

A Robust Ensemble Deep Learning Approach for Early and Accurate Tomato Leaf Disease Identification

P. Senthilraj¹, Dr.P. Parameswari²

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Abstract: Farmers and stakeholders stand to significantly minimize potential yield losses from disease outbreaks through the efficient and prompt identification of tomato diseases using easily accessible leaf images. This research introduces an inventive solution to this challenge by presenting a new method capable of visually distinguishing nine distinct infectious tomato leaf diseases from healthy leaves. These include blights, mold on leaf, bacterial spot, Septoria spot, mosaic virus, target two-spotted spider, and the virus like yellow leaf curl. To achieve this, the research employs an ensemble learning approach that combines the strengths of EfficientNetB5, DenseNet169, and VIT architectures. The method is evaluated using a comprehensive tomato leaf disease (TLD) dataset and yields impressive results. During training, it achieves an average accuracy of 99.6% with minimal deviation, and validation accuracy averages at 98.3%. Cross-validation tests demonstrate an average test accuracy of 99.1%, further emphasizing the model's reliability and consistency. In addition to accuracy, the research prioritizes model interpretability, utilizing gradient-weight based classified activation maps (GCAM) and global interpretable method-agnostic explanations. This transparency not only enhances predictive accuracy but also instills trust and facilitates the model's integration into agricultural processes. The ensemble learning model, combining transfer learning and efficient network architectures, emerges as a leading solution, boasting remarkable performance in terms of accuracy during training and testing. This research provides agricultural professionals with a practical and efficient methodology for early plant disease diagnosis, contributing significantly to disease outbreak prevention and economic loss mitigation.

Keywords: Disease classification, Agricultural practices, Yield loss, Deep learning, Interpretability and GCAM.

Introduction

Plants play a vital role in our survival by supplying us with nourishment and safeguarding us from harmful radiation. Life on Earth would be nearly unimaginable without the presence of plants. In addition to giving all land-dwelling animals food, they protect the ozone layer from ultraviolet light from the sun. Because of their high nutritional value and safety for human consumption, tomatoes are grown all over the world [1]. The globe consumes over 160,000,000 metric tonnes of tomatoes annually [2]. Many people think that trading tomatoes may help rural communities make much-needed revenue, which would have a big effect on poverty levels [3]. When it comes to growing and harvesting, Because of their wide range of applications and excellent nutritional value, tomatoes have a significant economic impact on agriculture. Owing to their pharmacological benefits [1], tomatoes are beneficial in preventing ailments like gum bleeding, high blood pressure, and hepatitis. Their anti-cancer properties are also extensively documented. The demand for tomatoes is rising due to their increasing prominence. Almost 80% of the agricultural yield [2] is

statistically linked to small-scale producers. However, these producers lose around half of their harvests annually due to diseases and pests. Tomatoes are highly susceptible to diseases and parasites, which highlights the need of studying the identification of diseases in field crops. FAOSTAT estimates that 186,821 million kilogrammes of tomatoes were produced worldwide in 2020 [1]. The main engine of economic expansion and the cornerstone of human civilisation is agriculture. The multitude of plant illnesses that farmers need to protect the crops they grow from has shown to be a major hindrance to agricultural output. Taking preventative measures and learning how to control plant diseases are crucial for increasing crop yield. Detecting plant diseases at an early stage is crucial for maximizing agricultural output while conserving resources and minimizing crop losses, especially with the ease of computerized management. It is imperative to guarantee timely and precise disease diagnosis and categorization in order to maintain the quantity and quality of tomatoes.

Different plant diseases may arise due to a variety of environmental factors. The illness triangle illustrates the relationship between three essential elements: the living thing, the surroundings, and the pathogen that causes the illness. Since its creation in the 1950s, the disease triangle has been widely utilised to illustrate how diseases spread. For a disease to manifest, all three components of the triangle must be present; if anyone is

¹Research Scholar, Department of Computer Science Karuppamm Mariappan College, Muthur- 638105 Tamil Nadu, India
professor.psenthil@gmail.com

²Principal Palanisamy College of Arts and Science, Perundurai – 638052
paramtech20@gmail.com

absent, the disease cannot develop. Many non-living factors, such as air circulation, temperature, moisture, pH, and irrigation, hold considerable sway over plants. Organisms like fungi, bacteria, and viruses have the capacity to attack plants, with the infectious agent being the microorganism responsible for causing plant diseases. A plant defined as a "host" is one that has contracted a disease. When every risk factor is present at the same time, disease onset happens [3]. After infecting a plant, most diseases exhibit rapid transmission rates since their symptoms typically advance upward through the plant. As a result, swift transmission is common among the majority of diseases once they infiltrate a plant.

Plant afflictions can arise from a variety of sources, including harmful fungi, bacteria, viruses, and unfavorable weather conditions. These diseases have the potential to disturb vital plant processes like photosynthesis, pollination, fertilization, and germination. This underscores the significance of accurately identifying these diseases at the earliest possible stage, as permitted by current medical knowledge.

Instead of relying exclusively on the expertise of human professionals, technology can now be utilized to identify whether a plant is diseased and, if so, to determine the specific type of disease. With ongoing advancements in the quality of images captured by technological devices, the precision of tasks involving object recognition, classification procedures, image processing, and artificial intelligence algorithms is also increasing. In terms of efficacy, deep learning (DL) and machine learning (ML) have outperformed conventional optimisation and prediction techniques. Unlike conventional techniques that depend on human-derived features and are limited by data volume, modern systems can autonomously learn from vast datasets. Furthermore, ML and DL models show a great capacity to apply their knowledge to data that has never been seen before, which is a major advancement over earlier techniques. Models based on deep learning and machine learning are superior than conventional methods at recognising complex and nonlinear relationships in data. As a result, ML is particularly adept at handling complex scenarios with numerous dynamic components and intricate interactions. Artificial intelligence (AI) has gained widespread adoption across various fields such as communication, construction, magnetism, physics, and biology [4–8]. Plant disease detection and classification in this situation require precision and promptness [9]. AI is already capable of autonomously recognising plant diseases from unprocessed photos [10,11].

Numerous research investigations have been carried out to ascertain the origins of plant ailments. The majority of these studies employed existing datasets, models, and libraries for their analyses.

An image segmentation-based method was created by Singh and Misra [12] to streamline the process of finding and classifying plant leaf diseases for classification. With a total accuracy rate of 97.60%, they were able to distinguish between five distinct diseases by using a genetic algorithm. In order to identify illnesses, Zhang et al. [13] carefully examined an archive of cucumber leaf samples. In order to segment sick leaves and extract shape and colour information for disease diagnosis, the researchers used k-means clustering in their research. They classified these affected leaves with an accuracy of 86.00% by employing the sparse representation approach. Plant disease identification and diagnosis can be facilitated by the application of artificial intelligence in the form of (CNN) models [14]. The algorithm was trained using a dataset including 87,848 photos, which included 58 distinctive mixes of plant and disease utilised on 25 distinct species of plants. The data yielded an impressive performance rate of 99.53 percent.

Recent years have seen a significant improvement in areas like pattern gratitude [17,18], computer visualization [19,20], and image processing [15,16], especially in the agricultural sector where automation of pest and disease detection procedures is a primary focus. For classic computer vision models, the complex and laborious nature of tasks involving preprocessing and establishing picture characteristics presents challenges. The effectiveness of these systems is dependent on the precision of the extraction of features processes and the creation of learning algorithms [21–23]. The use of deep learning in the diagnosis of illness is growing in popularity as a result of improvements in computer power, capacity for storage, and availability of large datasets. Plant disease detection is a complex problem that has previously been difficult to diagnose, but this technology has been successfully employed in that regard. Deep learning is a specific kind of machine learning that serves a particular purpose. Among the most popular deep learning algorithms are CNNs, which are applied to tasks including object recognition, semantic segmentation, and classification of images [24, 25]. By learning to classify based on image data, CNNs excel in discerning patterns within images, objects, and scenes, eliminating the need for manual isolation of image features [26,27].

This article will assess and elucidate several prevalent deep learning approaches currently adopted. Even though the influence of disease identification on tomato crops has been the subject of multiple research, the

current model can still be improved. We suggest a CNN model that consists of two layers of convolution, two maximum pooling layers, a flattening layer, a tomato plant disease detection layer that uses data from the layer that is hidden, and other layers to solve this. This empowers farmers to independently address concerns without relying on agricultural specialists, including the identification of various threats to crops. Our methodology is designed to make it easier to identify plant diseases early on, which will increase agricultural output overall and lead to increased food supply.

The driving force behind this endeavor is the need for an automated method to diagnose diseases potentially affecting tomato plants. Several contributions in this study fill gaps in previous research:

- The research introduces a novel method for classifying nine distinct infectious tomato leaf diseases using easily accessible leaf images. This goes beyond traditional methods by utilizing computer vision and deep learning methods for diagnosing illnesses.
- The study improves the resilience and accuracy of disease classification by utilising an ensemble learning approach that combines the EfficientNetB5, DenseNet169, and ViT architectures.
- The ensemble model combines transfer learning and efficient network architectures, optimizing both accuracy and cost-effectiveness. This is important for practical implementation in agriculture, where resources can be limited.
- To enhance model interpretability, the research incorporates gradient-weight based classified activation maps (GCAM) and global interpretable method-agnostic explanations.

This study presents an architecture that uses data augmentation in conjunction with three dissimilar machine learning models—EfficientNet, DenseNet169, and the transformer ViT model—for the early detection and categorization of illnesses in tomato leaves. The goal is to develop a robust framework for screening tomato leaf images to identify disease indicators based on the specific pathogens that affect tomato leaves.

Review of related works

Employing state-of-the-art technologies like machine learning and advanced neural network architectures such as Inception V3 net, VGG 16 net, and Squeeze Net, researchers from diverse institutions have devised automated systems for detecting plant diseases. Their focus is on accurate diagnosis of ailments present in tomato leaf tissue.

The precision of pre-trained network models in detecting and categorizing tomato diseases falls within the range of 94.00% to 95.00% [28,29]. Six different types of tomato leaf diseases were recognised and categorised from an array of 300 images using the Tree Classification Models and Segment technique [30]. A unique method that achieves 93.75% accuracy in diagnosing illnesses affecting leaves has been proposed [31]. In order to accurately identify and classify plant leaf diseases, a classification strategy and image processing software are required [32]. Capturing images through an 8-megapixel smartphone camera, data was segregated into healthy and afflicted categories. The image processing process encompassed three key steps: contrast enhancement, image segmentation, and unique feature detection. The classification tasks were performed by feed-forward neural networks and multilayered artificial neural networks, and the results were compared with the (MLP) and (RBF) networks. The results were noticeably better. Plant leaf photos were categorised into both healthy and diseased parts during the research period, but the underlying cause of the problem was not found. With 87.2% accuracy, the researchers diagnosed leaf ailments using a classification method that included colour space evaluation, colour time, histogram, and colour coherence.

To effectively detect diseases harming tomato crops, researchers used models with an overall size of 13,262, such as AlexNet and VGG 19. With this model, 97.49% accuracy was attained [33]. For dairy crops, a virus identification rate of 95.00% was attained by combining transfer learning with a CNN model [34]. With neural network-trained transferable learning and an AlexNet-based deep learning technique, tomato plant leaf surfaces could be identified and classified with 95.75% accuracy [35,36]. The Resnet-50 model was developed to recognize 1000 diverse diseases that pose a threat to tomato leaves. This was accomplished by labelling a set of 3000 images with descriptive labels for various illnesses, including "lesion blight," "late blight," and "yellow curl leaf." The model was improved by using a Leaky ReLU network activating method and increasing the first convolution layer's kernel size to 11x11.

The disease classification performance improved to 98.30% correctness and 98.00% precision after multiple iterations [37]. A comparatively simple eight-layer CNN algorithm was developed for the identification and organization of tomato leaf diseases [38], utilising the PlantVillage data set [39], which aggregates data on various agricultural products. Using the tomato leaf dataset, this method improved illness diagnosis through the use of deep learning algorithms.

CNNs have become a dependable diagnostic tool for plant diseases in recent times [40, 41]. Some research efforts have concentrated on enhancing the quality of feature detection in high-stakes scenarios by overcoming challenges arising from variations in illumination and background consistency. Others have focused on augmenting feature detection by identifying intricate contexts. Certain studies have even developed real-time models to expedite disease detection in plants [44,45]. Early disease detection has also been pursued through model development by different researchers [46,47]. For instance, a study discussed in Reference [48] delves into digital images of tomato leaves, deploying a CNN and AI-derived algorithm-based classification model that accurately identifies five distinct diseases with a precision of 96.55%. Models based on deep neural networks have been used in many studies to identify illnesses in tomato leaf data. Reference [49] finds that the VGG16 model performs better than the other four different alternatives (LeNet, VGG16, ResNet, and Xception). It performs best when used to classify nine distinct diseases with a precision of 99.25%. The effectiveness of models based on deep neural networks in identifying illnesses in tomato leaves was examined in a different study. Models like AlexNet, GoogleNet, and LeNet routinely addressed the identical problem with 95.00% accuracy or greater, according to Reference [50]. Agarwal et al. [51] constructed a CNN framework for categorising data into ten categories. They then

compared it with various ML models (such as decision trees and arbitrary forests) and DL techniques (such as VGG16, Inceptionv3, and MobileNet). This approach resulted in a remarkable 99.20% increase in accuracy.

Many studies have attempted to improve classification accuracy by combining different classification networks, including multinomial logistic regression, random forests, and support vector machines [52]. These networks can be applied in conjunction with extracted leaf characteristics. By employing MobileNetv2 and NASNetMobile, leaf features were efficiently extracted, and the combination of these techniques has been demonstrated to significantly boost classification accuracy. Successful identification of plant diseases has been achieved in various studies through the utilization of algorithms like Mask R-CNN [53]. Techniques like Gabor filters, K-nearest neighbours, and KNN have been used to reduce computational costs and model sizes in an effort to lessen the resource and time requirements associated with deep learning calculations. The authors in Ref. [54] employed a SqueezeNet design with just 33 filters to address these issues. To address these issues, YOLO-Tomato, which is founded on the YOLOv3 design, was introduced. The authors used this to improve tomato identification in Refs. [55–57]. YOLOv3 incorporates a dense architecture that promotes feature reuse, facilitating the learning of a more accurate and compact model.

Table 1: Summary of the previous relevant works

Ref. No.	Method	Advantages	Disadvantages
28,29	ML & Neural Networks	High accuracy (94.00% to 95.00%)	Computationally expensive, requiring specialized hardware like GPUs or TPUs
30	Tree Classification & Segmentation	Early disease detection, non-invasive	Dependent on image quality and lighting
31	DCNN Approach	Achieved 93.75% accuracy in classification	Lack of interpretability
32	Image Processing & Classification	Precise identification of diseases	Not be able to abstract complex features
33	AlexNet & VGG 19 Models	High accuracy (97.49%)	Model complexity and resource requirements not mentioned
34	Transfer Learning & CNN	Achieved 95.00% virus detection rate	Finding the right hyperparameters can be a time-consuming process
35	AlexNet-based Model	95.75% accuracy in identifying conditions	Struggle when dealing with imbalanced datasets
37	Resnet-50 Model	Increased classification performance (98.30%)	Limited to Available Data
38	Simplified CNN Model	Utilized the PlantVillage dataset	Susceptible to overfitting
48	CNN & AI Algorithm-based Model	Accurate identification of five diseases (96.55%)	Time-consuming and expensive
49	Deep Neural Network Models	VGG16 achieved the best performance (99.25%)	Lack of Contextual Understanding

50	Various Deep Neural Network Models	Consistently achieved high accuracy (95.00% or higher)	Vulnerability to Adversarial Attacks
51	CNN & ML/DL Models	Remarkable 99.20% increase in accuracy	May suffer from vanishing gradients
52	Diverse Classification Networks	Augmented classification accuracy	Problematic for deployment on resource-constrained devices
53	Mask R-CNN	Successful identification of plant diseases	Computational resource requirements not discussed
54	Ensemble Algorithms	Efficient models to mitigate computational expenses	Requires Annotated Data
55-57	YOLOv3	Enhanced tomato identification	Challenges in Multi-Class Scenarios

Methods and materials

The identification of diseases affecting tomato leaves can be challenging due to their intricate structures and the diverse array of diseases that impact tomatoes. Deep learning has been a powerful tool in recent years to help in computer-assisted disease detection. Neural networks with deep layers, which can extract intricate patterns from enormous image collections, are used in this technique. The recommended method for disease detection in tomatoes through deep learning involves several key stages. Initially, a collection of images of leaves from tomatoes is assembled, comprising specimens of both undamaged and healthy leaves. These images are preprocessed and then used to train a CNN or other deep neural network model to recognise complex patterns in the images. After being trained, the model is able to classify new photos as either normal or as associated with particular diseases. The model's accuracy and performance can be improved by adjusting its

parameters and adding new data. Finally, the accuracy and generalisation capabilities of the model are evaluated by evaluating its performance on an independent set of photos. Figure 1 shows the basic layout of the suggested system for identifying and categorising illnesses in tomato plant leaves.

Dataset utilized

This study made use of the Tomato Leaf illnesses Dataset, which included 11,000 photos of tomato leaves with ten different illnesses. This Kaggle dataset is available to the general audience. While Figure 2 shows a visual representation of a sample of tomato leaf illnesses, Table 1 gives an overview of the characteristics of the illnesses in tomato leaves and the quantity of samples in each class. The following URL will allow you to access the dataset: <https://www.kaggle.com/datasets/kaustubhb999/tomatoleaf> (accessed on January 20, 2023).

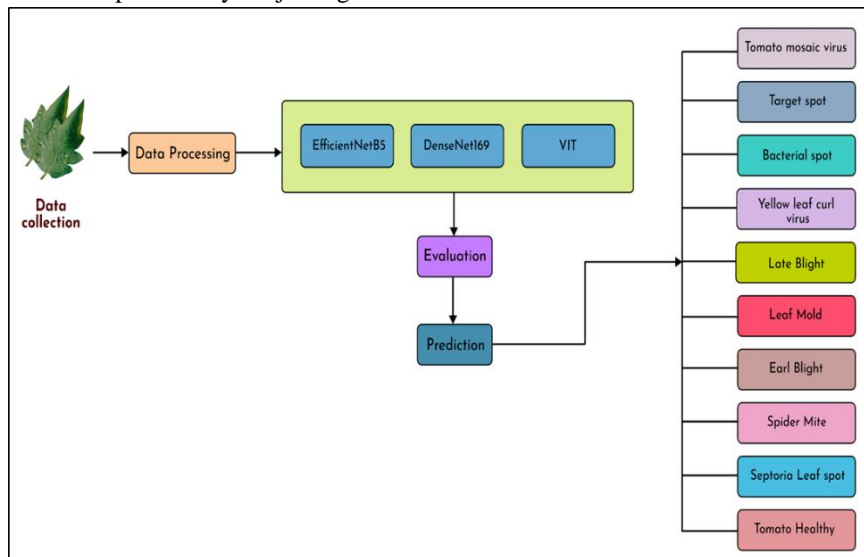


Figure 1: The way the suggested method is structured

Table 2: Features of the tomato leaf classes

Classes	Samples count	Description
Mosaic virus	1100	A viral illness called mosaic virus can seriously damage tomato plants, lowering their development and production. Stunted development, malformed fruit, and the emergence of

		mosaic-like designs in dark and light green on leaves are among the symptoms. Tomato varieties that are resistant to the illness and agricultural techniques like upholding cleanliness can help minimise its spread. Contact with contaminated plant material can result in the transmission of the disease.
Target spot	1100	Target spot, brought on by the mould <i>Corynespora cassiicola</i> , causes depressed, circular lesions on leaves and stems that are ringed with concentric circles. Fungicides and good agricultural practises, such as crop rotation and sanitation, can help control it, even if it can lead to defoliation and decreased fruit output.
Early blight	1100	Commonly occurring early blight can seriously harm tomato plants, lowering yields and degrading fruit quality. The symptoms include dark brown spots organised in circular patterns on the lower leaves and brown, depressed lesions on the leaves. Fungicides and agricultural techniques including crop rotation and pruning can help manage it, although it can result in defoliation and a reduction in fruit production.
Spider mites	1100	By eating on the undersides of departs these tiny arachnids can seriously injure tomato plants, resulting in discoloration and restricted growth. Predatory mites, insecticide soaps, and agricultural techniques including crop rotation and sanitation can all be used to control them.
Septoria leaf spot	1100	The fungus <i>Septoria lycopersici</i> is the cause of Septoria leaf spot, which is characterised by tiny, round lesions on tomato plants' lower leaves that have yellow halos and dark brown centres. Fungicides and agricultural techniques like crop rotation and sanitation can help manage it, even if there may still be a considerable loss of production and defoliation.
Healthy Leaves	1100	Images of healthy tomato leaves may be found in this category and can be used as a point of comparison when comparing them to leaves that are diseased.

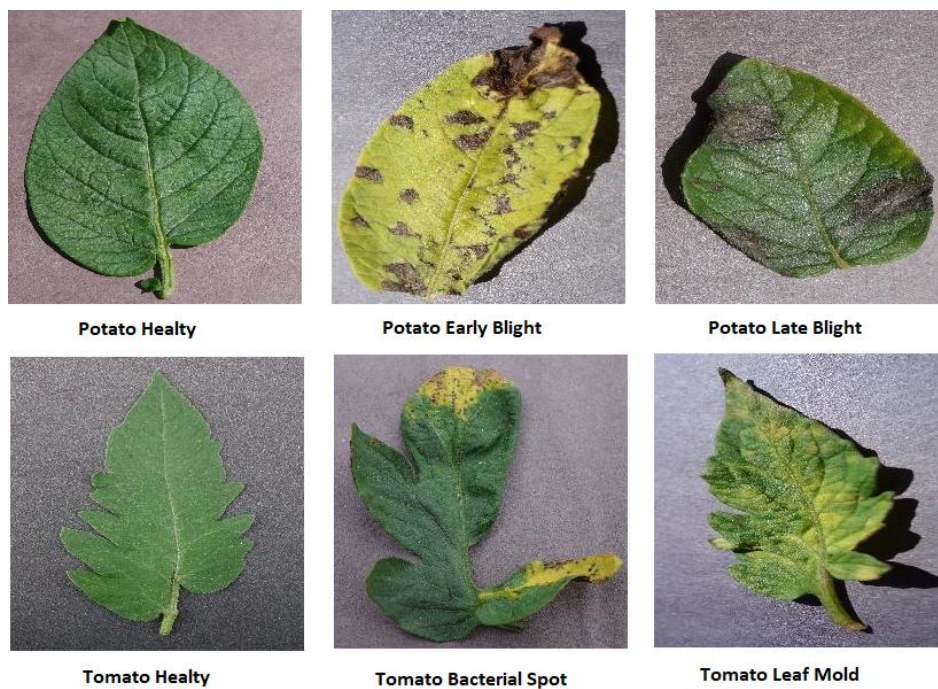


Figure 2. Examples of demonstrated datasets

Data Preprocessing

Data preparation is a crucial step that raises the calibre of the data and increases the effectiveness of the algorithms for classification employed in the picture classification process. The main objective of data preparations is to get pictures ready for use in deep learning models by eliminating noise, fixing errors, and managing anomalies that can affect the model's accuracy. This entails setting

up the data in a way that makes model analysis efficient. Common preprocessing methods, such as image scaling and normalisation, are frequently used in deep learning algorithms for image categorization. Resizing an image entails changing its proportions to match a predetermined size so that the model may be trained. This not only simplifies the model but also ensures consistent training on images of uniform size. Normalization, on the other hand, entails harmonizing

brightness and contrast levels across images, thus ensuring uniform quality throughout the dataset. By using these preprocessing methods, the dataset is more consistent and of higher quality, which increases model accuracy. PIL and OpenCV are two examples of image processing libraries that can be used to apply these techniques.

Transfer Learning Algorithms

A model can be learned on a particular assignment and then transferred to another that is related to it using transfer learning techniques. This can be especially handy when a task is identical to one that was previously resolved or when there is a dearth of labelled data for that particular task. By utilising the information and characteristics discovered from a pretrained model, it can save a great deal of time and money. Transfer learning can also enhance the performance of the model by lowering the likelihood of overfitting and facilitating a better generalisation of the model to a new dataset. When considering whether to employ transfer learning, it is important to consider the amount of labelled data accessible in the new task as well as the degree of similarity among the model that was previously trained and the new task. If the new job differs significantly from the one for which the model that was previously trained was designed, or if a significant amount of labelled data is available, it may be better to train a system from scratch. Transfer learning can reduce the need for labelled data while improving model performance. It may be used to a wide range of models, including CNNs, and can be put into practise through feature-based or fine-tuning methods.

DenseNet121 Model

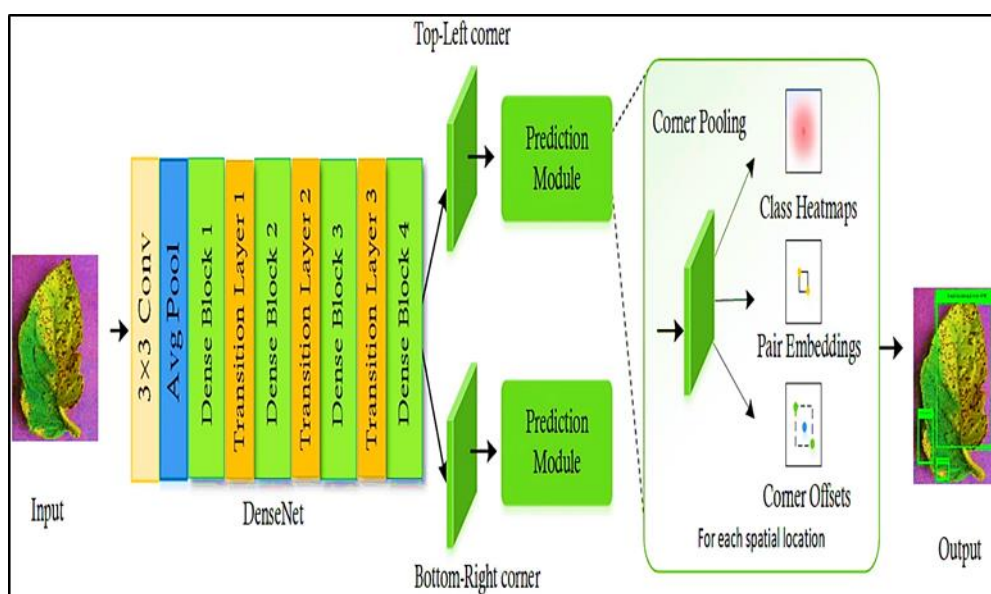


Figure 3. DenseNet model for detecting tomato diseases

Efficient net Model

DenseNet121, introduced by Huang et al. in 2017, is a widely recognized CNN architecture belonging to the DenseNet family. It is characterized by dense cross-layer linkages that enhance accuracy and promote efficient information transmission. The multiple dense blocks that make up the DenseNet121 structure each have a variety of convolutional layers that are intimately related to every layer that comes after them [58–61].

In this work, we apply a pretrained DenseNet121 model to tomato disease detection. Using transfer learning is a popular technique in this case, where weights from the large ImageNet dataset are used to initialise the pretrained model. In order to modify the model, a new layer arrangement was added. This setup consists of two completely linked layers with 512 and 256 neurons each, a global pooled mean layer, and two batch normalisation layers. The pretrained model's top layer is replaced by these additional layers. After the first layer is fully connected, a new activation layer is given a ReLU activation function. Finally, the output layer is augmented with a softmax activation layer containing 10 neurons, corresponding to the 10 distinct tomato disease types. The visual depiction of this process is shown in Figure 3.

This architecture was chosen because DenseNet models perform well in a variety of image classification tasks and because of their small size, which makes them appropriate for transfer learning. The addition of batch normalisation layers improves training stability and convergence, while the global average pooling layer aids in parameter reduction. The critical parameters of the DenseNet121 model.

Plant disease classification is one of the many computer vision jobs that have seen widespread adoption of

convolutional neural network designs like Efficient net. Other activities include image processing and classification. The learnt model's weights were initialized using a sizable image processing dataset, a popular technique that makes advantage of the transfer learning principle. To adapt the algorithm to a new photo classification problem, a new set of levels were added to the highest layer of the initial Efficientnet model. This classifier, superimposed on the pretrained model, underwent a series of transformations to tailor it for the new task.

A GlobalAveragePooling2D layer, which aggregates map features along the height and width dimensions, receives the output from the pretrained model. As a result, a feature vector with a fixed captures the key elements of the input image. This vector is handled by two fully connected layers, each including 512 and 256 neurons. These layers acquire the ability to convert the vector of features into a representation with a high level

that is relevant to the new image classification task and contains important discriminative information. Batch normalising layers are combined to enhance training stability and speed up convergence after each fully linked layer. An activation layer employing ReLU's activation function includes a nonlinearity factor after the second completely linked layer, enabling the network to store more intricate representations. Ten cells and a softmax activation mechanism make up the final fully interconnected layer, which receives the output of the next fully connected layer. This layer generates a distribution of probabilities for each of the dataset's ten classifications. It gains the ability to translate the basic representation to the final network output, which is the input image's projected class label. Figure 4 shows the structure of the ResNet50V2 model, which was developed to identify tomato illnesses. For information on the parameters used in creating the ResNet50V2 model for tomatoes disease detection, see Table 3.

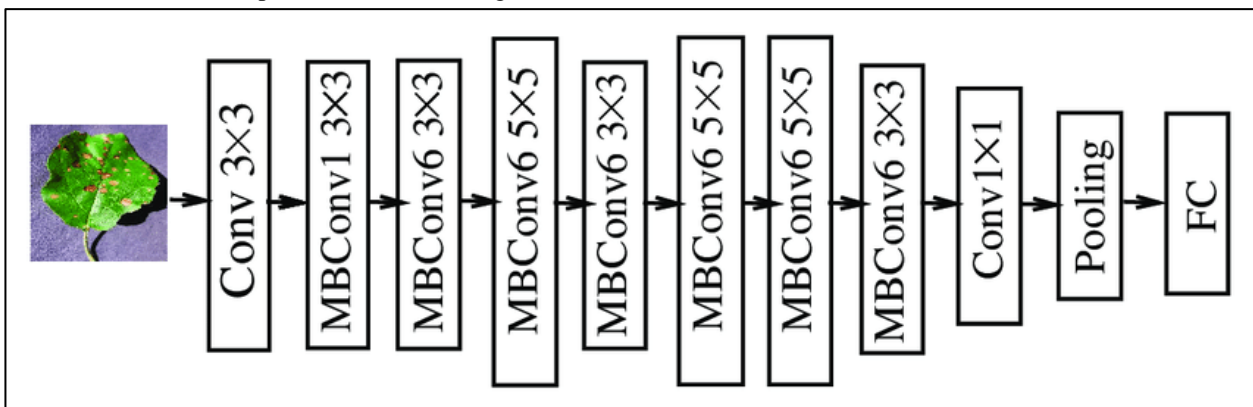


Figure 4. E-Net model for detecting tomato diseases

Vision Transformer

When it comes to deep learning, the (VIT) is a unique design that is receiving a lot of attention, especially for picture categorization problems. VITs use a transformer-based design, which has shown to be very effective in applications related to processing natural languages, in contrast to traditional Convolutional Neural Networks (CNNs).

There are several basic components that make up the VIT design. The input image is first split up into a large number of fixed-size pieces. An anchoring layer completes the remaining duties once each patch has been flattened to generate a 1D vector. This layer facilitates the translation of each patches to a higher-dimensional field of features. The transformer encoder receives these patched embeddings after that. Figure 5 illustrates how this encoder uses a series of self-attention techniques that

are essential to understanding the contextual relationships between the patches.

The following describes the steps involved in learning the data and adding it to a VIT classification model. A "patches" layer processes the incoming image to create a grid of non-overlapping 6×6 patches. The 2D image is transformed into a 3D tensor using the framework (batch settings, patch dimension \times patch width \times the total number of channels). The number of color channels is indicated by the full quantity of channel, which is typically three for RGB images. The "patch encoder" layer processes this patch tensor and then gives each patch a learnt linear transformation (through a dense layer). Additionally, a learnable position embedding is applied to each patch, enhancing the model's ability to note spatial relationships between patches and detect relative positions within the image.



Figure 5. Image after transformer encoder

For every input image, the model's predictions are produced by this specific layer. During training, the model is optimized using the amount of weight loss normalizing procedure of the AdamW optimizer, which is a variant of the Adam optimizer. Sparse categorical cross-entropy is the chosen loss function; this method is

commonly employed to tackle problems related to multiclass classification. The framework of the ViT transform model, which is utilised to diagnose tomato diseases, is depicted in Figure 6. Table 4 lists the important variables that are relevant to the ViT model.

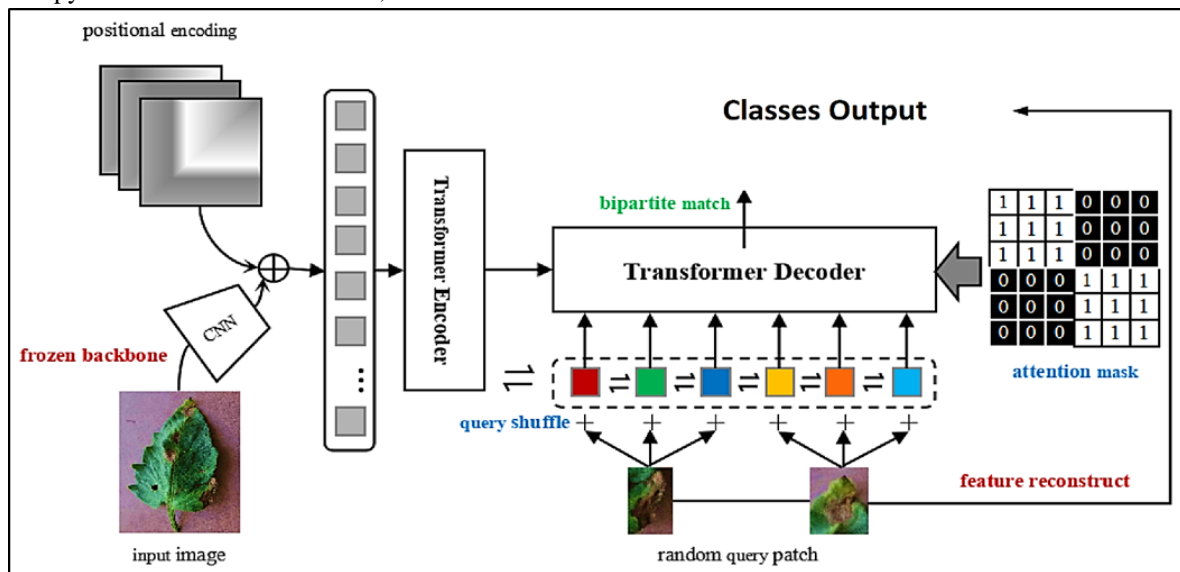


Figure 6. ViT model for identifying tomato diseases

Explainable AI

Conventional evaluation metrics fall short in capturing the processes employed by an AI system to generate an outcome and fail to provide a means of interpreting the result. As a result, it is imperative for an AI algorithm to effectively elucidate its decision-making process. This becomes especially crucial in domains where high-stakes decisions are involved, as there is a growing demand for transparency in deep learning-based systems [55]. Professionals must be able to comprehend the information generated by the deep learning model and leverage this understanding to make precise diagnoses, particularly in the case of identifying specific types of TLD (Top-Level Domain) varieties. In this context, two

commonly used tools, LIME and GradCAM, are employed. This research utilizes explainable AI (XAI) algorithms to achieve these objectives.

GradCAM calculates the gradient of a specific result, like a class score, in relation to a chosen layer's convolutional features. Semantic segmentation can also make advantage of it. The softmax layer in our model helps with semantic segmentation by generating a score for every class and pixel. Equation (2) describes the GradCAM mapping between 'N' pixels and the feature map 'A' for a specific class 'C'.

$$M^c = ReLU(\sum_K \alpha_c^K A^K) \quad (1)$$

$$\alpha_c^K = \frac{1}{N} \sum_{i,j} \left(\frac{dy^c}{dA_{i,j}^K} \right) \quad (2)$$

Implementation Details

On Google Colab [57], the suggested deep learning approach and explainable AI (XAI) algorithms were run on an NVIDIA K80 graphic processing unit with 12 GB of RAM. For implementation, we used Python [56] and Keras [54]. TensorFlow version 2.5 is compatible with Python version 3.7 and Keras version 2.5.0, which are both included in the runtime environment offered by Google Colab. Two callbacks were incorporated into the suggested model for both training and validation.. To track validation loss and lower the rate of learning by a factor of 0.5, the first callback was utilised. In order to achieve early halting, outcomes of the top four epochs were retained in the second callback. To mitigate the risk of overfitting, both callbacks were utilized within a training span of 50 epochs.

Evaluation Metrics

We evaluated the model's ability to identify TLD photos using widely-used performance criteria, including accuracy(A) (7), recall(R) (5), F-score(F) (6), and precision(P) (4), as described in reference [58].

$$(P) = \frac{T_P}{T_P+F_P} \quad (3)$$

$$(R) = \frac{T_P}{T_P+F_N} \quad (4)$$

$$(F) = 2 \times \frac{P \times R}{P+R} \quad (5)$$

$$(A) = \frac{T_P+T_N}{T_P+T_N+F_P+F_N} \quad (6)$$

Here, " T_P " stands for "true positive," " T_N " for "true negative," " F_P " for "false positive," and " F_N " for "false negative." We used the confusion matrix to conduct distinct assessments for every class in addition to evaluating the efficacy of the model.

Results and Discussion

Comparing Current Pre-Trained Deep Learning Models

We evaluated the performance of the enhanced EfficientNetB5 model against several well-known transfer-learning techniques using MobileNet [17], Xception [19], VGG16 [18], ResNet50 [20], and DenseNet121 [21] as substitutes for pre-trained deep learning (DL) models. Utilizing the TLD dataset, we applied transfer learning while following the same implementation requirements as mentioned in Section 3.3. Considering the variety of current deep learning models, which range from heavyweight (requiring an extensive amount of trainable parameters) to thin (requiring fewer trainable parameters), we chose to incorporate both types of models (heavyweight models represented by MobileNet, and heavyweight models like VGG-16, ResNet50, etc.). Table 2 shows that, in terms of correctness and loss, the suggested DL model using EfficientNetB5 performed better than the other models.

Table 3 provides a comparison of the proposed model with the models from MobileNet, Xception, VGG16, ResNet50, and DenseNet121.

DL MODEL	TA	TL	VA	VL	TsA	TsL
MobileNets	98.91	0.2067	97.11	1.28	98.01	0.9067
Xception	98.91	0.2847	98.72	1.36	96.33	0.4032
VGG16	84.22	2.1876	80.11	2.256	95.67	3.45
Resnet50	98.96	0.3315	98.82	1.245	97.89	0.456
DenseNet121	98.91	0.2345	97.82	1.30	98.31	0.31089
This work (EfficientNet)	98.85	1.18	98.07	1.25	98.08	0.21

With regard to test accuracy, the suggested DL model that made use of EfficientNetB5 came out on top, scoring 99.07%, outperforming models such as MobileNet (94.0%), Xception (95.32%), VGG16 (93.35%), ResNet50 (96.03%), and DenseNet121 (96.3%). Our suggested DL model fared better in terms of accuracy than the second-greatest model, DenseNet121, by a margin of 2.77% when compared to the state-of-the-art pretrained DL models. With a test

accuracy of 93.35%, the lowest in the same comparative group, VGG16 performed 5.72 percentage points worse than the suggested DL model using EfficientNetB5..

Explaining the Model Using EfficientNetB5

We evaluated standard statistical validation protocols, which included analysing the model's accuracy and loss in the training, confirmation, and test data as well as measures like recall, precision, and F1-score. There was

a 50 epoch pre-established cutoff point for the training process. During training, the model's accuracy, on average, was 99.84%, with a 0.10 percentage point

deviation, and the validation accuracy reached 98.28% with a variance of 0.20 percentage points (please see Table 3 for details)."

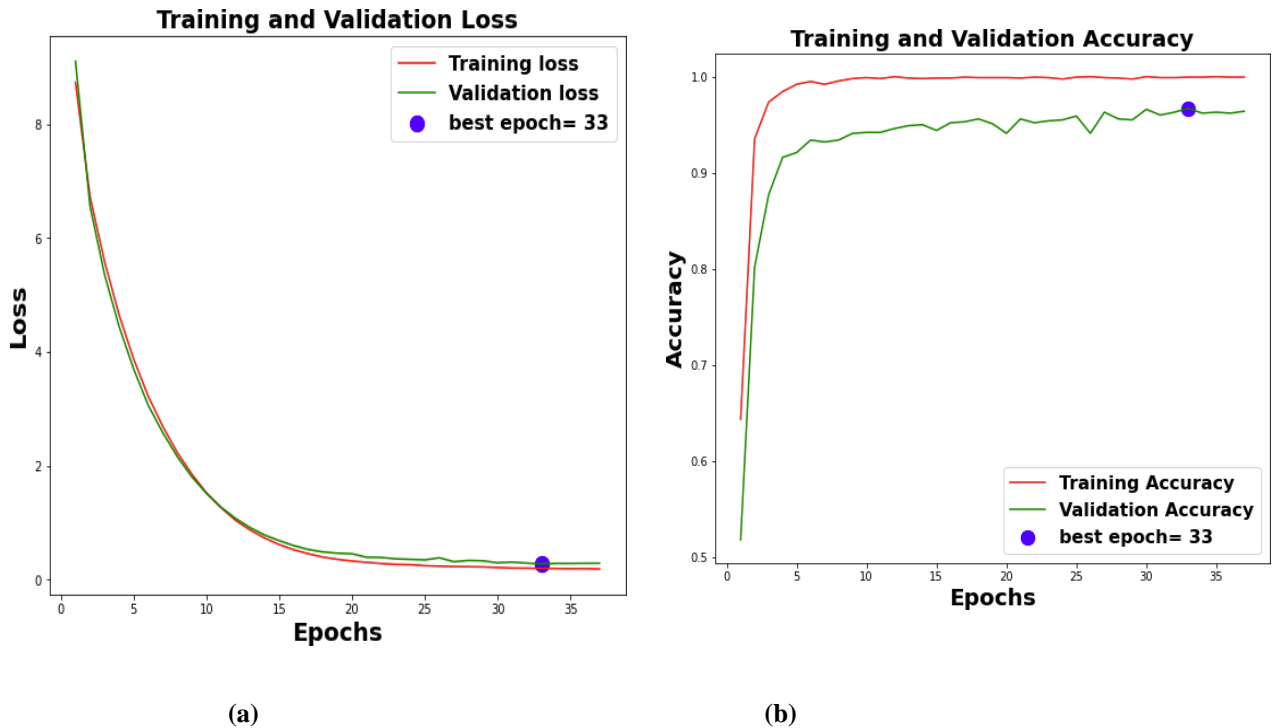


Figure 7: displays the outcomes of the validation and training procedure. In panel (a), across 10 folds, the average training accuracy registered at 99.84% while the average validation accuracy was 99.07% b), the training loss stood at 0.18, and the validation loss was 0.24

Table 4. The percentages for ten-fold training, testing, and proof are as follows:

	TA	TL	VA	VL	TsA	TsL
K1	98.86	1.287	99.01	1.345	98.12	1.298
K2	98.96	1.287	98.03	1.456	98.23	1.287
K3	98.92	1.276	99.45	2.675	98.13	0.189
K4	99.91	1.281	98.51	2.678	98.14	0.178
K5	99.86	1.286	98.43	2.765	98.67	0.876
K6	98.98	1.345	99.21	0.345	97.87	2.567
K7	98.87	1.456	87.45	0.345	96.78	1.786
K8	98.67	1.546	98.54	2.546	96.78	5.678
K9	98.78	1.234	76.87	3.765	98.77	6.789
K10	98.77	1.234	98.78	7.876	98.7	8.987
$\mu \pm \sigma$	99.89 \pm 1.12	1.456	98.74	9.876	98.99	9.878

After testing the model on a set of tests that was not included in the data used for training, we were able to get a 99.07% test accuracy with a 0.38% variance and a 0.20 test loss with a 0.03 variability. Table 4 presents precision, F1-scores, and recall values for each distinct category.

We determined the AUC ROC values for each class in order to evaluate the efficacy of our suggested model, as

indicated in Figure 9. The model effectively classified the data, as shown by an average AUC ROC score of 1 for each class. The AUC ROC scores for the various classes also showed how well the model performed in each category. These results show how effectively the model solves the multi-class classification issue.

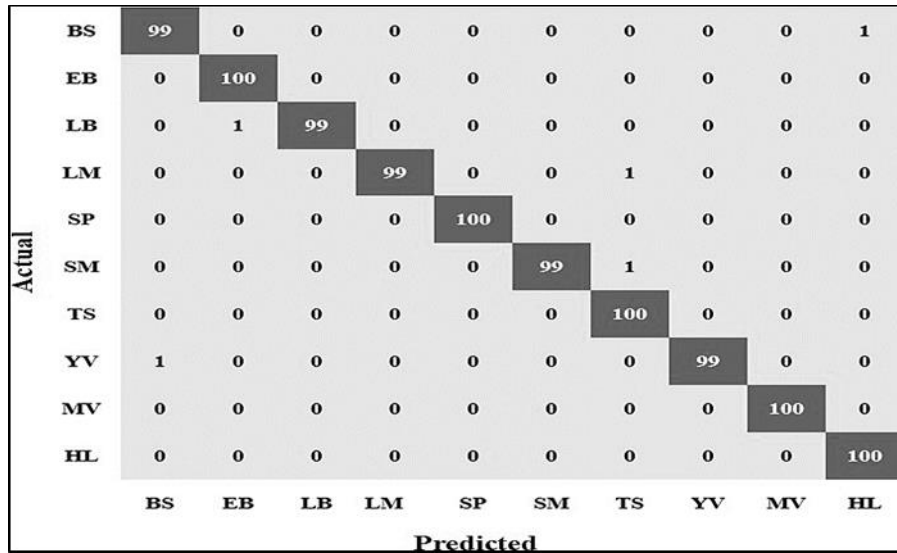


Figure 8. The diagram offers an illustration of the confusion matrix. 'BS', 'EB', 'LB', 'LM', 'SP', 'SM', 'TS', 'YV', 'MV', and 'HL' are the acronyms for bacterial spot, early blight, late blight, leaf mould, Septoria leaf spot, spider mite, target spot, yellow curl virus, and mosaic virus, in that order

Table 5. Individual predictions, recall rates, F1-scores, and the number of samples (support) for each class within the TLD dataset's test subset

	PRECISION	RECALL	F1-SCORE
Spot of Bacterial	0.98	0.98	0.100
Blight of Early	0.98	1.01	0.985
Blight of Late	1.02	0.98	0.986
Mold of leaf	1.02	0.98	1.023
Leaf spot septoria	1.02	1.02	0.983
Mite of spider	1.02	1.98	0.956
Spot of Target	1.02	1.02	1.043
Viruses in yellow curl	1.02	0.97	0.984
Virus in mosaic	1.01	1.01	0.987
Healthy	0.98	1.01	0.996
Accuracy			0.987
Average in macro	0.98	0.97	
Average in weight	0.98	0.97	

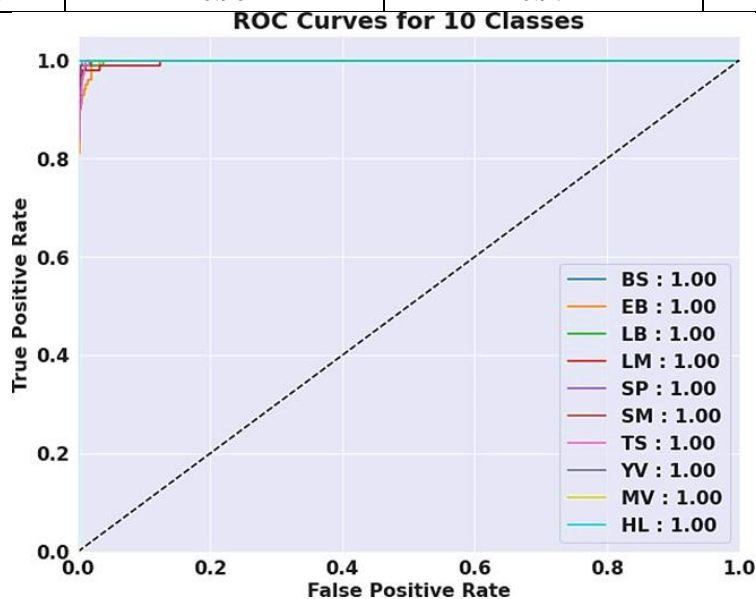


Figure 9. The suggested model's AUC-ROC results, which show an AUC score of 1.0

XAI-Based Model Explanation


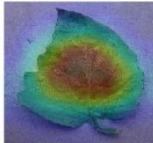


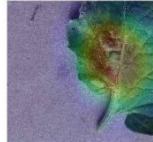


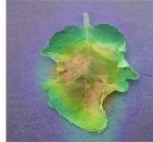


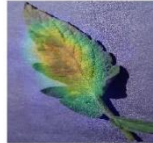

GradCAM


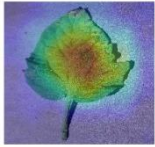
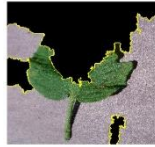

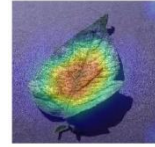


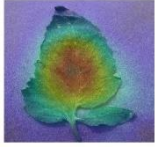


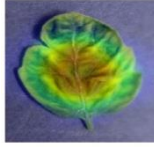


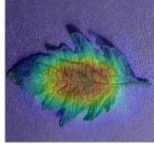

GradCAM was utilised to utilise the spatial information held by convolutional layers to extract significant portions of TLD pictures that were required for classification. To conduct a comprehensive analysis of each of the TLD samples from each group and assess the effectiveness of the recommended visual explanation methodologies, we looked at the heatmaps generated by these techniques. Table 5 shows the heatmap that was created..

The heatmap for bacterial spot illustrates how the central portion of the leaf is crucial for classification, as can be

observed in the initial column of Table 5. The heatmap's depiction of early blight is consistent with the right portion of the image being highlighted as having greater influence. GradCAM is used to identify leaf mould by concentrating on the leaf's yellow area. On the other hand, certain portions of the leaf picture backgrounds are also highlighted when looking at the GradCAM heatmap for the intended spot class (as displayed in the fifth row of Table 5), with most of the gradient centred on the photos. Testing the subject on a set of separate test photographs (see Section 6) confirms that although the setting has little effect, the model takes background information into consideration when making decisions.

Table 6. Interpretations of TLD interpretable AI results

Category	Leaf	GradCAM	LIME
Bacterial spot			
Blight in early			
Blight in late			
Molded leaf			

Septoria			
Spider-mite			
Targeted spot			
Yellowish leaf			
Mosaic virus			

Global interpretable method-agnostic explanation

We produced a 150-row matrix of generated at random ones and zeros, coupled with columns representing superpixels. A 3 by 3 kernel with a maximum separation of 100 units was used to perturb this matrix after it had been partitioned at a ratio of 0.2. To be precise, the top 20 numerical characteristics were subjected to these perturbations. After that, we reversed the means-centering and scaling processes and used a normal (0, 1) sampling strategy to align these features with the training data's mean and standard deviation. We created a robust binary feature and used it to produce categorical characteristics based on the initial distribution. This method made sure that when a characteristic matched the instance that was specified, it was given an unambiguous value of 1. Table 5 shows the TLD segmentation at the person level.

In the context of the bacterial spot shown in the first row of Table 5, it's evident that the bacterial spot is present on the leaf. Furthermore, the central portion of the leaf significantly influences the classification, a fact reflected in the way LIME segments the leaf. Examination of the LIME output for early blight indicates that EfficientNetB5 correctly activates in the relevant leaf region. In a similar vein, the network uses the yellow part of the leaf as a key characteristic to identify a leaf as having leaf mould.

Comparing with the Most Advanced Techniques

Table 7 shows the comparison of our suggested model's classification performance with the most advanced techniques currently in use. In order to ensure coherence and relevance in evaluating performance, we opted to assess our model against the latest disease detection models that leverage deep learning techniques for TLD categorization. We chose seven current deep learning

techniques to give a thorough comparison. Both transfer learning-based DL models and commercial CNN algorithms that were developed from scratch were included in this comparative group. Remarkably, out of the four articles, only two integrated CNNs with LIME as a customizable eXplainable AI (XAI) technique to

enhance interpretability. Transfer learning was used in all three additional research to classify the TLD dataset, but XAI techniques were not used in any of them. Notably, our suggested approach fared better than any other cutting-edge techniques.

Table 7. Our model is compared to the most advanced techniques using the TLD dataset

Techniques	Accuracy in percentage	XAIs
CNNs (Module with attention)	98.25%	X
B7 with EfficientNet	99.8%	X
VGGNets,GoogleNets,AlexNet	92.57%,90.69% & 96.26%	X
Compact-CNNs	98.71%	GradCAMs
Deep-CNNs	99.50%	X
Densenet Xception	98.20%	X
XAI-CNN	99.6%	LIMEs
EfficientNetB5	99.85%±0.20%	GradCAMs,LIMEs


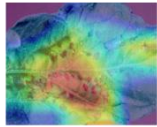

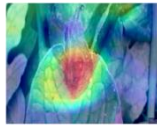
Independent Validation

When developing a model, it is best to use test data that is different from the dataset used for training. A bias in the PlantVillage (PV) dataset was found in the study by Noyan et al. [48] and was linked to the background colour. As a result, we had to apply our representation to photos of tomato leaves that we had collected from another source [59], which included 32,535 images that depicted eleven distinct tomato leaf illnesses. A 250x200 pixel resizing was applied to these photos. Notably, our suggested model was not trained, tested, or validated using these photos. They were fed into the model, and for every disease category, real-time validation was carried out.

We next evaluated GradCAM results and computed the expected probability for these example images, which are compiled in Table 7. The GradCAM results effectively pinpointed the infected areas of the leaf, while no such markings were found in the healthy sections. For a detailed breakdown of results by disease class, please refer to Table 8.

Regarding precision, leaf mould and spider mites both attained an accuracy percentage of 80%, with the other disease categories performing less well. The average accuracy was 96%, with certain categories reaching 100% correctness.

Table 8. Real outputs

Image	Forecast Possibility	GradCAM
	Bacterial spot (80.56%)	
	Blight in early (90.26%)	










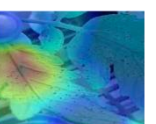






	Blight in late (91.60%)	
	Molded leaf (93.42%)	
	Septoria spot (90.35%)	
	Spider-mite (88.41%)	
	Targeted spot (96.87%)	
	Yellowish leaf (87.58%)	
	Mosaic (85.33%)	
	Healthy (95.19%)	

Table 9: Correctness for each class in the separate data set

Class	Accuracy
BS	100%
EB	100%
LB	100%

LM	80%
SP	100%
SM	80%
TS	100%
YV	100%
MV	100%
HL	100%
Average	96%

The results and Upcoming Projects

In this research, we introduced a framework for generating explanations (XAI) and developed a Convolutional Neural Network (CNN) model to classify Tomato Leaf Diseases (TLD) into nine distinct categories. We named our model BotanicX-AI, and it was constructed using transfer learning with EfficientNetB5, prioritizing explanation-driven insights. GradCAM and LIME were employed to provide in-depth explanations for the model's predictions. To benchmark our work, we compared our model to existing pre-trained deep learning models for TLD detection, all of which shared a common fine-tuned architecture. We also conducted ablation studies to identify the most effective deep learning model. Our XAI-based CNN model achieved impressive test and training accuracies of $99.07\% \pm 0.38\%$ and $99.84\% \pm 0.10\%$, respectively. Both GradCAM and LIME explanations successfully pinpointed the specific regions of the images that influenced the TLD categorization. This study demonstrates that the combination of XAI and EfficientNetB5 yields accurate explanations for the results, enhancing classification precision.

During our investigation, we observed that GradCAM faced limitations in identifying the image regions relevant to the model's predictions due to the gradient-averaging phase. To address this issue, we recommend exploring alternative approaches such as HiResCAM, a generative adversarial network (GAN), and Kernel SHapley Additive exPlanations (SHAP). These techniques should be considered for testing and further refinement.

We also recommend enlarging the PlantVillage dataset to include tomato leaf diseases. This extension would assist in reducing the problem of background bias brought up in [48]. Moreover, our suggested model has potential for assessment with datasets that include extra information and pictures because it is based on the EfficientNetB5 architecture.

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