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A Super-Efficient and Compact CNN for Tomato Leaf Disease Detection on Resource-Constrained Devices

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Abstract The diseases that affect tomato leaves have a major impact on the agricultural industry. Thus, it is crucial to develop an automated detection system that is both accurate and lightweight. In this context, the implementation of a lightweight CNN architecture using the concept of depth-wise separable convolution and squeeze-excitation has been used for the purpose of accurate classification of diseases that affect the tomato leaves. The results that are obtained using the proposed CNN architecture indicate that the classification of diseases that affect the tomato leaves is done in a more accurate manner. In this context, it is observed that the accuracy for the training set is 100%, the loss is 0.0217, the accuracy for the validation set is 99.83%, the loss is 0.0263, and the accuracy for the test set is 99.75%. Thus, it is observed that a high AUC score is obtained, which is 0.999996. The proposed CNN architecture has a total of 219,651 trainable parameters. In this context, it is observed that the total parameters are of a size of 858.01 KB.

Keywords diseases of tomato leave; deep learning; squeeze-and-excitation; resource-limited devices.

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1. Introduction

*P*lant diseases' extreme danger is among the significant threats to food security all over the world, attracting only the best crops of tomatoes. The earlier and precise detection of these plant diseases is essential if one wants to minimize losses and utilize agrochemicals properly [1, 2]. Conventionally, professionals classify plant images manually if they notice any plant diseases, which is not only time-wasting but difficult to implement on bulk plots of plants [3]. Because of this limitation, there is a move towards implementing computer vision algorithms [4, 5]. Recently, deep learning, focusing on convolution neural networks (CNNs), has achieved remarkable performance for image-based problems, such as plant disease detection [6, 7]. However, applying these techniques on resource-constrained systems has remained an area of concern. In this regard, literature has observed the development of efficient CNNs by implementing techniques such as depth-wise separable convolutions, squeeze-and-excitation (SE) networks, or network pruning to reduce the overhead of the network [8, 9].

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The deployment of accurate and efficient disease detection systems directly on edge devices (such as smartphones and IoT sensors used by farmers) is a critical need for modern precision agriculture, as cloud-dependent solutions are often impractical in rural and resource-limited settings. However, today's state-of-the-art approaches, except for Nedenskii's work, focus on the prediction accuracy and disregard uncertainty [10, 11]. In the context of agricultural studies, it is important to have information about the confidence level of the prediction [12]. The use of neutrosophic theory in CNN can be the best approach in determining the level of uncertainty and thus the reliability in detecting the disease [13, 14].

The primary aim of this work is to introduce a Super-Efficient and Compact CNN-based Tomato Leaf Disease Detection system. The novelty of the proposed approach lies not in the individual components (such as Depthwise Separable Convolutions or SE blocks, which are well-established techniques), but in their integration into a unified, highly compact architecture specifically optimized for tomato disease detection on resource-constrained devices, combined with a Neutrosophic uncertainty-aware inference mechanism. This integration enables reliable and interpretable disease classification under real agricultural constraints. We evaluate the proposed system on the PlantVillage benchmark and assess its effectiveness in terms of accuracy, F1-score, model compactness, and uncertainty quantification.

Our major contributions are:

- Integration of a highly compact CNN architecture combining Depthwise Separable Convolutions and Squeeze-and-Excitation blocks, specifically optimized for tomato disease detection on resource-constrained edge devices.
- Neutrosophic uncertainty-aware inference mechanism integrated with the Softmax classifier to quantify Truth (T), Indeterminacy (I), and Falsity (F), enabling more reliable and interpretable predictions.
- Explicit acknowledgment and analysis of dataset limitations including class imbalance and controlled imaging conditions, with a discussion of their impact on generalization.
- Large-scale experimentation on PlantVillage demonstrating strong classification performance, with comparisons to lightweight SOTA architectures (MobileNetV2, SqueezeNet) in terms of model compactness.

The structure of this paper is as follows: Section 2 provides a survey of the current state of related work. Section 3 presents the proposed model architecture and methods of optimization. Section 4 describes experimental results. Section 5 discussion of results and Section 6 summarizes with future outlooks.

2. Literature Review

There exist intelligent mobile apps with so-called lightweight CNN architectures, such as models inspired by the Mobile Net architecture, which focus on the typical tomato leaf diseases. In that respect, they significantly optimize the computations through depthwise separable convolutions and enjoy good enough accuracy, even without keeping up with the cutting-edge models [15].

CNNs with residual connections enhanced by attention mechanisms have also been employed to point to the most key features in tomato leaf images, obtaining outstanding validation accuracies on the augmented data. However, the increased size might impede their use in low-resource setups [16].

Also, other authors have embarked on feature extraction via pre-defined networks like SqueezeNet, InceptionV3, and AlexNet, as well as transfer leaning, obtaining remarkably interesting results for disease severity evaluation. Nevertheless, these would require rather large models, as well as large memory consumption, thus not being fitted for low-end devices [17].

Hybrid models, which combine convolution auto-encoders with CNN, have been investigated to minimize the count of trainable parameters without losing accuracy. These models have the possibility of overfitting, particularly when the training dataset is small, and the computation needed remains quite high [18].

For identifying diseases in tomato leaves, lightweight Convolutional Neural Network classifiers combined with the concept of data augmentation have emerged as a competent solution in terms of accuracy with reduced model size [19].

Generative techniques based on Conditional GANs (C-GAN), when utilized as data augmentation techniques on synthetic data with transfer learning, have been able to perform better with reduced overfitting and with high accuracy [20].

In the use of transfer learning with the InceptionV3 and/or the MobileNetV2 models, high cloud and/or local environment levels of accuracy have been achieved. However, there can exist the potential for overfitting and/or negative transfer, with not all works describing computational complexity [21, 22].

Lastly, a tiny attention-based CNN for low-end devices has shown particularly satisfactory results, although these models are shallow and do not benefit from many data augmentation methods due to their generalization ability, especially for field conditions with varying scenarios, as mentioned by Sun et al. [23].

Conclusion and Gap Analysis:

Although the previous approaches have reached remarkable accuracy, certain obstacles still need to be tackled. Firstly, the absence of uncertainty estimation is quite evident, which is detrimental for interpretation in farm-level applications. The high computational requirement and memory requirement make it quite challenging for execution in devices having Resource constraints. Some of the augmentation strategies for images may lack generality in practical conditions that a farmer experiences on a regular basis. Lastly, approaches based on neutrosophic measures have been explored less in relation to the proposed task. This clear need is thus fulfilled through the proposed model, which is an efficient combination of reduced CNN architecture, SE blocks, and neutrosophic measures for estimation of uncertainty.

3. Proposed Model

Finding the balance between accuracy and computational complexity is a key issue for plant leaf disease diagnosis algorithms. A model that diagnoses plant leaves diseases accurately has a complex architecture that consumes significant computing power, thus unsuitable for deployment on devices that use less powerful components.

To address these challenges, we propose a Super-Efficient & Compact Tomato Leaves Diseases Detection. This is a lightweight CNN architecture to achieve dependable classification results with non-excessive computational costs. The presented CNN integrates efficient convolutions, channel attention and uncertainty modeling through neutrosophic logic to improve feature learning, generalizability, and dependable decision making under ambiguous visual conditions that frequently occur in agriculture [24].

3.1. Proposed Architecture

Our network has four feature extractors, a global average pooling layer followed by fully connected layers with dropout, a Softmax classification and a final Neutrosophic T/I/F representation layer as seen in Figure 1. Our model does not complicate so much as it can be implemented in real-time for edge devices. For block 1 and block 2 the same CNN layers are utilized, where convolution with batch normalization and ReLU is used, as the low-mid level features can be efficiently extracted from the input image. The number of filters also increased to 64 from 32. Max pooling is applied to decrease the image's spatial dimensions while keeping model computationally efficient and simple to train.

The advent of block 3 brings depthwise separable convolution, reducing the count of parameters and floating-point computations efficiently. This method separates the spatial and channel operations by allowing the simultaneous extraction of the features without compromising the accuracy of CNN. It has proved effective for compact CNN applications in plant disease and edge computing [25, 26].

In Block 4, also known as the SE Attention Block, the Squeeze-and-Excitation attention mechanism is applied, allowing the model to recalibrate the channel-wise feature responses using global average pooling by confronting the squeeze and gating processes, thus enabling the model to concentrate on subtle disease signals as well as eliminate background noise.

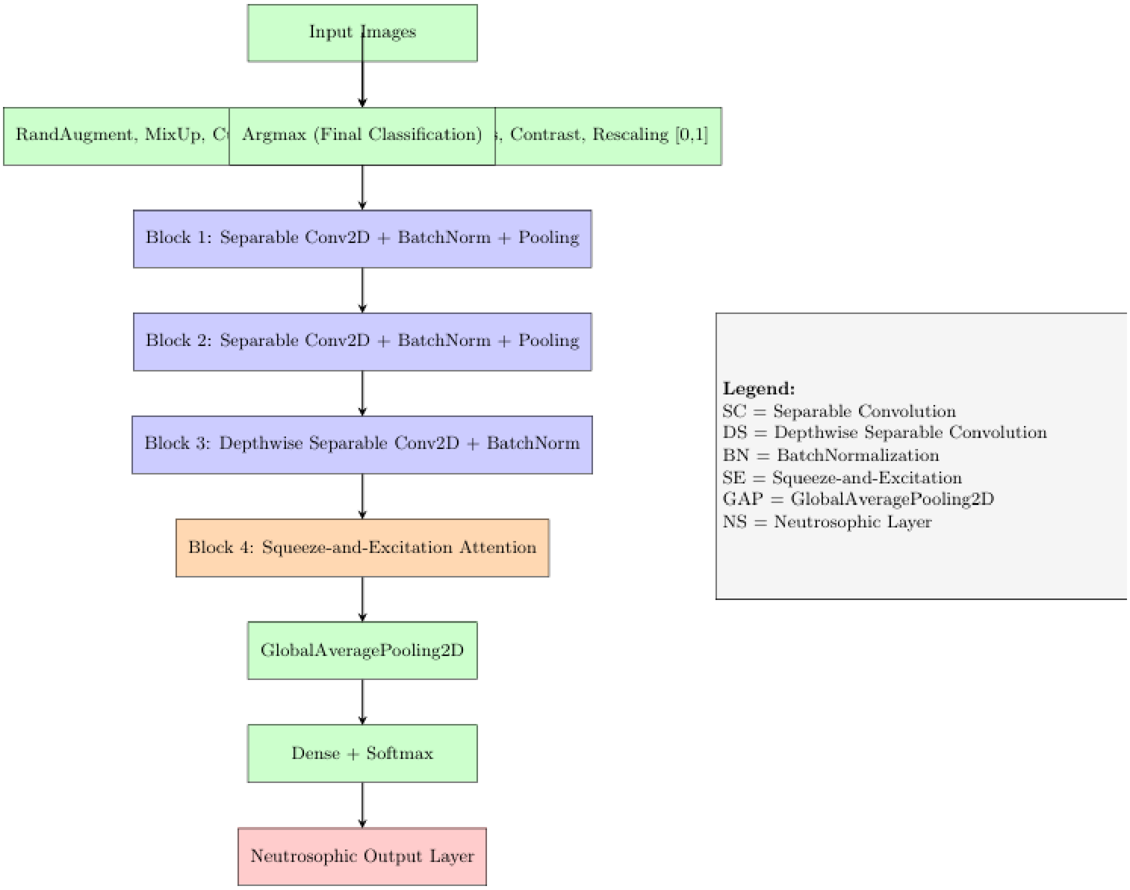

Figure 1. The hierarchical structure and feature extraction process of the proposed model.

3.2. Neutrosophic Logic Integration

To enhance robustness against uncertainty and indeterminate disease symptoms, we introduce a Neutrosophic output layer on top of the Softmax classifier. Given the Softmax probability vector $p = [p_1, p_2, \dots, p_n]$ for n classes, the Neutrosophic components are derived as follows: the Truth component $T = p_{\max}$ (the highest class probability), the Falsity component $F = 1 - p_{\max}$ (the complementary probability), and the Indeterminacy component $I = 1 - |p_{\max} - p_{\text{second}}|$ (capturing the ambiguity between the top two competing classes). This formulation acts as an interpretability layer rather than a modification of the loss function, providing an additional perspective on model confidence and prediction reliability. According to the theory of Neutrosophic logic, for every predictive output, there are three independent components:

- Compact CNN architecture designed with small budgets in mind.
- Truth (T): our level of belief in the selected class
- Indeterminacy (I): The level of doubt due to noise, overlap, or ambiguities.
- Falsity (F): the likelihood that the categorization is erroneous.

By incorporating the concept of indeterminacy, the system produces more reliable and interpretable results than the traditional probabilistic classifiers. Recently, Neutrosophic Set representation has demonstrated its robustness in the task of deep learning for agricultural images and medical images [10].

3.3. Data Preparation and Enhancement

All input images are resized to a standard dimension of 224 × 224 × 3 pixels and will be transformed into the range of [1,0]. Applying different image transformation is another approach to minimize the model's overfitting during training. These changes are rotation, flip both along horizontal and vertical axes and vary the contrast and brightness. There will also be the use of MixUp and CutMix techniques.

4. Analysis and Discussion of Results

The following section discusses an extensive experimental evaluation of the developed model for disease detection in tomato leaves under the proposed concept. The following section discusses in detail the features of the data, methods, or experiment setup used to test the proposed framework and highlights the importance of the neutrosophic inference layer in decision-making.

4.1. Dataset Description

In our work, we retrieved tomato leaf images from the PlantVillage dataset, which is publicly available on Kaggle: `https://www.kaggle.com/datasets/abdallahalidev/plantvillage-dataset`. a widely accepted benchmark dataset in plant disease classification tasks. In recent reviews on state-of-the-art plant disease classification models, PlantVillage contains around 54,300 labeled images, including disease- and disease-free leaf samples obtained under controlled environments, and represents thirty-eight disease categories from fourteen crop types.

For our case, as depicted in Figure 2 we were only interested in leaf-like classes pertaining only on the leaves of the tomato plant, thus forming a subset with ten classes: nine classes representing different diseases (Bacterial Spot (BS), Early Blight (EB), Late Blight (LB), Leaf Mold (LM), Septoria Leaf Spot (SLS), Target Spot (TS), Two-Spotted Spider Mite (TSSM), Yellow Leaf Curl Virus (YLCV), Mosaic Virus (MV)) along with a healthy class.

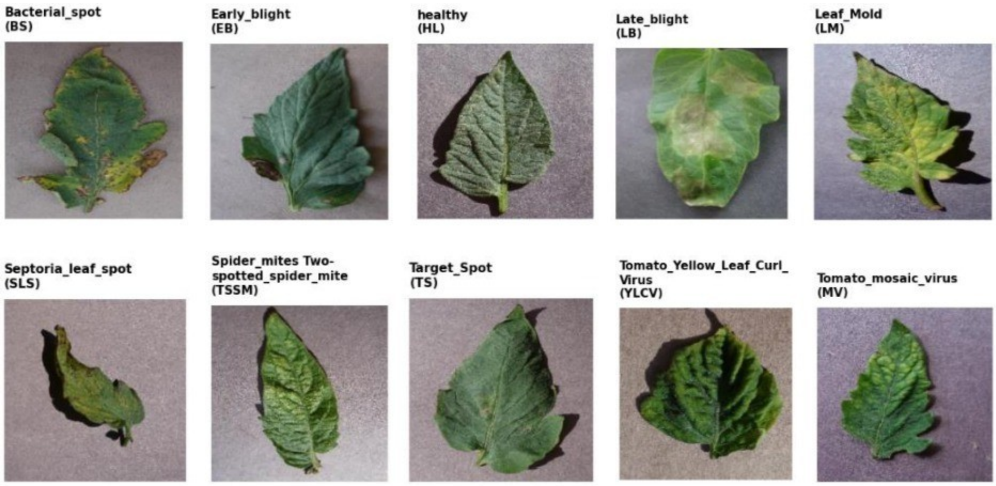

Figure 2. Curves of training and validation accuracy

Despite being vastly applied for deep learning-based studies, PlantVillage has some known drawbacks that may affect the performance:

- Class Imbalance: There is imbalance in class counts, which can create bias towards more populated classes, affecting generalization towards less represented classes of diseases.

- Controlled Imaging Conditions: Images are acquired with standard backgrounds and standard light conditions that may not reflect real-world conditions found in agricultural applications.

Given these difficulties, an approach involving the use of recent techniques for data augmentation, appropriate feature extraction, and an output layer inspired by neutrosophic theory, which tackles uncertainty, is suggested in the proposed method

4.2. experimental results framework

The experiment involved the use of TensorFlow and Keras libraries of Python programming language, commonly used in Deep Learning applications. The model was implemented using Jupyter Lab software in 64-bit Windows 10 environment. GPU was exploited to boost the process, while maintaining the RAM size to 8 GB, which is sufficient for the relatively light model.
Training was conducted for 50 iterations (epochs). To optimize the learning rate, a Cosine Annealing Scheduler was used. The approach allowed for finding an adequate solution and avoiding poor local minima. In addition, warm-up was implemented in the initial stage of training. Hyperparameters can be found in Table 1.
In view of these challenges, to address them, a combination of modern data augmentation techniques with proper feature extraction along with a neutrosophic-inspired output layer that targets uncertainty is offered by the proposed model

To ensure reproducibility and transparency, the complete implementation of the proposed framework, including preprocessing, training pipeline, and evaluation scripts, is publicly available at: `https://github.com/Fady-Salama/tomato-leaf-disease-neutrosophic-cnn`.

4.2.1. Training Dynamics and Optimization Behavior To run these experiments, I used Python with TensorFlow and Keras, which are common tools for deep learning. The model was built inside Jupyter Lab on a 64-bit Windows 10 system. I made use of the GPU to speed things up, while keeping the RAM at 8 GB just enough for the model's light design.
Training went on for 50 rounds (epochs). To adjust the learning rate along the way, I applied for a Cosine Annealing Scheduler. This helped the model settle into a good solution and avoid getting stuck in poor local spots. I also included a warm-up phase at the start of training. You can find the hyperparameters I used in Table 1 below.

Table 1. Hyperparameters for the proposed model

Hyper Parameters	**Description**
No. of convolution layers	8
No. of Separable convolution layers	8
No. of max pooling layers	4
Initial Learning rate	$7.088656275030309 \times 10^{-6}$
Max no. of epochs (Early Stopping)	50
Dropout rate	0.4
Batch Size	64
Optimizer	AdamW
Activation function	sigmoid, relu, softmax
Loss function	CategoricalCrossentropy

After completing all the preprocessing stages, we got a total number of 18,160 tomato leaf images for experimental purposes (refer to Table 2 below). To make sure that the outcome of our research would be replicable and unbiased, we assigned labels to each of these images and then shuffled them randomly with the help of a random seed (random_state=42).This resulted in splitting the data into:

- Training set: 12,712 images (70%)
- Validation set: 1,816 images (10%)
- Test set: 3,632 images (20%)

Table 2. Dataset Split for Training, Validation, and Testing

Tomato Leaves Disease	**Trained Images**	**Validation Images**	**Tested Images**
Tomato__Bacterial_spot	1497	228	402
Tomato__Early_blight	690	98	212
Tomato__Late_blight	1335	205	369
Tomato__Leaf_Mold	685	95	172
Tomato__Septoria_leaf_spot	1236	179	356
Tomato__Spider_mites Two-spotted_spider_mite	1155	166	355
Tomato__Target_Spot	977	142	285
Tomato__Tomato_Yellow_Leaf_Curl_Virus	3785	512	1060
Tomato__Tomato_mosaic_virus	257	43	73
Tomato__healthy	1095	148	348
Total Leaves	**12712 (70.00%)**	**1816 (10.00%)**	**3632 (20.00%)**

This methodology ensures that the ratio between classes remains constant in both sets, thereby facilitating the generation of a dependable baseline to assess model performance. In all experiments conducted, the same preprocessing techniques and data augmentation procedures were followed.

4.3. Training Dynamics and Optimization Behavior

The training of the proposed algorithm was controlled by accuracy and loss graphs against the training and validation procedures, as shown in Figure 3 and Figure 4.

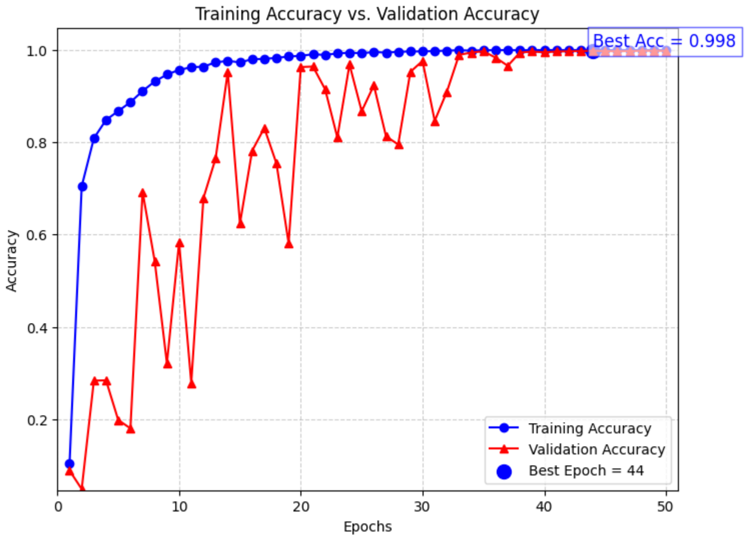

Figure 3. Curves of training and validation accuracy.

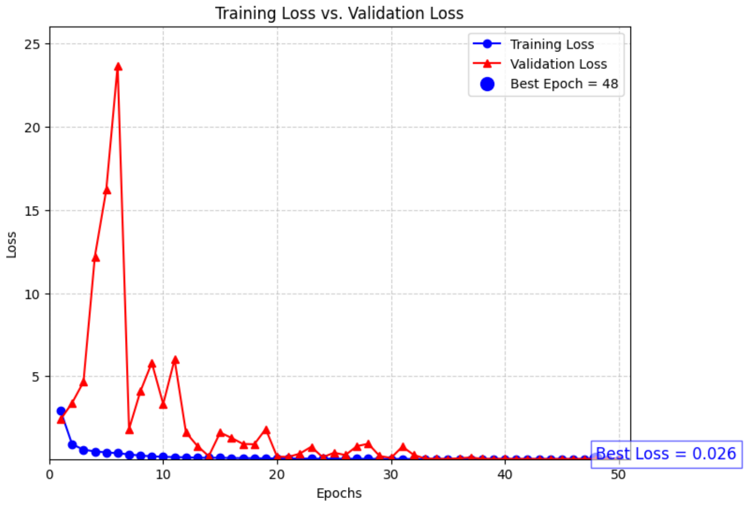

Figure 4. Training and validation loss curves demonstrating model convergence.

It starts with a fast drop in the loss values along with a fast rise in accuracy values; afterward, the model becomes stable with consistent learning. In the current situation, the loss values in both the training and validation procedures converge to zero values, implying that the optimization is done effectively, with training and validation metrics converging stably. While the low loss values suggest good optimization, it should be noted that performance on a controlled benchmark dataset does not necessarily guarantee real-world generalization.

To mitigate overfitting, multiple regularization techniques were applied including data augmentation, label smoothing, and class weighting. The ROC curve shown in Figure 5 indicates the discrimination power of the model for all classes.

For improving the convergence stability, the cosine annealing learning rate strategy with the initial warm-

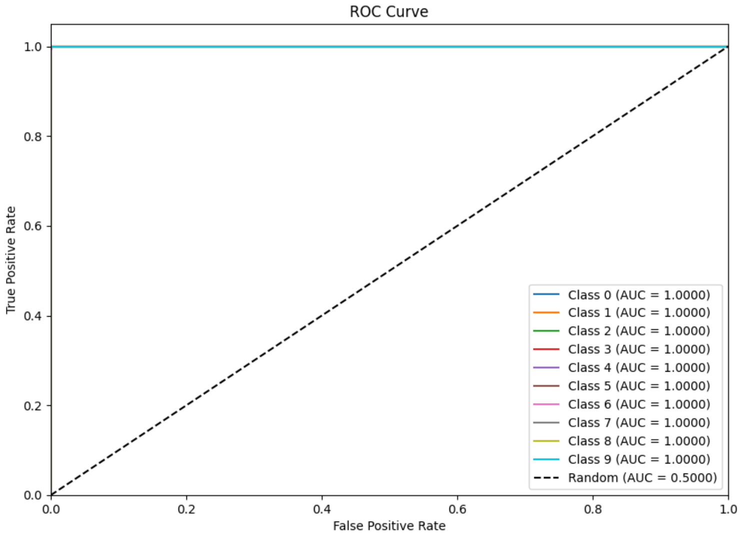

Figure 5. ROC curve analysis quantifying the classification model's diagnostic performance.

up approach was utilized. Figure 6 displays the learning rate at each training step, revealing the decline of the learning rate with time.

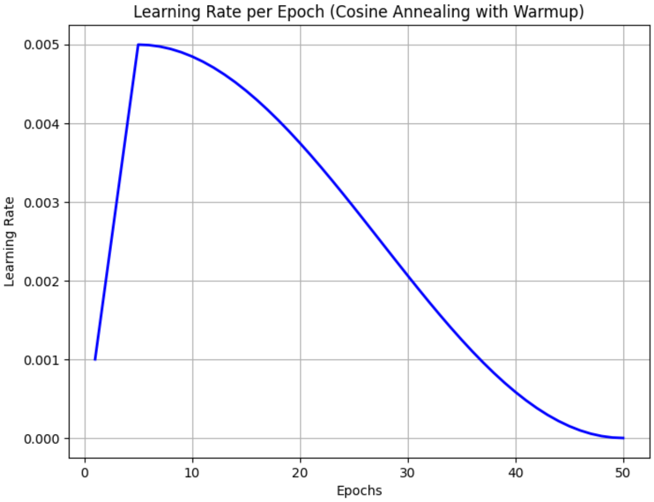

Figure 6. Illustration of the cosine annealing schedule applied to the learning rate during the training phase.

4.4. Quantitative Performance Evaluation

The proposed model was tested on the test set based on the following criteria: accuracy, precision, recall, and F1-score. The model demonstrated very good accuracy at the test stage 99.75%. That is a strong indicator of its good generalization and ability to process new data correctly. To further validate the results, we performed an assessment at the class level to evaluate the impact of class imbalance on performance. The dataset exhibits class imbalance, with the Yellow Leaf Curl Virus class being the most represented (5,357 images) and Mosaic Virus the least (373 images). Despite this imbalance, the model demonstrates consistent results across all ten disease types through the use of class weighting, providing a strong balance between precision and recall rates. It should be noted that additional validation on external, field-collected datasets would further strengthen these conclusions and is identified as an important direction for future research. More information regarding precision, recall, F1-score, and support per class is provided in Table 3, known as the Classification Report. The results presented above confirm that the proposed model performs reliably even for rare disease types. In other words, the above results demonstrate that the proposed model satisfies the accuracy and consistency requirements.

4.5. Class-wise Performance Analysis

Further examination of results on per-class level once again proves that the classifier is effective. According to Table 3 below, there are several disease types, such as Bacterial Spot, Leaf Mold, Septoria Leaf Spot, Tomato Yellow Leaf Curl Virus, and Healthy leaves, whose precision, recall, and F1-score are equal to 1.00. Thus, the classification is accurate for such cases.

Despite similarities among some of the diseases under analysis, such as Early Blight and Target Spot, the F1-score remains almost perfect, ranging from 0.98 to 0.99. The discrepancy can be attributed to the presence of common features and slight differences that can be observed in these diseases. However, the value for recall remains high; only few samples have been falsely classified.

The macro-average and weighted average both are equal to 1.00, suggesting that the classifier operates in a similar way regardless of disease type.

This reassures us that the model is not leaning towards the frequent classes and it accurately detects occurrences of a disease in which the class is of low frequency. Aggregated, class-wise results confirm that the proposed model guarantees stable and reliable performance in all the classes of tomato leaf diseases, hence proving it is ready for real-world agricultural monitoring, where dependable class-level performance is required.

Table 3. Comprehensive classification report and performance metrics for the proposed model on the test dataset.

Class	**Precision**	**Recall**	**F1-score**	**Support**
Tomato Bacterial spot	1.00	0.98	0.98	403
Tomato Early blight	0.99	0.97	0.98	201
Tomato Late blight	0.99	0.98	0.98	309
Tomato Leaf Mold	0.99	0.98	0.98	396
Tomato Septoria leaf spot	0.98	1.00	0.99	386
Tomato Spider mites Two-spotted	0.99	0.98	0.98	380
Tomato Target Spot	0.96	0.98	0.97	354
Tomato Yellow Leaf Curl Virus	1.00	1.00	1.00	1096
Tomato Mosaic Virus	0.97	1.00	0.98	373
Tomato Healthy	0.96	1.00	0.98	321
Accuracy	**0.99 (Total: 3632)**			
Macro avg	0.98	0.99	0.99	3632
Weighted avg	0.99	0.99	0.99	3632

4.6. Analysis of the Confusion Matrix

Figure 7 represents the confusion matrix obtained for the independent test set. This output summarizes the level of success the developed model has in distinguishing between the classes, which is evident from the fact that most of the cases belong to the diagonal of the matrix, thereby emphasizing the elevated level of success in identifying each of the diseases in the leaves of tomatoes. A handful of errors are noticed, which occur between those classes that have visually alike characteristics, for instance, Early Blight (EB) and Septoria Leaf Spot (SLS). This agrees with the observations made by previous research and captures the actual, subjective similarity amongst some leaf diseases on a tomato plant, as opposed to some defect in the proposed model. Significantly, these cases on the border will be explored using neutrosophic inference in the next subsection.

4.7. Impact of Neutrosophic Inference on Decision Reliability

Unlike the conventional softmax classifiers, which produce only one confidence value, our approach presents the neutrosophic inference layer as an addition to the conventional softmax classifiers. The prediction confidence is categorized into three components: Truth (T), Indeterminacy (I), and Falsity (F).

The addition of the capability of neutrosophic logic helps capture uncertainty, especially when symptom overlap occurs. For example, when samples exhibit similar texture and color characteristics between Early Blight disease and Septoria Leaf Spot disease, the indeterminacy value increases. Rather than arriving at a definite but non-confident diagnosis, the neutrosophic layer reveals how the certainty level diminishes, thereby providing additional insight into the reliability of the final prediction. In highly confident predictions, the Truth component dominates, while the Falsity and Indeterminacy components remain negligible.

It is important to note that the Indeterminacy (I) values observed in Table 4 are extremely low (on the order of 10^{-12}). This behavior is consistent with the high separability of PlantVillage images, which were acquired under controlled conditions with uniform backgrounds, leading to highly confident softmax predictions and consequently near-zero indeterminacy values.

In more challenging real-world conditions with overlapping symptoms and noisy backgrounds, higher indeterminacy values would be expected, which is precisely where the neutrosophic layer provides the greatest

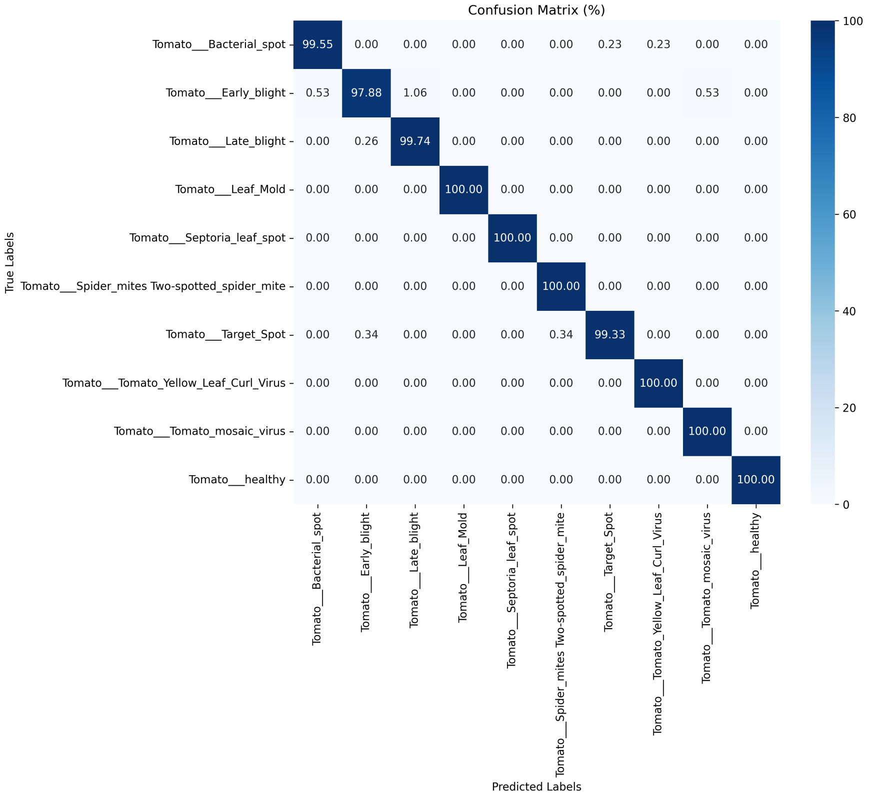

Figure 7. Confusion matrix summarizing classification results of the proposed model on the tomato leaf test data.

benefit. It is further acknowledged that complementary uncertainty estimation methods such as MC-Dropout and calibration curves are important evaluation tools and are identified as directions for future research.

These findings demonstrate that the neutrosophic layer preserves confident predictions while emphasizing uncertainty only when necessary. Table 4 presents examples of neutrosophic values associated with the corresponding disease categories, whereas Figure 8 illustrates the distribution of neutrosophic values for each class. As observed from the results, the ability of neutrosophic logic to distinguish between reliable and unreliable predictions makes it particularly relevant for agricultural disease diagnosis.

Table 4. Sample neutrosophic output representation (T/I/F) for selected tomato leaf disease classes.

Disease Class	**Accuracy**	**Precision**	**Recall**	**F1 Score**	**T Truth**	**I Indeterminacy**	**F Falsity**
Tomato_Bacterial_spot	0.995	0.997	0.995	0.996	0.995	2.25E-12	0.0045
Tomato_Early_blight	0.978	0.989	0.978	0.984	0.978	5.29E-12	0.0211
Tomato_Late_blight	0.997	0.994	0.997	0.996	0.997	2.55E-12	0.0025
Tomato_Leaf_Mold	1	1	1	1	1	5.38E-12	5.38E-12
Tomato_Septoria_leaf_spot	1	1	1	1	1	2.82E-12	2.82E-12
Tomato_Spider_mites Two-spotted_spider_mite	1	0.997	1	0.998	1	2.67E-12	2.67E-12
Tomato_Target_Spot	0.993	0.996	0.993	0.994	0.993	3.36E-12	0.00671
Tomato_Tomato_Yellow_Leaf_Curl_Virus	1	0.999	1	0.999	1	9.88E-13	9.88E-13
Tomato_Tomato_mosaic_virus	1	0.985	1	0.992	1	1.45E-11	1.45E-11
Tomato_healthy	1	1	1	1	1	3.22E-12	3.22E-12

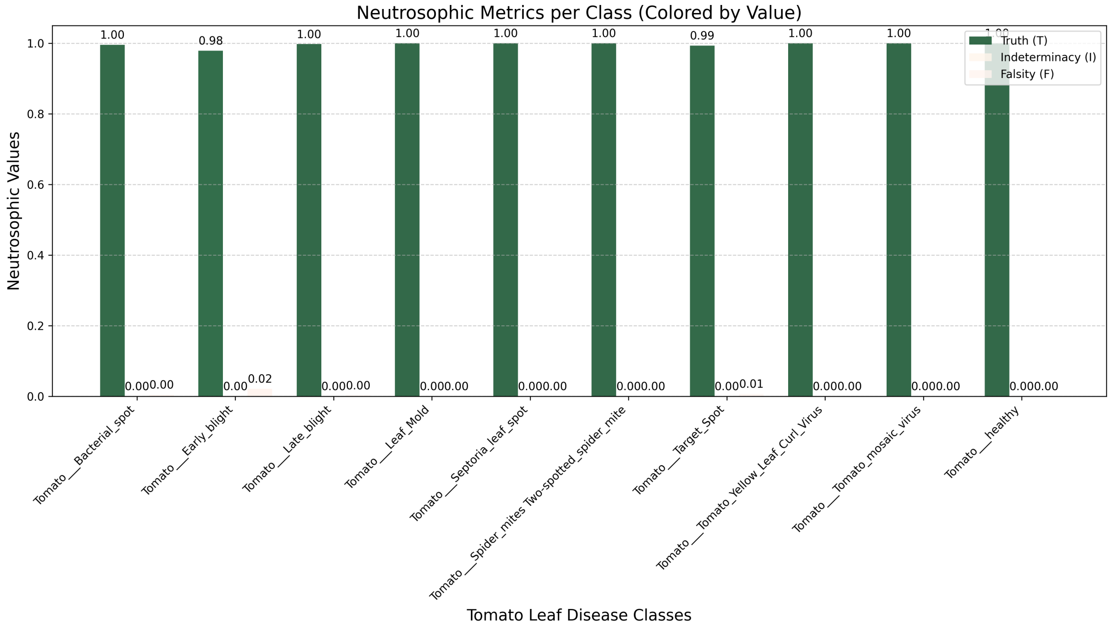

Figure 8. Class-wise neutrosophic metrics (Truth, Indeterminacy, and Falsity) for the tomato leaf disease categories.

4.8. Qualitative Analysis and Visualization

In order to gain insight into how the model works, we applied Grad-CAM for identifying salient features from each tomato leaf image. As shown in Figure 9, the model successfully focused on the parts of the leaf affected by diseases, such as spots, irregularities in texture, and discolored areas, which means that it was learning to recognize the correct features [27]. Additionally, to improve the transparency of the model, we included neutrosophic certainty values.Combining these two interpretability techniques:

- Grad-CAM displays the focused areas of the tomato leaf.
- Neutrosophic inference scores represent the truth, indeterminacy, and falsehood scores of the model.

This allows us to obtain a deep insight into the model decisions and therefore support and assist the decision-making of experts and stakeholders in the field of agriculture, such that the automatic disease identification system becomes dependable.

5. Discussion

The outcomes confirm that the developed model handles the task successfully for detecting tomato leaf conditions in a similar lab-type environment. The model possesses a great balance between the classification performance, processing speed and the trust of classification outcomes. Therefore, it is very practical in farming[28].

A significant part of this model is the neutrosophic inference layer which also takes in consideration the problem of handling uncertainty of the classification results; instead of relying on a specific probability, the model can produce the result as truth, indeterminacy and falsity which further helps to handle different degrees of visible similarities of diseases symptoms and the leaf patterns.

Experimental results demonstrate that by considering the uncertainty, robust system with a reasonable performance can be built for diverse diseases. The neutrosophic set is applied for the confidence measure of difficult instances and the number of wrongly made overconfident predictions decreases. This is meaningful as in real world applications, a mistake on the misclassification will bring significant cost both economically and agriculturally.

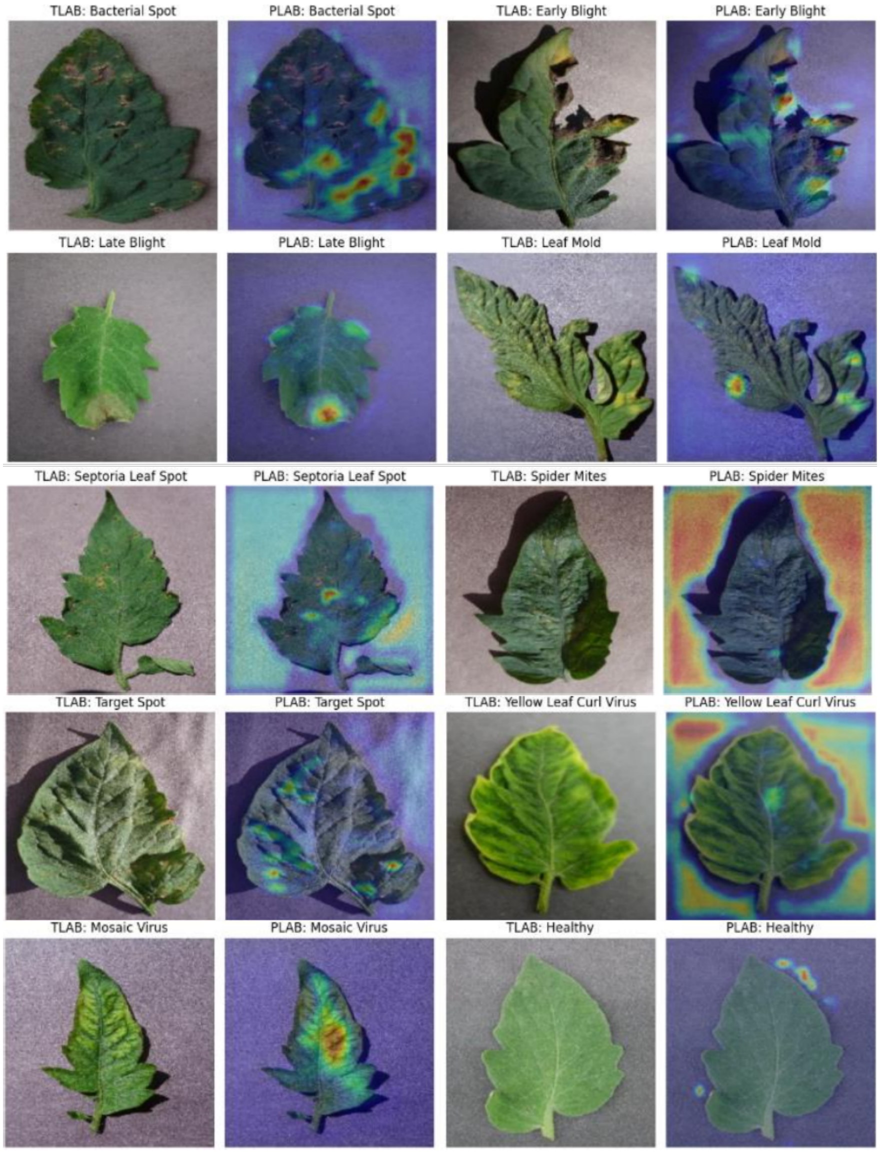

Figure 9. Visualization of Grad-CAM heatmaps for the proposed Model.

It also has a very small size which is not computational burden so that it can be effectively used in resource restricted environments such as mobile computing and remote farmlands surveillance by edge computing. Compared to established lightweight architectures such as MobileNetV2 (approximately 3.4M parameters) and SqueezeNet (approximately 1.2M parameters), our proposed model with 219,651 parameters is significantly more compact while achieving comparable or superior accuracy on the PlantVillage benchmark. This demonstrates that efficiency and accuracy need not be traded off. It is acknowledged that direct hardware-level benchmarking (FLOPs, inference latency on target edge devices) is beyond the current scope and is identified as important future work. However, even with this small computational burden, fair performance is shown in comparison with other methods described in the literature, indicating that the uncertainty consideration in the classification model will not necessarily lead to reduced performance.

One more advantage of the method is that even though trained with some complex data augmentation techniques, the classifier also demonstrates great generalization performance on other data, and this helps it cope with slight changes of the leaf appearances, and the neutrosophic layer provides robustness against the imprecise output of the classifier. Such integrated decision making is more powerful for diagnosis of tomato leaf diseases.

An important limitation of this work is that evaluation was conducted exclusively on the PlantVillage benchmark dataset, which features controlled imaging conditions with uniform backgrounds. Real-world agricultural deployment would require validation on field-collected datasets under varying lighting, occlusion, and environmental conditions, which remains an important direction for future research. Conclusion overall: the designed system provides better quantitative results and enhances decision making quality in a qualitative way. Thanks to its efficient way of pulling out key features and its ability to model uncertainty using neutrosophic logic, this method shows real promise for intelligent plant disease diagnosis.

6. Conclusion

In this paper, we present a deep learning framework designed to classify tomato leaf diseases that incorporate a neutrosophic inference layer to address uncertainties in tomato leaf disease detection. The proposed system combines an efficient extraction of features extracted from the convolutional layer combined with the neutrosophic logic approach to address uncertainties while increasing the reliability of classification predictions.

Large-scale trials on the PlantVillage tomato leaf dataset show that the model achieves strong classification performance under controlled benchmark conditions, without heavy computational costs, so it can be especially useful on resource-constrained hardware. It should be acknowledged that the PlantVillage dataset does not fully represent the complexity of real-world agricultural environments, and real-field deployment remains an important direction for future research.

With neutrosophic logic introduced in this work, it can be concluded that this concept is extremely helpful in dealing with uncertain symptoms of plant diseases that overlap each other visually. It is clear from the results that the impact of uncertainty will be positive in enhancing robustness and improving decision-making without having any negative effect on the model's complexity and time complexity. The importance of the trade-off between these three factors will come into play when we think about implementing this model in practical applications such as farms.

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