Journal of the Brazilian Computer Society, 2025, 31:1, doi: 10.5753/jbcs.2025.4581

Enhancing Disease and Pest Detection in Greenhouse Tomato Cultivation Using Advanced Machine Learning on New Dataset of Images

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Received: 05 June 2024 • **Accepted:** 06 February 2025 • **Published:** 13 March 2025

Abstract Increasing food production is a continuous need. In this context, agriculture is a fundamental part of meeting the ever-increasing demand for food. Plant diseases are one of the factors that compromise food production goals, and the characteristics and climate of each production region influence them. Tomatoes are one of the world's most consumed vegetables and are widely affected by various diseases. However, tomato cultivation in greenhouses allows its continuous production. In this context, this research work focuses on the problem of identifying diseases in scenarios of tomato cultivation in greenhouses, where we have specific occurrences of diseases that are affected by regional climatic conditions. Brazil is a major producer of tomatoes, producing more than 3 million tons annually, with 8% of this production being made in the state of Paraná. This study was developed through data collection in collaboration with greenhouse tomato producers from an important region in North Paraná. For this study, we created new datasets with two image sizes: the Tomato Leaf Image Dataset (TLID) with image sizes of 256×256 pixels and 15,256 images, and the Patch Tomato Leaf Image Dataset (PTLID) with patch sizes of 32×32 pixels and 227,218 images. Both datasets comprise seven classes, including four types of diseases, two combinations of diseases on the same leaf, and the healthy leaf. Machine Learning techniques have been widely used to identify plant diseases. This work presents two machine learning methods tested with both datasets. In the proposed models, we combine three convolutional neural networks, a customized CNN, VGG19, and Resnet50, and two voting classification methods using hard and soft decisions. The evaluation performed on the datasets showed that when the patches are used, the results improve significantly, reaching an accuracy of 90.48%. It is also possible to identify the stage of the disease.

Keywords: Plant Diseases, Tomato Diseases, Greenhouses, Convolutional Neural Networks, Ensemble, Deep Learning

1 Introduction

The demand for food increases concomitantly with the growth of the world population, which should reach almost ten billion people by 2050 [Food and of the United Nations, 2017]. In this context, agriculture is fundamental for the food supply, representing, in the economic aspect, 4% of the global gross domestic product (GDP), reaching more than 25% in developing countries [Bank, 2022]. To ensure continuous supply, two aspects directly related to productivity and fruit quality stand out: i) climatic interference by biotic and abiotic agents acting on the plant continuously, altering its metabolism [Lopes and Ávila, 2005], and ii) plant diseases, since in warmer regions, the occurrence of diseases is more pronounced than in colder regions.

Diseases in crops are typically identified by farmers or specialized technicians, who may recommend laboratory tests for more accurate diagnosis, especially when symptoms are similar. Pesticides are commonly used to combat these diseases, but improper application can harm human health and contaminate soil, water, and air. It can also reduce soil fertility and pollute groundwater and water bodies. Tomatoes, widely consumed and rich in nutrients like lycopene, vitamins, and minerals, are particularly vulnerable to diseases. According to the FAO, global tomato production reached 70 million tons in 2014, while Brazil's production was around 4 million tons in 2021 [IBGE, 2022; Leite and Fialho, 2018]. Tomato production can occur in open fields, aimed at the sauce and extract industry, or in greenhouses, intended for fresh consumption, which requires high-quality fruits for sale. Greenhouse cultivation, usually carried out by small farmers with family labor, allows for year-round production but requires constant monitoring to prevent diseases that may compromise quality and market value. Over 200 diseases and physiological disorders affect tomato cultivation worldwide [Lopes and Ávila, 2005], with symptoms appearing primarily on leaves but also affecting leaflets, stems, roots, and fruits, caused by fungi, bacteria, nematodes, and viruses.

Detecting plant diseases is a critical issue studied over the years to produce healthy food and reduce production costs. In this context, precision agriculture can be the solution to mitigate the effects of these diseases [Balasundram *et al.*, 2020]. In most current studies, with machine learning and deep learning, image processing techniques are used to identify and classify plant leaf diseases [Kini *et al.*, 2023]. Through remote sensing devices, these technologies can detect diseases at the beginning, allowing measures to be taken before they spread and compromise the production and quality of food [Khanal *et al.*, 2020; Bharadwaj *et al.*, 2024].

Although several machine learning-based disease identification methods are proposed in the literature, there is a recurring problem: the limited amount of existing data in the agricultural area. The available databases do not include all diseases that can affect tomato [Hughes and Salathe, 2016; Turkoglu *et al.*, 2022] crops because there is a wide variety of diseases [Lopes and Ávila, 2005], and gathering images of these diseases depends on knowledge, for example, of the timing of their occurrence in the crop and timely photography registration. Another very important factor to consider is the occurrence of two diseases on the same leaf, which allows understanding how the algorithm will behave when identifying both diseases. Diseases also vary from region to region and from one crop type to another [Ghini *et al.*, 2008; Lopes and Ávila, 2005]. Greenhouse tomato leaves are crucial because they are never washed by rainwater or irrigation methods, causing the accumulation of particles, dust, and fertilizer residues on their surface [Campagnol R, 2015]. **Figure 1** shows images of a healthy tomato leaf and others with different diseases and their combinations.

Considering that the greenhouse environment favors the development of specific diseases, different from those that occur in the open field [Vida *et al.*, 2004; Vox *et al.*, 2010] and also that vary from one region to another due to climatic factors [Ghini R, 2011; Angelotti F, 2017], here we propose a specific method for the recognition of diseases in the cultivation of tomatoes in environments of greenhouses with a regional focus. There is a lack of specific databases with images of diseases associated with cultivating tomatoes in greenhouses. This cultivation scenario has peculiarities regarding the types and characteristics of diseases that may be present in tomatoes.

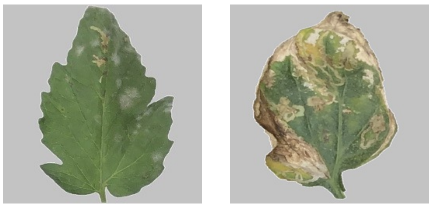
Through this study, we intend to answer the following research questions:

- Q1: Do the diseases present in greenhouse tomato cultivation have regional specificities?
- Q2: How do identification algorithms behave using unprocessed images collected by smartphones?
- Q3: Is it possible to increase accuracy in disease identification by combining machine learning algorithms?
- Q4: Is it possible to identify the presence of multiple diseases on tomato leaves and their degree of contamination using machine learning-based strategies?

Therefore, in this work, we created a new database for studies and research in the specific task addressed here. We carried out the collection of images *in loco* using a smartphone in a large producing region for the assembly of the new database. In addition to healthy leaves, we identified six types of diseases and a combination of diseases on the same leaf. From this database, we developed a specific strategy for classifying diseases in tomatoes using three deep-learning algorithms: customized CNN, VGG19, and Resnet50. The proposed strategy also applies combination and voting methods to identify each class accurately.

(a) Healthy leaf. (b) Leaf Miner.

(c) Bacterial Spot. (d) Powdery Mildew.



(e) Powdery mildew and Leaf Miner. (f) Bacterial Spot and Leaf Miner.

(g) Whitefly.

Figure 1. Example of a healthy leaf and diseased leaves.

The contribution of this work is threefold, as follows:

(i) Dataset of tomato leaf comprising 7 classes and 15,256 images of diseases and pests, encompassing both healthy and diseased leaves, as well as the combination of two diseases on the same leaf, collected from a specific producing region that employs greenhouse cultivation. The dataset will be made publicly available to facilitate future research.
(ii) Proposal of deep learning-based methods for tomato disease identification, using a combination of classifiers.
(iii) Experimental results to introduce the new dataset, which can be considered as a baseline performance for further research.

The remainder of this paper is structured as follows: Section 2 presents related works on disease detection from plant leaves using machine learning and deep learning methods, predominantly considering specific works for tomatoes. In Section 3, we contextualize the study and formulate the research problem. Section 4 provides details on the new dataset construction. In Section 5, we present the proposed tomato leaf disease classification methods. Section 6 describes the results and analyses of the proposed method. Section 7 presents the conclusion and future work.

2 Related Work

Plant diseases cause production losses and alter fruit quality. Therefore, one of the significant challenges is the early detection of diseases, which will make it possible to reduce these losses. In this context, several methods using *machine learning* and *deep learning* models have been proposed and have been widely used in different cultures, achieving significant results. The primary studies identified in the literature are presented below.

Despite the promising results presented by standard machine learning classifiers, deep learning algorithms have shown to be more efficient in identifying plant diseases. Convolutional neural networks are excellent when it comes to feature extraction. Several studies have used these networks to classify diseases in tomato plants.

In the study by [Brahimi *et al.*, 2017], the authors compared the performance of the deep models AlexNet and GoogleNet with that of the shallow models Random Forest and SVM. This comparison was important as it demonstrated the effectiveness of deep models for image classification. For this purpose, the PlantVillage dataset was used with all available images of tomato leaves.

The authors [Sardogan *et al.*, 2018] used a combination of CNN with the Learning Vector Quantization (LVQ) algorithm. The study partially utilized the PlantVillage dataset, considering only four diseases. It was concluded that the combination of these two methods was effective in recognizing the analyzed diseases.

The authors [Tm *et al.*, 2018] used the PlantVillage dataset with all available tomato leaf images and a simple convolutional neural network architecture, with a minimal number of layers, to classify tomato leaf diseases into different classes. The study demonstrated that even a simple classifier can efficiently classify images of tomato diseases.

In [Meeradevi *et al.*, 2020], the authors used the VGG16 architecture along with the PlantVillage dataset in a balanced manner, but considered only a few disease classes. The model, when used alone, exhibited overfitting. However, by applying L2 regularization, the overfitting issue was addressed, resulting in good model performance.

The authors [Sharma *et al.*, 2020] utilized four machine learning techniques: logistic regression, KNN, SVM, and CNN. Image processing and segmentation techniques were applied to enhance the performance of the classifiers in identifying diseases. The dataset was obtained from online sources such as Kaggle and GitHub. Among the presented techniques, the CNN achieved the best results, highlighting the superiority of these networks in image classification.

In [Hong *et al.*, 2020], the authors compared five deep network architectures DenseNet-Xception, Xception, ResNet50, MobileNet, and ShuffleNet to determine which one would yield the best results in identifying diseases in tomatoes. For this purpose, images of tomato leaves from the PlantVillage dataset were used. The study revealed that networks employing different types of convolutions, such as the dense and separable connections of DenseNet-Xception, achieved superior recognition accuracy compared to ResNet, which uses residual connections, and the lightweight networks MobileNet and ShuffleNet.

A comparison of architectures was conducted by [Gehlot and Saini, 2020], using the PlantVillage dataset to identify diseases in tomato plants. The pretrained networks analyzed were AlexNet, VGG-16, GoogleNet, DenseNet-121, and ResNet-101. DenseNet-121 achieved the highest accuracy and had the smallest size, while ResNet-101 and VGG-16 showed similar performance, but ResNet-101 is larger, making it unsuitable for smaller devices.

In the work presented by [Pushpa *et al.*, 2021], the authors compared VGG16, LeNet-5, and AlexNet and applied image processing techniques. The dataset was sourced from PlantVillage, containing images of healthy and diseased leaves. When comparing the three models, AlexNet and VGG16 demonstrated the best performance, achieving the highest accuracy, thereby proving that models with deeper architectures can achieve better performance.

The PlantVillage dataset was used by [Tan *et al.*, 2021], who applied color and texture feature extraction techniques. Various traditional classifiers were considered, such as SVM (Support Vector Machine), KNN, and Random Forest, along with deep learning architectures AlexNet, VGG16, ResNet34, EfficientNet-b0, and MobileNetV2 for comparison. The results indicated that the deep learning model ResNet34 achieved the highest accuracy in classification.

A new CNN architecture was proposed in [Sakkarvarthi *et al.*, 2022]. The PlantVillage dataset for tomatoes was used partially. The new architecture was compared with other pretrained networks, such as ResNet152, VGG19, and InceptionV3, and the proposed model outperformed the other networks.

In [Omar *et al.*, 2022], the authors also created a model based on CNN. The PlantVillage dataset was used, considering the nine classes of tomato diseases and one healthy class. The model achieved good results but did not surpass those of the pretrained networks obtained for the same dataset.

The study conducted by [Malunao *et al.*, 2022] developed a machine vision system to recognize leaf diseases in tomato plants using DNN (Deep Neural Network) and the YOLOv3 (”You Only Look Once”). The combination of these two approaches ensured high accuracy in classifying tomato diseases.

In [Pradhan and Kumar, 2022], the authors proposed a deep approach based on CNN to identify tomato leaf diseases. The experiments were conducted using the PlantVillage dataset and were used to test the performance of pretrained models, including DenseNet169, InceptionResNet V2, InceptionV3, VGG16, VGG19, DenseNet201, MobileNet, MobileNetV2, and Xception. The new method could be an alternative option to traditional disease identification methods.

In [Turkoglu *et al.*, 2022], different methods were compared to obtain deep convolutional networks trained for the classification of plant diseases and pests. State-of-the-art pretrained deep networks (AlexNet, GoogleNet, ResNet18, ResNet50, ResNet101, and DenseNet201) were used with transfer learning to classify images, as well as feature extractors combined with an SVM classifier. The database was constructed from images of various crops observed in Turkey. The results demonstrated the effectiveness of the proposed models compared to other state-of-the-art algorithms.

In the research conducted by [Khalid *et al.*, 2023], the proposed technique evaluated three deep learning models for classifying diseases in tomato leaf images: ResNet-152, EfficientNet-B4, and VGG-16. The PlantVillage dataset was used, considering only three diseases. Although all networks achieved excellent results, VGG-16 reached the highest accuracy. The results demonstrate that CNNs are highly suitable for the efficient detection of plant diseases.

Based on the review presented in this section, it is observed that several studies explore techniques for identifying diseases in tomato plants using machine learning methods. It is also noted that deep learning has emerged as the technique with the best performance for this purpose. Most studies use the PlantVillage dataset due to its flexibility for different approaches, the wide variety of crops, and the diversity of diseases it contains. However, some important factors should be considered, such as the way the images were collected. According to the creator of the dataset, the leaves were removed from the plants and photographed separately. This process can eliminate some important characteristics present in the leaves in their natural environment, such as spots, insects, residues from applied products, dust, and others. Additionally, many studies rely exclusively on this dataset, which, although valuable, does not cover all diseases that affect tomato crops and does not account for the possibility that a single tomato plant may be simultaneously infected by multiple diseases.

Table 1 summarizes the main characteristics of the related work described in this section. It is important to remark that in most of the studies on tomato disease identification, the same database was used, varying only the number of images considered. In this sense, we can point out that our study methodology is more correlated to the studies of [Tarik *et al.*, 2021] and [Ahmed *et al.*, 2019], as both also collected their own images of diseased plants and considered those most critical for their geographic region.

3 Contextualization and Problem Formulation

Plant diseases vary according to the climate of each region, which determines or intensifies the appearance of diseases. In countries of continental dimensions, such as Brazil, the climate varies throughout the territory, with the southern region being the coldest and having a predominance of subtropical climate. This type of climate favors the emergence of some important diseases that compromise tomato production. Culturing in a greenhouse helps reduce the effects of climate on plants. Greenhouses protect against weather conditions such as cold fronts, excessive rainfall, hail, winds, and direct sunlight, thus maintaining the integrity of the plants. On the other hand, despite the benefits of the greenhouse, it also favors the appearance of some diseases because, in this type of cultivation, the leaves are not washed by rain or dew. Generally, the irrigation methods are done by dripping, thus preventing the plant from being washed.

There are several studies to identify tomato diseases, in which the PlantVillage database [Hughes and Salathe, 2016] is used with several diseases that attack the plant. However, tomatoes can be attacked by more than 200 different diseases [Lopes and Ávila, 2005]. Because it is a very sensitive and fragile plant, it can also be attacked simultaneously by more than five diseases. Despite being a robust base, PlantVillage [Hughes and Salathe, 2016] does not cover all tomato diseases. The climate of each region influences the diseases. This means that the diseases in a certain region do not occur in another with a different climate.

Generally, cultivation in greenhouses is done by small farmers, the so-called family farming. Family members usually labor for this type of cultivation to avoid higher production costs. When the plantation is affected by a disease, it spreads quickly, requiring an evaluation by a specialized technician, which increases the cost of the product. The early identification of diseases can reduce costs both with a specialized professional and with pesticides. Through a device accessible to most people, such as the *smartphone*, producers could easily capture images and get help in identifying diseases through an application.

For data collection, we considered an important greenhouse tomato-producing region situated in the south of Brazil. We built a new database with new diseases and their combination. We examined the behavior of three machine-learning methods for disease classification in greenhouse-grown tomatoes. This study serves as a baseline for research using the database introduced here.

4 Dataset Construction

This section presents the two databases used in this work, with images of diseases and healthy tomato leaves. The Tomato Leaf Image Dataset (TLID) has images of whole leaves, and the Patch-based Tomato Leaf Image Dataset (PTLID) has images of diseased and non-diseased parts of the leaves.

4.1 Tomato Leaf Image Dataset (TLID)

The availability of databases is an indispensable necessity for developing disease identification techniques using machine learning algorithms. In the agricultural area, depending on the type of crop and planting conditions, there is not a sufficient and up-to-date amount of images for studies and research development. Therefore, collecting and assembling a specific database of images of tomato diseases was a precondition for this work, which focuses on cultivating tomatoes in a greenhouse. TLID was built through several visits to producers between December and June on three properties, each with several greenhouses, which made it possible to find different diseases at different stages of development. As shown in **Figure 2**, tomato branches were photographed. All the leaf images were cut and scaled, one by one, using an image processing software, totaling 15,256 specific images in

Ref.	Year	Cultivation	Model	Dataset	Images	Classes	Acc%
Brahimi *et al.* [2017]	2017	Tomato	AlexNet/GoogleNet Random Forest/SVM	PlantVillage	14,828	9	99.18%
Sardogan *et al.* [2018]	2018	Tomato	CNN/LVQ	PlantVillage	500	5	86.00%
Tm *et al.* [2018]	2018	Tomato	LeNet	PlantVillage	18,160	10	95.00%
Meeradevi *et al.* [2020]	2020	Tomato	VGG16	PlantVillage	2,317	6	95.00%
Sharma *et al.* [2020]	2020	Tomato	CNN/Logistic regression KNN/SVM/CNN	PlantVillage	20,000	19	98.00%
Hong *et al.* [2020]	2020	Tomato	DenseNetXception Resnet50/MobileNet SuffleNet	PlantVillage	13,112	19	97.10%
Gehlot and Saini [2020]	2020	Tomato	ResNet101/AlexNet DenseNet121/VGG16 GoogleNet	PlantVillage	14,529	10	99.69%
Pushpa *et al.* [2021]	2021	Tomato	AlexNet/VGG-16 Lenet-5	PlantVillage	7,070	10	96.64%
Tan *et al.* [2021]	2021	Tomato	AlexNet/ResNet34 VGG16/EfficientNet-b0 MobileNetV2	PlantVillage	18,160	10	99.70%
Sakkarvarthi *et al.* [2022]	2022	Tomato	CNN/InceptionV3 ResNet152/VGG19	PlantVillage	3,000	10	88.17%
Omar *et al.* [2022]	2022	Tomato	CNN	PlantVillage	13,467	9	92.00%
Malunao *et al.* [2022]	2022	Tomato	YOLOv3	PlantVillage	300	3	98.28%
Pradhan and Kumar [2022]	2022	Tomato	DenseNet169/VGG-19 InceptionResNetV2 InceptionV3/VGG-16 DenseNet201/MobileNet MobileNetV2/Xception	PlantVillage	14,532	10	96.00%
Turkoglu *et al.* [2022]	2022	Others	AlexNet/GoogleNet ResNet18/ResNet50 ResNet101 DenseNet201	Others	4,447	15	96.83%
Khalid *et al.* [2023]	2023	Tomato	EficientNet-B4 ResNet152/VGG16	PlantVillage	5,524	3	98.00%

Table 1. Summary of the Related Works.

a size of 256×256 pixels. These images are smaller than the original size, allowing better use by classification methods.

(a) Plant branch Miner.

(b) Branch of plant Bacterial Spot.

Figure 2. Examples of images of tomato branches photographed for study.

Plant diseases can be caused by various agents such as fungi, bacteria, mycoplasmas, viruses, viroids, and nematodes. Specifically, our data collection found diseases caused by fungi, viruses, and bacteria. These diseases are different from each other, but in some phases, some similarities can make their correct identification difficult. In our collection, we identified healthy leaves, four types of diseases called leaf Miner, Bacterial Spot, Powdery Mildew, and Whitefly, as well as the combination of Powdery Mildew and leaf Miner and Bacterial Spot and leaf Miner. In **Table 2**, we show the types of diseases and the number of collected images. Both healthy leaves, those with diseases, and their combinations have characteristics that define them as a certain disease. These special characteristics are called labels or classes. We can consider that we found seven classes of images: Healthy, Leaf Miner, Powdery Mildew, Bacterial Spot, Whitefly, Powdery Mildew and Leaf Miner, and Bacterial Spot and Leaf Miner. These classes were validated by an agronomic engineer who could confirm the respective diseases by visually inspecting the images. **Figure 3** shows healthy leaves, with the incidence of shade from the greenhouse itself.

Figure 4 shows the types of attacks of the Miner Fly, which are mines on the surface of the leaf and feeding punc-

Table 2. Number of Images per Class.

Class ID	Class	Images
1	Healthy	2,688
2	Miner fly	2,255
3	Bacterial Spot	2,395
4	Powdery Mildew	2,181
5	Powdery Mildew and Leaf Miner	2,362
6	Bacterial Spot and Leaf Miner	2,503
7	Whitefly	872
	Total	**15,256**

tures made by the female. **Figure 5** shows the evolution of Bacterial Spot caused by bacteria, from its beginning to the most advanced stage of the disease, which compromises almost the entire leaf, making its photosynthesis process impossible. **Figure 6** shows the most important disease in protected cultivation, Powdery Mildew, caused by fungi, which can compromise almost 40% of production. In **Figure 7**, there is more than one disease on the same leaf, Miner and Powdery Mildew, as well as **Figure 8**, which shows Bacterial Spot and Miner. The Whitefly is shown in **Figure 9**, an insect that can cause direct damage to the plant through sap suction or indirect damage through the transmission of viruses.

It is important to note that because the cultivation is in a closed environment, it is impossible for the leaves to be washed by rain or irrigation system (performed by drip system), accumulating residues such as debris, fertilizer remnants, dust, etc. The photographed branches were not subtracted from the plants, so no original leaf characteristics were altered.

Figure 3. Healthy leaf with shade incidence.

Figure 4. Different types of Leaf Miner attacks.

Figure 5. Disease evolution Bacterial Spot.

4.2 Patch-based Tomato Leaf Image Dataset (PTLID)

In the construction of PTLID we decided to consider only the part infected with the disease. For this, we subdivided the leaves of Dataset TLID into 64 images 32×32 pixels sized. After the division, the patches containing the diseases were separated, disregarding the other parts. **Figure 10**(a) shows a leaf with size 256×256, and **Figure 10**(b) the diseased patches.

Figure 6. Evolution of Powdery Mildew disease.

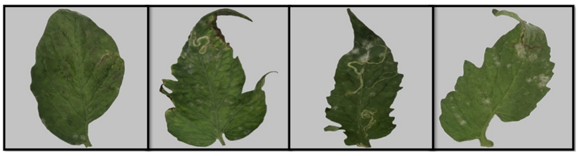
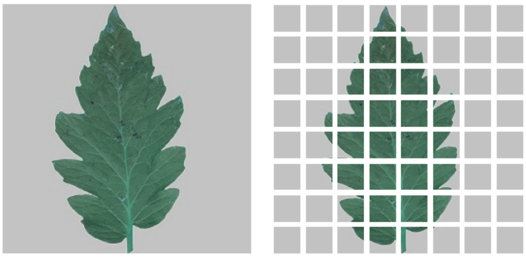


Figure 7. Combination of two diseases Powdery mildew and Leaf Miner.

Figure 8. Combination of two diseases, Bacterial Spot and Leaf Miner.

Figure 9. Whitefly.



(a) Leaf 256×256.

(b) Patches 32×32.

Figure 10. Different image sizes used in the proposed method.

Table 3 shows the number of images per class resulting from dividing the images into patches. In addition to the classes in TLID, images of Background were considered in this PTLID. A total of 227,218 images were counted and distributed among eight classes.

5 Proposed Method

The architecture proposed in this study includes three main steps: Dataset Construction, System Flow, and Ensemble Voting. The detailed block diagram of the proposed method is shown in **Figure 11**. In the Dataset Construction step,

Table 3. Number of Patches per Class.

Class ID	Class	Images
1	Healthy	48,676
2	Miner fly	11,099
3	Bacterial Spot	55,213
4	Powdery Mildew	60,628
5	Powdery Mildew plus Miner fly	10,653
6	Bacterial Spot plus Miner fly	15,435
7	White fly	1,060
8	Background	24,454
	Total	**227,218**

we used images from the databases described in Section 4. We have two databases with different image sizes, one with 256×256 pixels and another with patches of 32×32 pixels. The 256×256 images were resized at the network input to 224×224 pixels, while the 32×32 images were not altered. The image colors for both datasets are coded in RGB, and the format is JPG.

5.1 System Flow

In the system flow stage, we used data augmentation to increase the data set and, thus, avoid overfitting. However, we only used it with images that contained the entire leaf. This method was not applied to the patches as there were already enough images. The data were normalized, and the dataset was divided into 80% for training and validation and 20% for testing. The performance of three CNN models, namely a custom CNN, VGG19, and Resnet50, was evaluated. Each model is explained in detail below. The choice of these networks was based on preliminary analyses performed via simulation, where we tested different CNN architectures. We evaluated the performance of eight networks, whose performance on the new dataset is presented in **Table** 4. A more detailed discussion of this choice is presented in Section 6.

5.1.1 Customized CNN Model

CNN is a popular method in image classification due to the flexibility that the architecture can offer in terms of the number of convolutional layers, types and sizes of filters, and pooling and dropout procedures, among others, that can be used. This model's flexibility makes it possible to improve the network's performance. In this study, we created a new CNN architecture and adjusted hyperparameters such as the number of convolutional layers, fully connected layers, number of filters, and pooling procedures. The selection of hyperparameters was manually performed through simulations. This was the model that presented the best results. The proposed CNN architecture is shown in **Figure 12**. We used three convolutional blocks, each consisting of two convolutional layers followed by a pooling layer. Two fully connected layers were added at the end of the model, one with 512 and the other with seven neurons, representing the classes to be identified. We used Dropout between the fully connected layers to avoid overfitting. We tested optimizers RMSprop, Adadelta, and Adam, but the optimizer that achieved the best performance was Adam, with a parameter of 0.001. The architecture of all models remained the same for the two databases used. Only changing the image size at the network input according to the respective database.

5.1.2 Pre-Trained VGG19 Model

The VGG19 network [Simonyan and Zisserman, 2015] is a pre-trained network model composed of 16 convolution layers and three fully connected layers. These networks use knowledge obtained on a similar problem already solved. The VGG19 network was trained on the ImageNet database, which contains one million images from 1000 categories. It is a very popular method for image classification due to the use of multiple 3×3 filters in each convolutional layer. The architecture of the VGG19 network is shown in **Figure 13**. The first 16 layers are used for feature extraction, and the last three are used for classification. For this work, we adapted and included two fully connected layers at the end of the model concatenation, one with 512 neurons and another with seven representing the number of output classes. The *Dropout* is applied between the two fully connected layers to avoid overfitting. The Adam optimizer was used with the parameter of 0.0001. The architecture of the VGG19 model adapted for our work is shown in **Figure 14**.

5.1.3 Pre-Trained Resnet50 Model

While in the training of conventional neural networks, each layer learns low-level and high-level features, in Resnet (Residual Neural Network) [He *et al.*, 2016] instead of learning with features, the model tries to learn some residue. Deep residual networks are convolutional neural networks that are 50 layers deep. In addition to Resnet50, other variants exist, such as ResNet101 and ResNet152. **Figure 15** shows our adjusted Resnet50 model for classifying tomato diseases in greenhouses. Two fully connected layers were added, one with 512 and another with seven neurons representing the output classes. We use *dropout* between dense layers to avoid *overfitting*. The first layer has 64 filters with a kernel size of 7×7, followed by a *maxpooling* layer of size 3×3. The first layer group consists of three identical blocks. Likewise, groups two, three, and four have four, four, and three identical blocks, respectively. Among some groups, the lines marked with blue color represent the identity block that connects two layers of different sizes. After all these blocks, 38 fully connected layers are responsible for the classification task. We also used *droupout* between these two connected layers to prevent *overfitting*.

5.2 Performance Evaluation Metrics

The output of the models will result in a probability for each class in the database, which can be a specific disease, a disease combination, or a healthy leaf. In this phase, the models' prediction results are compared with each class's actual classification in order to evaluate the performance of the models.

Different metrics evaluated the classification results for the methods used, *Accuracy* (A), *Precision* (P), *Recall* (R) and *F1 score*, defined by the equations (1)-(4), respectively. The parameter TP (True Positive) represents correctly predicted positive values, FP (False Positive) represents incor-

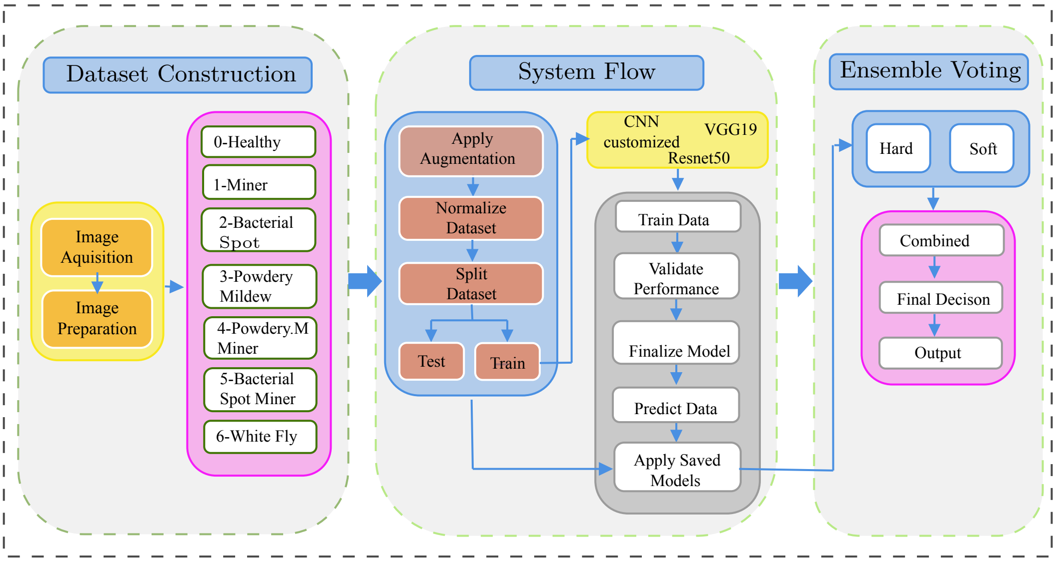


Figure 11. Block diagram of the proposed method.

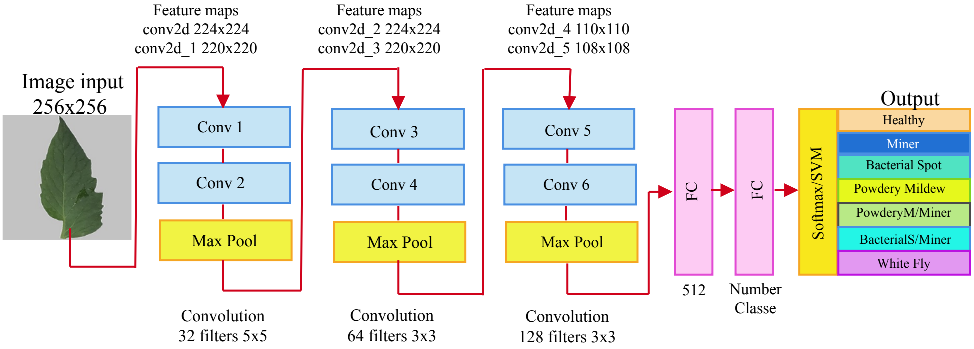


Figure 12. The architecture of the customized CNN model.

rectly predicted positive values, TN (True Negative) represents correctly predicted negative values and FN (False Negative) represents incorrectly predicted negative values.

$$Accuracy\ (\%) = \frac{\mathrm{TP}+\mathrm{TN}}{\mathrm{TP}+\mathrm{FP}+\mathrm{TN}+\mathrm{FN}} \times 100 \qquad (1)$$

$$Precision\ (\%) = \frac{\mathrm{TP}}{\mathrm{TP}+\mathrm{FP}} \times 100 \qquad (2)$$

$$Recall\ (\%) = \frac{\mathrm{TP}}{\mathrm{TP}+\mathrm{FN}} \times 100 \qquad (3)$$

$$F1\ (\%) = \frac{2\cdot\mathrm{P}\cdot\mathrm{R}}{\mathrm{P}+\mathrm{R}} \times 100 \qquad (4)$$

5.3 Support Vector Machine - SVM

Initially, the SVM algorithm was designed to address binary classification problems [Vapnik, 1995]. Over time, it was extended and adapted to handle multi-class classification challenges as well [Crammer *et al.*, 2002]. Its objective is to find the optimal hyperplane $f(w,x) = w \cdot x + \mathrm{b}$ to separate two classes in a given dataset, with features $x \in \mathbb{R}^m$. SVM learns the parameters w by solving the optimization problem defined by Eq. (5),

$$\min \frac{1}{p}\cdot w + C \cdot \sum_{i=1}^{p} \max\left(0, 1 - y_i^{'} \cdot (w^T x_i + b)\right) \qquad (5)$$

where $w^T\ w$ is the Manhattan norm (also known as L1 norm), C is the penalty parameter (may be an arbitrary value or a selected value using hyperparameter tuning), $y^{'}$ is the actual label, and $w^T x_i + b$ is the predictor function. Eq. (5) is known as L1-SVM, with the standard hinge loss. Its differentiable counterpart (L2-SVM) defined by Eq. (6), provides more stable results,

$$\min \frac{1}{p}\cdot \|w\|_2^2 + C \cdot \sum_{i=1}^{p} \max\left(0, 1 - y_i^{'} \cdot (w^T x_i + b))^2\right) \qquad (6)$$

where $||w||^2$ is the Euclidean norm (also known as L2 norm), with the squared hinge loss. To implement the SVM, we used the sklearn library in Python. We chose the kernel='linear' parameter because we observed that most classes are linearly separable. Additionally, we used the default value for the C parameter, which is $C = 1.0$, as defined in Python.

5.4 Ensemble Voting

Another method employed in our proposal is Ensemble Voting. The idea of ensemble methods is that the results of multiple machine learning models can be combined to increase

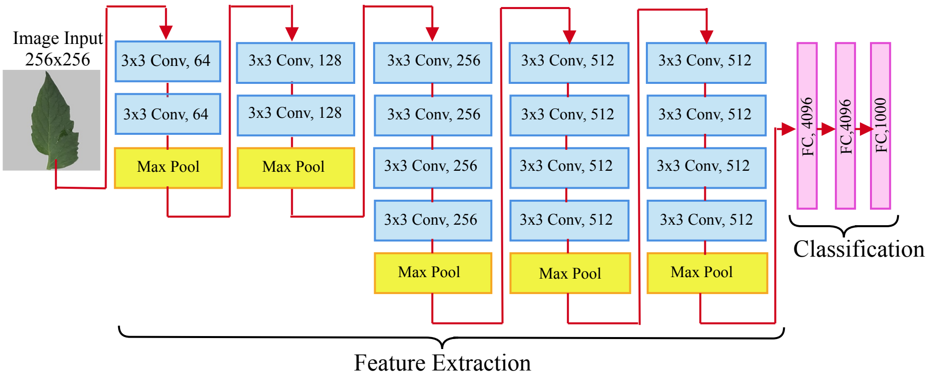


Figure 13. VGG19 network architecture.

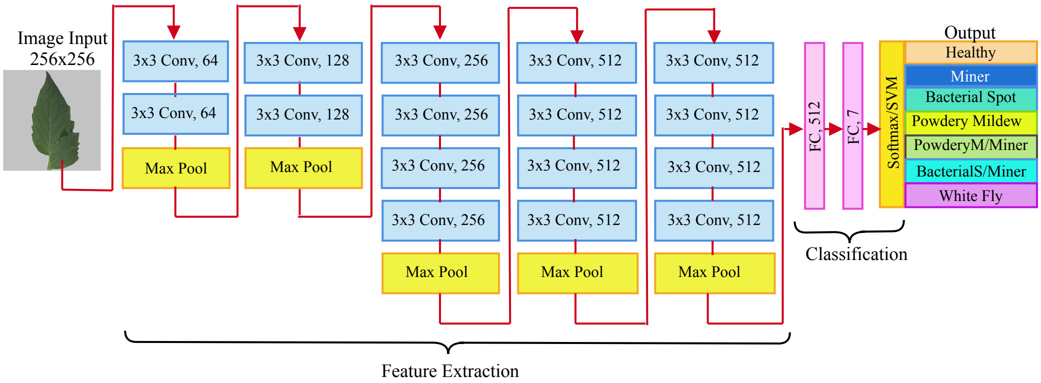


Figure 14. Adapted VGG19 network architecture.

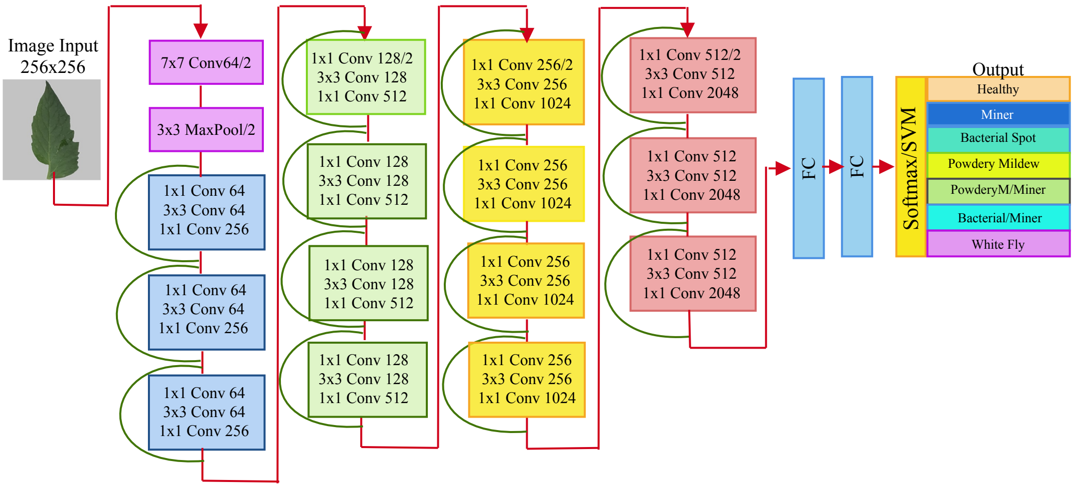


Figure 15. Resnet50 Architecture.

identification accuracy [X. Dong *et al.*, 2020]. There are several types of ensemble methods: voting, bagging, boosting, and stacking. This study used the voting method [Burka *et al.*, 2022]. Voting can be performed in two ways in classification problems: Hard voting, in which each model votes for a class, choosing the one with the most votes, and Soft voting, which considers the probabilities of a model not being entirely sure of a class and considers the class with the highest probability.

Each classifier, i, takes an input and generates a vector with the probabilities of the classes, $\mathbf{p}_i = [p_{i1}, p_{i2}, \cdots, p_{ik}]$, where $\sum_k p_{ik} = 1$. Each CNN has its own architecture, and the probabilities they generate are combined through voting. Hard voting is based on calculating the predicted category for each network,

$$y_i = \arg\max(\{p_{i1}, p_{i2}, \cdots, p_{ik}\}) \tag{7}$$

where the final category is determined through the mode of all of them:

$$y = \text{mode}(\{y_1, y_2, \cdots, y_n\}). \tag{8}$$

Soft voting can be done as a weighted sum of the probabilities given by each CNN. The probability of belonging to the class k predicted by the ensemble [Cruz *et al.*, 2021] is calculated using the following equation,

$$P_k = \sum_{i=1}^{n} w_i \cdot p_{ik} \tag{9}$$

where n is the number of CNNs considered in the ensemble. The w_i weights are assigned based on the training performance of the networks, where the highest weights correspond to the smallest errors. The selected category, y, is the one with the highest probability:

$$y = \arg\max(\{P_1, P_2, \cdots, P_k\}) \tag{10}$$

6 Results and Discussions

In this study, we utilized Convolutional Neural Networks and Ensemble Methods to assess two potential approaches for identifying tomato diseases, as depicted in **Figure 16**. The first approach, referred to as *Method A*, utilizes the images from the TLID dataset, as described in Section 4.1, and evaluates the entire leaf on a global scale. The second approach involves using the PTLID dataset, as outlined in Section 4.2. This approach, known as *Method B*, evaluates the image locally, focusing exclusively on the regions of the image that display diseases.

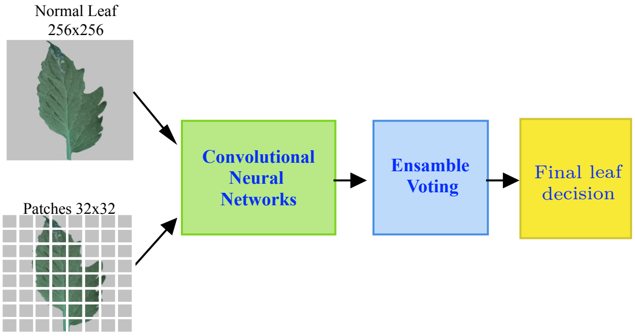


Figure 16. Methods used to classify tomato diseases

Several network models were tested as shown in **Table 4**. Some networks yielded better results than others. However, we couldn't choose a network solely based on its performance, as our objective was to test the same networks for both TLID and PTLID datasets. In this context, the PTLID dataset has a particularity: its image size is 32×32. This poses a challenge for a very deep network, requiring image resizing, which becomes unfeasible due to the quantity of images in this dataset. Thus, among the tested networks, we opted for three models: the custom CNN, Resnet50, and VGG19. Other lightweight network models, such as ShuffleNet, GhostNet, and ResNet-18, were also tested, achieving accuracies between 50% and 75%. However, these models would need enhancements to improve their performance on the dataset. The architectures proposed in this paper, although using more complex models, could already be implemented on mobile devices with higher processing capacity or could be implemented using cloud processing.

6.1 Method A – Full-size Leaf Image Processing

Method A was conducted as a global classification of the leaf. **Figure 17** shows this process. An image with a tomato leaf taken from the TLID dataset, and resized to 224×224 pixels, is used as input to the network. The network architectures experimented were CNN, VGG-19, and ResNet-50. We still use two ensemble hard and soft voting methods to determine the final decision. We consider the individual results using validation data from the three methods CNN, VGG19, and Resnet50 with two types of network output Softmax and SVM, to obtain a joint result that is more accurate than when used individually. We use the validation set with 3,051 images for this. We also apply data augmentation in this experiment, as the diversity of the dataset can increase the generalizability and robustness of the model [Pulgar *et al.*, 2017]. The batch size was set to 64, and we used the Adam optimizer with a ratio of 0.0001 for the pre-trained models and 0.001 for the customized CNN.

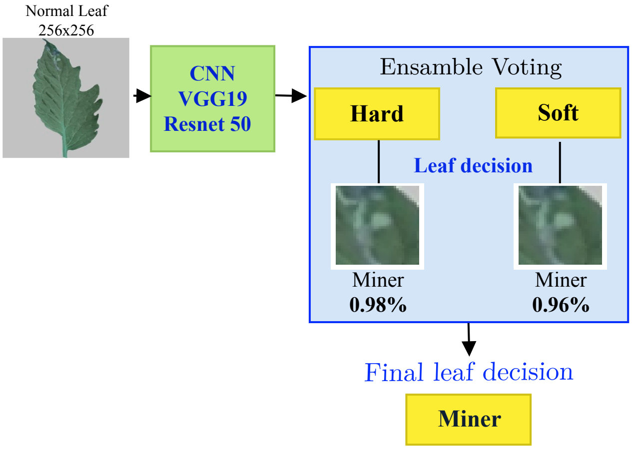


Figure 17. Block diagram of global detection and classification method.

Table 5 shows the individual results of the three classifiers considered in this work. We use accuracy, precision, recall, and F1 Score as metrics. We can see a balance in the results of the methods with very little difference between them. However, the results for softmax were better than the results for SVM. Additionally, we conducted some tests to evaluate the impact of using the PCA (Principal Component Analysis) technique on the classifier that achieved the best result with network output softmax (VGG19+SVM). We tested different types of kernels for SVM, including linear, polynomial, and Gaussian. The Gaussian kernel achieved the best accuracy in the experiments. The results are also shown in **Table 5**. The best accuracy was obtained by the VGG19 architecture, with 86.56%, followed by the Resnet50 with an accuracy of 82.76%, and finally, the specific CNN with an accuracy of 79.61%. To prove the effectiveness of the tested methods, we used the same models with the PlantVillage database, and the accuracy of this dataset was superior to 96%. These differences in performance between the two databases, using the same method, highlight the specificities of the new database presented in this article concerning the cultivation of tomatoes in greenhouses. Afterward, we found the accuracy of each network by considering the validation data to obtain the accuracy for hard and soft voting for both network outputs. Again, the softmax output stands out over SVM. According to **Table 6**, the ensemble Hard method obtained 85.84%, and the Soft method obtained 82.76%.

As discussed in Section 2, for the creation of the PlantVil-

Table 4. Accuracy scores of deep networks using TLID dataset (%)

Alexnet	78.43%
CNN	79.61%
EfficientNet	74.80%
InceptionV3	68.14%
MobileNet	82.69%
Resnet50	82.76%
Resnet152V2	83.09%
VGG19	86.56%

lage database, the leaves were harvested and then photographed. As a result, important characteristics that are part of the tomato growing environment may have been lost, such as various types of insects, specks, dust, and fertilizer residues, among other residues. The fact that most leaves are free of these important attributes can influence the final result of the algorithm, making that scenario less realistic.

The performance of the models is evaluated in terms of classification accuracy. The confusion matrix was generated to visualize the classification performance of TLID using the CNN customized, VGG19 and Resnet50 models. **Figure 18** shows the customized CNN model, **Figure 19** shows the behavior of the VGG19 model and **Figure 20** the Resnet50 model. The instance that classified the images most accurately was the healthy class for all matrices, as it doesn't have too little noise in the leaf. The classes that combined two diseases were confused with those with one. For example, the 'Bacterial Spot class and Miner' caused confusion between both the 'Bacterial Spot' class and the 'Miner' class. Other confusions between the classes were due to the similarities between the diseases in their different phases. These confusions between the classes compromised the accuracy of the models, causing them to remain below 86%.

6.2 Method B – Leaf Patch Images Processing

Greenhouse tomato leaves may contain other attributes besides existing diseases due to their environment. This can compromise the overall assessment of the leaf. The objective of Method B is to make a local assessment of the leaf. For that, we tested the same classifiers used in Method A, and we tried to reduce the noise in the leaves, considering images of patches with a size of 32×32, in which only the respective diseases were present. **Table 7** shows the results obtained with the images of the patches when tested with the same methods as Method A and two Softmax and SVM network outputs. According to the results, it is possible to see that, again, the performance was very similar between the models; however, when using the Softmax network output, the results are better. VGG19 obtained the best performance among the models, with 90.19% of accuracy, CNN obtained 86.78%, and Resnet50 achieved 88.94%. It is possible to verify that all methods had a considerable change in performance when compared to Method A. The performance improvement was achieved because there was less confusion between classes. However, it is still possible to notice that, according to the confusion matrices shown in **Figure 21**, **Figure 22**, and **Figure 23**. As we can see, some confusion between the classes still remains.

For the voting method, we used validation data with 45,444 images. First, we find the accuracy of each classifier, and then we use the three classifiers together to find the voting accuracy of the Hard and Soft methods. **Table 8** shows the results for these two methods. The Hard method obtained the best overall result (i.e. 90.48%).

In the example shown **Figure 24** the Background and Healthy classes appear most frequently. The Background class is not considered in the final result because it is the background of the image. The patches of the Healthy class appeared in greater number in **Figure 24** because in this example the disease is clearly in its early stages with only 3 patches that presented the disease and the rest healthy patches. The number of times a disease class appears in the vector can indicate the stage of the disease, that is, if, for example, up to 3 patches appear in **Figure 24**, we could consider that the disease is in its early stages. If the example were different and had between 3 to 8 patches, we could consider it in an intermediate stage, etc. After creating this vector, we use the Ensemble Hard and Soft methods for each patch, providing a confidence percentage. In the end, we determine which disease each patch refers to. The block diagram shown in **Figure 24** illustrates the procedure described above.

Another interesting fact observed when using this method is that the algorithm can find diseases not previously labeled for the leaf. For example, **Figure 25** (a) shows an image labeled as White Fly, indicated by the red marks in the image. However, the algorithm also identified the disease Powdery Mildew, marked in white in the image. This disease, however, had not been labeled when the leaf was evaluated globally. The way the leaf patches were created allows the algorithm to identify other characteristics in more detail. In the local classification of the leaf, it enables a more precise classification of the type of disease, resulting in less confusion between classes as occurred in Method A. **Figure 25** (b) shows the classification of healthy patches (white marking), Bacterial Spot (red marking), and Bacterial and Mining Spot (blue marking), allowing greater precision in the identification of diseases.

This local leaf classification allows us to prove visibly existing diseases and evidence of diseases in early stages, disease-causing insects. Some early-stage diseases are barely noticeable. Method B allows for the accurate classification of diseases and others that may be in the early stages.

In relation to the research questions, we were able to reach the following conclusions:

Q1: *Do the diseases present in greenhouse tomato cultiva-*

Table 5. Individual Classifier Results for Method A.

		Evaluation Metrics			
Method	**Dataset**	**Accuracy**	**Precision**	**Recall**	**F1 Score**
CNN+Softmax	TLID	79.61%	79.17%	75.76%	76.63%
VGG19+Softmax	TLID	**86.56%**	**85.10%**	**84.88%**	**84.94%**
Resnet50+Softmax	TLID	82.76%	80.94%	80.85%	80.80%
CNN+SVM	TLID	66.08%	58.20%	59.56%	57.82%
VGG19+SVM	TLID	82.50%	82.72%	78.98%	79.86%
Resnet50+SVM	TLID	82.63%	82.07%	79.49%	79.97%
VGG19+SVM+PCA	TLID	84.23%	83.00%	83.00%	83.00%
CNN	PlantVillage	96.95%	96.61%	95.97%	96.23%
VGG19	PlantVillage	**98.70%**	**98.43%**	**98.19%**	**98.29%**
Resnet50	PlantVillage	96.18%	96.78%	95.11%	95.70%

Table 6. Voting Classifier Results for Method A and SVM.

			Accuracy		
	CNN	VGG19	Resnet50	Hard Voting Ensemble	Soft Voting Ensemble
Softmax	79.61%	86.56%	82.76%	**85.84%**	82.76%
SVM	66.08%	82.50%	82.63%	84.36%	82.62%

tion have regional specificities? Diseases are influenced by the climate of each region. For example, some diseases only occur in hot, dry weather, others in hot, humid weather. The climate favors its emergence or not.

Q2: *How do identification algorithms behave using unprocessed images collected by smartphones?*. The results suggest that because they are not processed, the image noise becomes more evident, making it difficult to extract features and consequently contributing to the algorithm confusing the classes, resulting in lower-than-expected performance.

Q3: *Is it possible to increase accuracy in disease identification by combining machine learning algorithms?*. We believe that due to the complexity of the database, the values when we combined the models together did not obtain such a significant improvement as when evaluated separately. In Method A, we can see that the classification accuracy for Ensemble Voting Hard reached 85.84%, lower than the highest value achieved by ensemble member VGG19. For the Ensemble Voting Soft, the value achieved was 82.76%, a value lower than the highest value achieved by one of the ensemble members. When evaluating Method B, we noticed that the values for Ensemble Voting Hard slightly increased compared to the highest value individually obtained by the models. The Ensemble Voting Soft only obtained a value equal to one of the ensemble members.

Q4: *Is it possible to identify the presence of multiple diseases on tomato leaves and their degree of contamination using machine learning-based strategies?* The complexity of the database, such as the similar characteristics between diseases evaluated in their different phases, made it possible to verify, according to the confusion matrices of the models evaluated, that there was a lot of confusion between the classes. Method B reduced confusion between classes. When tested with the overall size of the leaf (256×256), it allowed not only to find the expected disease but also to identify other diseases existing on the leaf. When we analyze the leaf globally with Method B, it is also possible to analyze the stage at which the disease is based on the number of disease patches found on the leaf.

7 Conclusions

This study proposes to identify machine learning models that are most suitable for recognizing foliar diseases in greenhouse tomatoes. Using two datasets, TLID considered the image size of 256×256 pixels, and PTLID, composed of images of 32×32 pixels. Both datasets are composed of healthy leaves and six classes of diseased leaves. The particularity of this database is that it was collected in a way that did not exclude specific characteristics of tomato leaves. We tested both datasets on three deep convolutional neural network models, a custom CNN, and two pre-trained networks, VGG19 and Resnet50. The results with TLID compared to PlantVillage were low, which may be due to the characteristics of the new database. To improve performance, we used PTLID, and the results presented in Section 6 were better than those of TLID. It was evident that for the TLID images, the pre-trained networks performed better than the CNN we customized. In PTLID, CNN and VGG19 performed better. The patches achieved a slightly better accuracy when tested with the three models, as shown in **Table 7**. Among the evaluated network architectures, the best performance was obtained by the VGG19 using patches. In this case, the use of voting methods also contributed to getting a little better accuracy rates. Future work will focus on image segmentation techniques to reduce noise in images and extend the idea of disease recognition to other crops, whether in greenhouses or not. Furthermore, we also intend to investigate the performance of multi-label classifiers in this scenario since multiple labels can be associated with a single sample. Finally, eXplainable Artificial Intelligence (XAI) techniques might be explored, aiming to provide insights into how the AI models are making decisions.

Table 7. Results for Method B.

Evaluation Metrics					
Method	Dataset	**Accuracy**	**Precision**	**Recall**	**F1 Score**
CNN+Softmax	PTLID	86.78%	79.43%	76.18%	77.57%
VGG19+Softmax	PTLID	**90.19%**	**84.90%**	**81.02%**	**82.60%**
Resnet50+Softmax	PTLID	88.94%	82.18%	78.72%	80.18%
CNN+SVM	PTLID	81.30%	66.57%	58.256%	59.93%
VGG19+SVM	PTLID	78.33%	67.05%	64.53%	64.61%
Resnet50+SVM	PTLID	88.76%	82.51%	77.13%	79.21%

Table 8. Voting Classifier Results for Method B.

Accuracy					
	CNN	VGG19	Resnet50	Hard Voting Ensemble	Soft Voting Ensemble
Softmax	86.78%	90.19%	88.94%	**90.48%**	88.94%
SVM	81.30%	78.33%	88.76%	88.81%	88.76%

Declarations

Acknowledgements

We thank the farmers who allowed access to their greenhouse cultivation areas to collect the images used to construct the dataset used in this study.

Funding

This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – Brasil (CAPES) – Finance Code 001.

Authors' Contributions

All authors contributed equally to this article and have read and approved the final manuscript.

Competing interests

The authors declare that they have no competing interests.

Availability of data and materials

The new datasets generated and analyzed during the current study are available in: `https://data.mendeley.com/datasets/kt64b2kh89/1`

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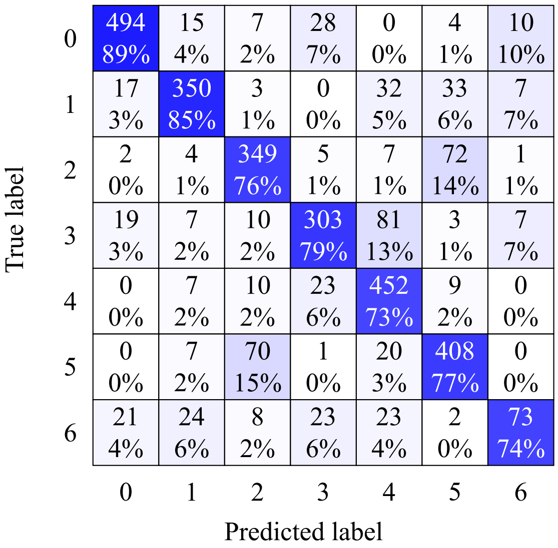
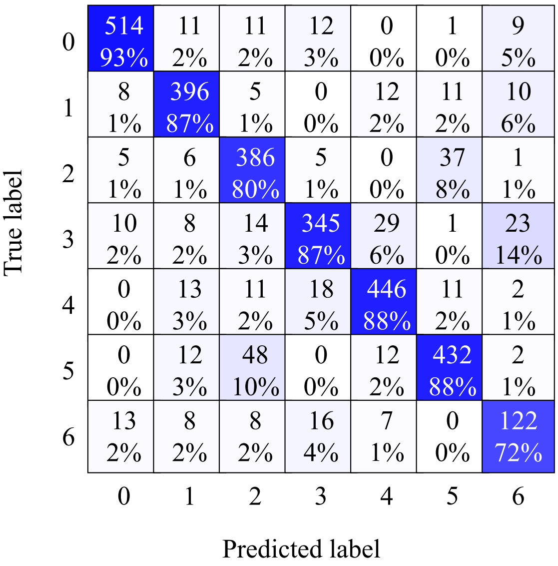


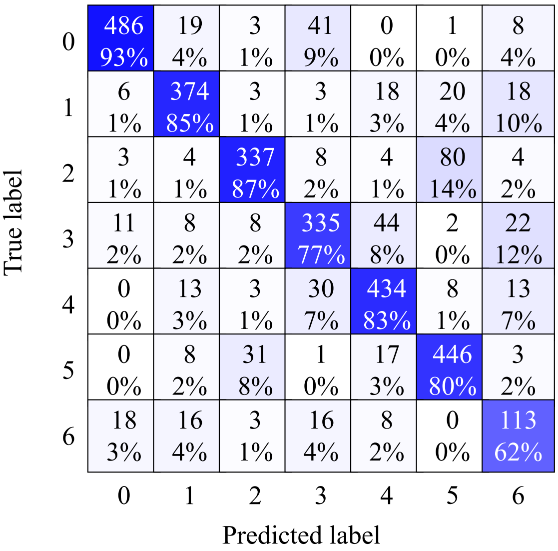
	0	1	2	3	4	5	6
0	494 89%	15 4%	7 2%	28 7%	0 0%	4 1%	10 10%
1	17 3%	350 85%	3 1%	0 0%	32 5%	33 6%	7 7%
2	2 0%	4 1%	349 76%	5 1%	7 1%	72 14%	1 1%
3	19 3%	7 2%	10 2%	303 79%	81 13%	3 1%	7 7%
4	0 0%	7 2%	10 2%	23 6%	452 73%	9 2%	0 0%
5	0 0%	7 2%	70 15%	1 0%	20 3%	408 77%	0 0%
6	21 4%	24 6%	8 2%	23 6%	23 4%	2 0%	73 74%

Figure 18. Method A - CNN Confusion matrix.



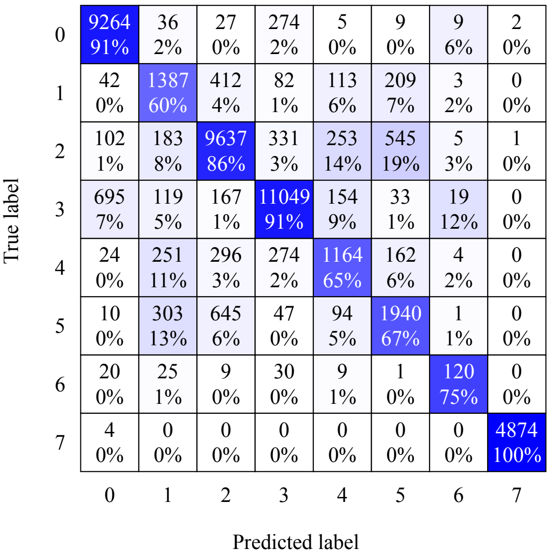
	0	1	2	3	4	5	6
0	514 93%	11 2%	11 2%	12 3%	0 0%	1 0%	9 5%
1	8 1%	396 87%	5 1%	0 0%	12 2%	11 2%	10 6%
2	5 1%	6 1%	386 80%	5 1%	0 0%	37 8%	1 1%
3	10 2%	8 2%	14 3%	345 87%	29 6%	1 0%	23 14%
4	0 0%	13 3%	11 2%	18 5%	446 88%	11 2%	2 1%
5	0 0%	12 3%	48 10%	0 0%	12 2%	432 88%	2 1%
6	13 2%	8 2%	8 2%	16 4%	7 1%	0 0%	122 72%

Figure 19. Method A - VGG19 Confusion matrix.



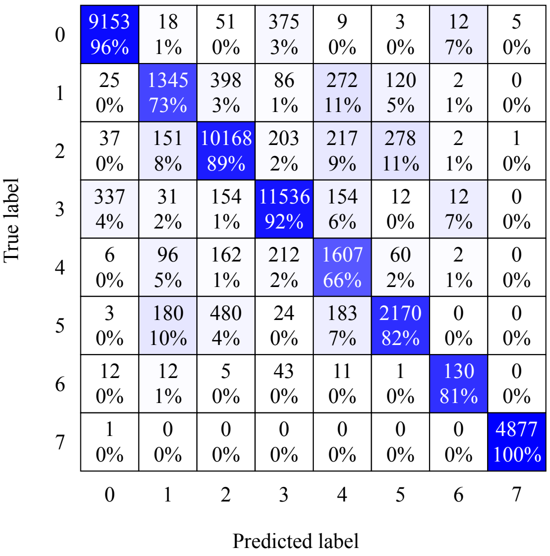
	0	1	2	3	4	5	6
0	486 93%	19 4%	3 1%	41 9%	0 0%	1 0%	8 4%
1	6 1%	374 85%	3 1%	3 1%	18 3%	20 4%	18 10%
2	3 1%	4 1%	337 87%	8 2%	4 1%	80 14%	4 2%
3	11 2%	8 2%	8 2%	335 77%	44 8%	2 0%	22 12%
4	0 0%	13 3%	3 1%	30 7%	434 83%	8 1%	13 7%
5	0 0%	8 2%	31 8%	1 0%	17 3%	446 80%	3 2%
6	18 3%	16 4%	3 1%	16 4%	8 2%	0 0%	113 62%

Figure 20. Method A - Resnet50 Confusion matrix.



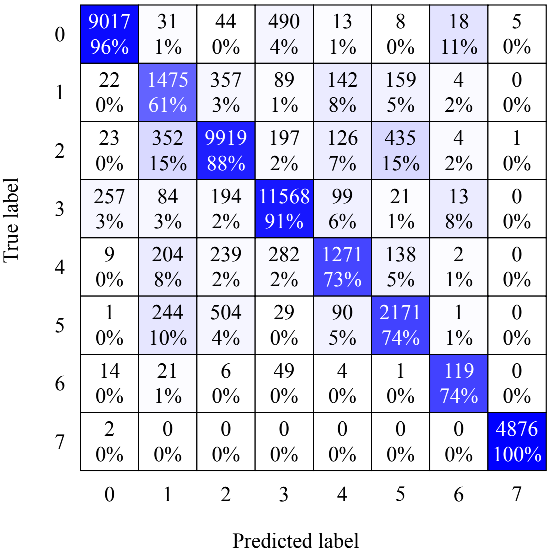
	0	1	2	3	4	5	6	7
0	9264 91%	36 2%	27 0%	274 2%	5 0%	9 0%	9 6%	2 0%
1	42 0%	1387 60%	412 4%	82 1%	113 6%	209 7%	3 2%	0 0%
2	102 1%	183 8%	9637 86%	331 3%	253 14%	545 19%	5 3%	1 0%
3	695 7%	119 5%	167 1%	11049 91%	154 9%	33 1%	19 12%	0 0%
4	24 0%	251 11%	296 3%	274 2%	1164 65%	162 6%	4 2%	0 0%
5	10 0%	303 13%	645 6%	47 0%	94 5%	1940 67%	1 1%	0 0%
6	20 0%	25 1%	9 0%	30 0%	9 1%	1 0%	120 75%	0 0%
7	4 0%	0 0%	0 0%	0 0%	0 0%	0 0%	0 0%	4874 100%

Figure 21. Method B - CNN Confusion matrix Patchs.



	0	1	2	3	4	5	6	7
0	9153 96%	18 1%	51 0%	375 3%	9 0%	3 0%	12 7%	5 0%
1	25 0%	1345 73%	398 3%	86 1%	272 11%	120 5%	2 1%	0 0%
2	37 0%	151 8%	10168 89%	203 2%	217 9%	278 11%	2 1%	1 0%
3	337 4%	31 2%	154 1%	11536 92%	154 6%	12 0%	12 7%	0 0%
4	6 0%	96 5%	162 1%	212 2%	1607 66%	60 2%	2 1%	0 0%
5	3 0%	180 10%	480 4%	24 0%	183 7%	2170 82%	0 0%	0 0%
6	12 0%	12 1%	5 0%	43 0%	11 0%	1 0%	130 81%	0 0%
7	1 0%	0 0%	0 0%	0 0%	0 0%	0 0%	0 0%	4877 100%

Figure 22. Method B - VGG19 Confusion matrix Patchs.



	0	1	2	3	4	5	6	7
0	9017 96%	31 1%	44 0%	490 4%	13 1%	8 0%	18 11%	5 0%
1	22 0%	1475 61%	357 3%	89 1%	142 8%	159 5%	4 2%	0 0%
2	23 0%	352 15%	9919 88%	197 2%	126 7%	435 15%	4 2%	1 0%
3	257 3%	84 3%	194 2%	11568 91%	99 6%	21 1%	13 8%	0 0%
4	9 0%	204 8%	239 2%	282 2%	1271 73%	138 5%	2 1%	0 0%
5	1 0%	244 10%	504 4%	29 0%	90 5%	2171 74%	1 1%	0 0%
6	14 0%	21 1%	6 0%	49 0%	4 0%	1 0%	119 74%	0 0%
7	2 0%	0 0%	0 0%	0 0%	0 0%	0 0%	0 0%	4876 100%

Figure 23. Method B - Resnet50 Confusion matrix Patchs.

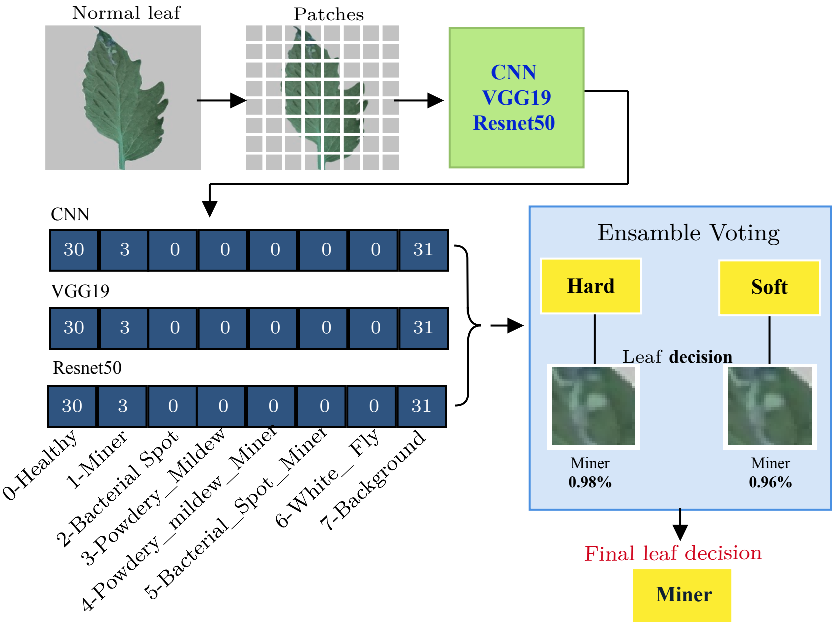
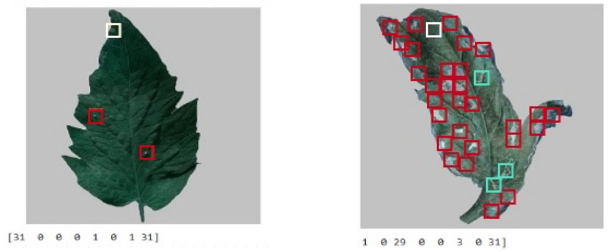


Figure 24. Local Tomato Leaf Disease Detection and Classification Block Diagram.



(a) Example of unlabeled disease identification

(b) Example of images with multiple labels

Figure 25. Examples of images classified using method B.

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