and training for Vision Transformer

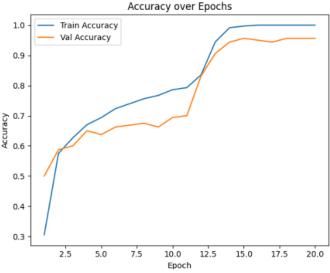


Figure 4.9: Training and Validation Results of Vision Transformer

Here are some disease by disease random chosen images and their prediction and their actual value using the vision transformers.

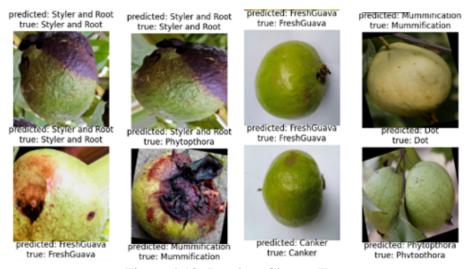


Figure 4.10: Random Chosen Tests

4.5 Support Vector Machine

The classification report comprehensively evaluates the SVM model's performance across various classes of guava diseases. The model demonstrates varying levels of precision, recall, and F1-score metrics for each class. Notably, the class "Dot" exhibits near-perfect precision, recall, and F1-score, indicating precise and accurate classification without significant false positives or negatives. However, classes such as "FreshGuava" and "Rust" show a bad precision and recall values, suggesting challenges in correctly identifying instances of these classes. Overall, the system achieves an accuracy of 78%, indicating its effectiveness in making correct predictions across all classes. The macro and weighted average metrics fur-

ther confirm the model's balanced results across all classes, with both averaging precision, recall, and F1-scores around 77-78%. These insights provide valuable guidance for understanding the SVM model's strengths and areas for improvement in classifying instances of guava illnesses from leaf images.

Classification R	Report:			
	precision	recall	f1-score	support
Styler and Root	0.71	0.80	0.75	40
Mummification	0.70	0.70	0.70	40
Dot	0.98	1.00	0.99	40
Scab	0.70	0.65	0.68	40
FreshGuava	0.65	0.65	0.65	40
Canker	0.87	0.82	0.85	40
Phytopthora	0.89	0.85	0.87	40
Rust	0.71	0.72	0.72	40
accuracy			0.78	320
macro avg	0.78	0.77	0.77	320
weighted avg	0.78	0.78	0.77	320

Figure 4.11: Classification Report of SVM

So, the recall, accuracy, precision, and F1 scores of the system are accuracy: 0.78, Precision: 0.78 (macro avg), 0.78 (weighted avg), Recall: 0.77 (macro avg), 0.78 (weighted avg), and F1-score: 0.77 (macro avg), 0.77 (weighted avg).

Metric	Value
Accuracy	0.78
Macro average of Precision	0.78
Weighted average of Precision	0.78
Macro average of Recall	0.77
Weighted average of Recall	0.78
Macro average of F1-score	0.77
Weighted average of F1-score	0.77

Table 4.3: Classification Metrics of SVM

So, the classification report gave us this. Now it's time for the confusion matrix of the sym model. In the support vector machine, we got lower results than the transfer learning method in every case like recall, f1 score, accuracy, precision, and support values of the system. The reason is the overfitting of training data. So, the confusion matrix is given below.

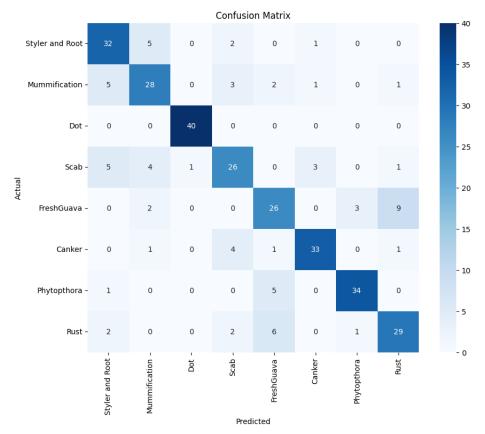


Figure 4.12: Confusion Matrix of SVM

Due to training overfitting, the SVM hasn't performed like the previous two deep learning models. Even though deep learning models usually perform way more than traditional machine learning, SVM does not very much. Actually, deep learning methods can handle overfitting and underfitting well. That's why they are far better than traditional approaches.

4.6 Discussion

As a part of the project, SVM (Support Vector Machine) was incorporated as an untraditional machine learning algorithm for the analysis of guava illness, which extracts the features of the leaf image manually. Vision Transformers, an advanced deep learning architecture that takes the raw image pixels not only for classification reasons but also captures spatial relations, were used to directly process the raw image pixels, capturing spatial relationships for improved accuracy. Transfer learning was achieved through fine-tuning pre-trained models which were previously trained on large image datasets and then adapting the learning features set for the task of guava disease classification thus improving the performance of models.

The accuracies of the three strategies are compared, and it is discovered that Vision Transformers attained the highest accuracy of 98% followed by Transfer Learning which scored a 97% accuracy and SVM scored 76%.

Algorithm	Accuracy (%)	
Vision Transformers	98	
Transfer Learning	97	
SVM	78	

Table 4.4: Comparing the Accuracy of Three Algorithms

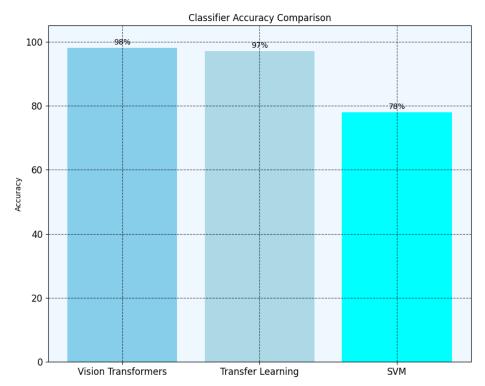


Figure 4.13: Comparing the Accuracy of Three Algorithms Histogram

So, that is how these three models are behaving testing our dataset of guavas.

Thus, in the process of assessing the effectiveness of the proposed system for detecting diseases in guava plants, we have excluded surveys of articles in the scientific literature. Certain to our review, current studies primarily aim at revealing techniques of vision machines in identifying and categorizing guava diseases. Yet, many of these works fail to provide significant numerical data and contain fewer comparisons with works of similar genres. However, a major problem in assuring a comparison of different methods is yet the complete lack of a standardized database for guava disease samples. Based on the available literature review, there are plenty of signs and trends regarding the research of guava disease detection; however, a vigorous study based on practical assumptions and guidelines is still lacking. However, the above challenges remain unattended, and this is where our project seeks to fill the gap through presenting a detailed narrative of numerical results related to the identification and categorization of guava diseases. Thus, in this context, it is our intention to provide an effective analysis of the comparative advantage of the proposed approach. Now, this is the comparison of our work with other's work.

Work Done	Object(s) Dealt with	Problem Domain	Sample Size	Feature Set Size	Class ific ation	Algorithm	Accuracy
					Yes	SVM	78%
This work	Guava	Recognition	4046	8	Yes	Transfer Learning	97%
					Yes	Vision Trans- formers	98%
Habib et al., 2020 [24]	Papaya (Both fruit and leaf)	Recognition	126	3	Yes	k-means clustering	90.15%
Kumar and Suhas (2016) [25]	Fruit	Recognition	243	NM	Yes	k-means clus- tering	87.47%
Kurniawati et al. (2009) [26]	Paddy (Leaf)	Recognition	94	5	Yes	Local entropy threshold	94.7%
Hasan et al. (2022) [27]	Guava	Recognition	550	10	No	AlexNet	83%
Tewari et al. (2023) [28]	Guava	Recognition	527	5	Yes	DenseNet201 Model	96%
Chopaade and Bhagyashri, (2016) [29]	Papaya, Mango, Banana (Leaf)	Detection	NM	NA	No	Histogram based thresh- olding	NA
Assad S. et al. (2022) [1]	Guava (Leaf)	Recognition	1834	5	Yes	The EfficinetNet-B3	94
Mostafa, A.M et al. (2022) [3]	Guava	Recognition	321	5	Yes	ResNet-101	97
Rozario et al. (2016) [30]	Apple, Banana, Potato, Tomato (Fruit)	Detection	63	NA	No	K-means clustering and Modified K-means clus- tering	NA
M. Abirami (2017) [8]	Guava (Leaf)	Recognition	465	5	Yes	GLD-Det	97%

Table 4.5: Comparing Our Task with Other People's Tasks

Chapter 5

Conclusions

5.1 Conclusions

In agriculture, plant diseases can cause serious problems for the quantity, quality, and staple food across the world. The treatment of these afflictions needs to be redoubled through proper and precise diagnosis, as well as effective treatments. Let's look at the details, elaboration of the deep learning methods, and an actual comparison with traditional methods for this aim. Plant disease, one of the most problematic issues in the agriculture product industry, has impacted crop loss and incurred economic damage. Many influencing factors can increase the danger of diseases like the change of climate, globalization, and agricultural production under intensive conditions. Under the circumstances, the poverty caused by fruit and vegetable loss puts the whole agricultural industry into a crisis and needs effective plant disease management to guarantee agricultural sustainability. To spare plant pathogens from taking over the crops or causing a catastrophe, it is both important and vital to understand these organisms early and act immediately. Hence the researched study highlights guava diseases and hazards that cause problems in farming and food security globally generally. The situation today unveils how critical it is to work out reliable detection and reticence techniques to guarantee the health of this crop against diseases that cause devastation. The key to the outstanding performance of this research lies in the exploitation of the superiority of deep learning, in particular, with the aid of Transfer Learning and Vision transformer (ViT) architecture, the realm of disease recognition experienced remarkable success by those methods which gave 97% accuracy for transfer learning and almost hitting 98% accuracy for ViT. These deep learning models hold great promise to become executive and economical models of medical identification and provide farmers and agricultural stakeholders with valuable tools for timely solutions and crop management. But we cannot underestimate the traditional machine learning methods, which still remain a critical tool for building a strong foundation for today's more advanced techniques as they give only up to less than 78% accuracy. Adopting the road ahead together to be accomplished through increased research

and development in the science of agriculture early disease detection or agricultural system of disease detection are necessary for bringing down the influence of diseases in guava and guarding the world food security system under waning money of agricultural problems.

5.2 Future Prospects of Our Work

There are several potential areas for future work and improvement in this project, some of which are:

- Enhanced Model Architectures: This can be implemented by powering up and sharpening the sophistication and efficiency of deep learning techniques such as Transfer Learning and Vision Transformer (ViT), which could, in turn, exercise the accuracy too, leading to even better and steadfast performance for fruit disease detection.
- **Fine-Tuning Strategies:** In the same way, the provision of reinforcement strategy for transfer learning model (e.g., differential learning rates, layer freezing, layer unfreezing) is another possible action to be taken. With this, the phenomenon can eventually generalize more and be able to adapt to the changing guava disease data sets.
- Data Augmentation Techniques: Pursuing alternative data augmentation schemes that uniquely benefit defying the guava disease images, i. e custom data processing transforms and analog data creation could be a winner of the dataset and the reductiveness of the result.
- Multi-Modal Fusion: Systematic usage of multi-modal data sources, (e. g. both (spectral imaging, hyperspectral imaging as well as infrared imaging) along with the pictures would help in this task of making the model more specific about diseases of guava.
- Real-Time Deployment: Through optimal model architectures fine tuning to accelerate the inference pipeline and deployment on edge devices and IoT systems, the onsite procedures of disease monitoring and timely interventions on guava farms become achievable.
- **Deployment in Mobile Applications:** Finally, compact versions of deep learning models especially for mobile devices can be executed through a user-friendly mobile application which in turn will enable farmers to use these technology solutions even on the go without installing a complex system.
- Collaborative Platforms: Through the construction of shared collaborative platforms and open-access repositories for record-sharing of guava disease datasets, pre-trained models and benchmarking reports could significantly aid research in disease detection amongst various agricultural organizations.

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