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Potato Plant Leaf Disease Detection Using Deep Learning Method

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ABSTRACT
In agriculture, plant disease detection and cures for those diseases are crucial for high crop production and yield sustainably. Improvements in the automated disease detection and analysis areas may provide important benefits for early action that would allow intervention at earlier stages for cure and preventing spread of the disease. As a result, damages on crop yield could be minimized. This study proposes a new deep-learning model that correctly classifies plant leaf diseases for the agriculture and food sectors. It focuses on the detection of plant diseases for potato leaves from images by designing a new convolutional neural network (CNN) architecture. The CNN methodology applies filters to input images, extracts key features, reduces dimensions while preserving important characteristics in images, and finally, performs classification. The experimental results conducted on a real-world dataset showed that a significant improvement (8.6%) in accuracy was achieved on average by the proposed model (98.28%) compared to the state-of-the-art models (89.67%) in the literature. The weighted averages of recall, precision, and f-score metrics were obtained around 0.978, meaning that the method was highly successful in disease diagnosis.

Keywords: Agriculture, Disease diagnosis, PlantVillage, Smart farming, Image classification, Deep learning, Convolutional neural networks

1. Introduction

Due to making better predictions and reliability, the development of digitalized systems has been popular in implementing applications for agriculture production areas and fields, such as the identification of crop varieties (Çınar & Koklu 2022; Bayram & Yıldız 2023), detection of weeds (Sabzi et al. 2018), and grading crops (Sabzi et al. 2015); the expansion and development of this technological area also seeks to investigate or detect plant diseases. As a result of unstable environmental conditions and climate change, plant diseases have increased rapidly, which may result in food shortages in places around the world in the near future.

The primary causes of plant diseases and their biotic and abiotic factors are represented in Figure 1, i.e. microorganisms and variables that result in environmental stress, respectively. Fungi, viral and bacterial pathogens differ in type of diseases they cause. They infect the crops by killing the cells of plants. The cause of fungal infection may be the result of infected seeds, crop rubbish, inappropriate soil, weeds, and other nearby crops. Plants may be infected by bacteria internally, which may not show any internal or external symptoms during the development of a disease. Viral infections are also difficult to detect which means that diagnosis can be challenging. The virus spreads through carriers of different bugs such as leafhoppers, whiteflies, cucumber beetles, and insects. Due to the presence of these factors (i.e., bacteria, fungi, viruses) and environmental changes (i.e., drought, frost), farmers are face numerous plant diseases that decrease the quality and yield of their crops. Additionally, the bacteria-infected plant spreads the infection to nearby plants and increases the rate of spreading. For these reasons, early-stage detection is crucial in order to protect plants from infection. It is reported that 80-90% of plant diseases occur on the plant leaves (Salih et al. 2020). With this in mind, this study focuses on the plant leaf, rather than the whole plant.

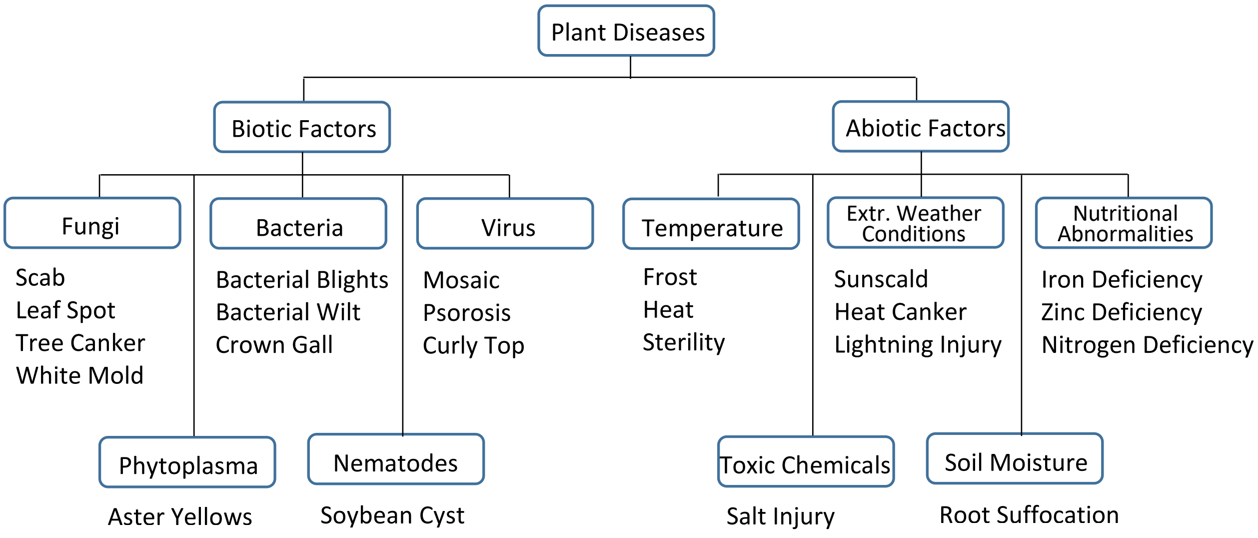

Figure 1- Factors & effects of diseases on plants

Visual identification of diseases by humans in plants of a large area is costly and time-consuming, depending on their ability which may not be accurate (Prajna 2021). The diseases could be very diverse because of the variety of plants and microorganisms. In addition, variations in the types of plant leaf diseases and the meteorological conditions due to climate change and global warming could increase the disease spread rate to the regions where they have not been seen before, in which even experts may be unfamiliar with (Sladojevic et al. 2016). Therefore, it is important to design a smart system that will help diagnose plant disease accurately and automatically (Gerdan Koc et al. 2022). A mobile application will further help non-expert farmers and farmers who do not have phytopathological and agronomic support infrastructure (Ferentinos 2018).

Plant diseases can have enormous impact on farming lands and forests, which threaten production and overall food quality and safety. Early stage and accurate detection of such diseases play a crucial role in prevention, guidance or management strategies. In recent years, artificial intelligence (AI) has expanded and developed and improved disease detection in agriculture. AI-based solutions provide alternative ways for automated disease diagnosis. These methods have the ability to work with large image datasets to create and train models, and diagnose and classify diseases using patterns with a high success prediction probability. The progress in such areas create capabilities that enhance disease detection, early-stage intervention, diagnosis, and suggestions for further-steps including cures.

The significant developments in machine learning (ML) technologies can result in the design and implement of an architecture for automated systems which could help to attain fast and accurate results to detect plant diseases. For example, Mathew et al. (2022) proposed a machine-learning-based automated system with a combination of support vector machine (SVM), k-nearest neighbors (KNN), and decision tree (DT) methods for classifying the diseases on potato leaves. Some studies worked with commonly-used approaches; for example, Sharma et al. (2021) compared the prediction success rates between SVM, DT, and KNN. Moreover, Iqbal & Talukder (2020) investigated the performances of logistic regression (LR), random forest (RF), naive Bayes (NB), linear discriminant analysis (LDA), KNN, SVM, and DT. Ismail et al. (2020) compared linear, quadratic, and cubic SVMs for the plant disease detection task and reported that cubic SVM obtained higher accuracy than others. Pardede et al. (2018) compared different kernels (linear, radial basis function, and polynomial) for SVM and stated that the linear kernel achieved the best accuracy. Some studies proposed a hybrid methodology like Singh & Kaur (2020) by combining the k-means algorithm with SVM and Mukherjee (2020) by creating the architecture using SVM and fuzzy logic.

Deep learning (DL) is a developed sub-category of machine learning that computes more complex problems with a variety of data types like videos and images. DL techniques received a great deal of attention because of their capability to achieve higher prediction accuracy than traditional ML algorithms. Recently, some efforts (Moharekar et al. 2022; Shwetha & Sneha 2022; Ahmed & Yadav 2023) have been made that focused on DL algorithms to improve prediction accuracies in the detection of plant diseases. Several research papers (Sarker et al. 2022; Kumar & Patel 2023) compared various DL architectures such as convolutional neural network (CNN), residual network (ResNet), and visual geometry group (VGG). Nanehkaran et al. 2023 used pre-trained model architectures like GoogleNet, Zeiler and Fergus Network (ZFNet), and AlexNet, which were trained by a high variety of data and capability of working with different tasks. Atik (2022); Ertem & Özbay (2022) investigated the performances of different architectures like AlexNet, GoogleNet, ShuffleNet, and ResNet with tomato leaves. Contributions in DL in the agriculture area have been made by the works of Monowar et al. (2022), He et al. (2022), Tiwari et al. (2020), Oppenheim & Shani (2017), and Patil et al. (2017). One deep learning technique, CNN, is fast becoming a popular classification method due to its ability to overcome challenges encountered in complex problems (Ghosh & Roy 2021; Saeed et al. 2021; Jasim & Al-Tuwaijari 2020; Chaitanya & Yasudha 2020). Therefore, this study employed the CNN technique for disease detection and classification on potato leaves.

In the literature, different ML and DL algorithms have been tested for plant leaf disease classification in different countries, under different environmental conditions, and for different plants such as rice (Nanehkaran et al. 2023), tomatoes (He et al. 2022), peppers (Bhagat & Kumar 2023), apples (He et al. 2022), maize (Nanehkaran et al. 2023), peaches (Wagle & Harikrishnan 2021), cherries (Kurmi & Gangwar 2022), corn (Ciran & Özbay 2022; Pardede et al. 2018), cucumbers (Nanehkaran et al. 2023), apricots (Türkoğlu et al. 2020), olive (Dikici et al. 2022), lemons (Saygılı 2023), and strawberries (Wagle & Harikrishnan 2021). This study focuses on the detection of diseases for potato crops due to their large scale and varied uses.

The main contributions of this paper can be summarized as follows. (i) It proposes a new deep-learning model that correctly classifies plant diseases for the agriculture sector. (ii) This study is original in that it especially focuses on the detection of plant diseases for potato leaves by designing a CNN architecture.

2. Material and Methods

2.1. Dataset description

The PlantVillage dataset (Hughes & Salathe 2015) is a resource in the agriculture area and plant pathology. The dataset contains a collection of labeled images with various plant types such as tomato, potato, pepper, and more. The dataset contains the collected and reported diseases for each plant and is used as an open-source dataset to develop and evaluate machine learning, deep learning, or any other models to design and detect diseases through classification. In our study, we used potato plant diseases from the PlantVillage dataset. It contains 2152 images of potato leaves divided into 3 categories: healthy, early blight, and late blight. Figure 2 shows example leaf images that belong to potato plants.

Healthy Early Blight Late Blight

Figure 2- Sample images of potato leaf diseases

The PlantVillage dataset is a well-known and popular dataset for crop disease with a significant number of public records available. All images in the dataset were captured by Land Grant Universities in the USA (Penn State, Cornell, Florida State, and others). They aimed to diagnose plant diseases by using advanced technologies to support farmers around the globe, by providing the knowledge they need to protect and improve crop health. The diseases of plants were identified and labeled by plant pathology experts. These experts directly worked in the field with two technicians providing the diagnosis and used standard phenotyping approaches in plant pathology. The dataset only contains the images of expertly identified leaves, and, therefore, these images are sufficient for each disease to be used in classification. The details about the technical validation of the dataset can be found in the related article (Hughes & Salathe 2015).

To classify images correctly, it is important to perform a pre-processing stage which includes resizing and rescaling operations. These processes help the algorithm to minimize the possible errors by capturing the characteristic features of diseases while preparing to feed the algorithm. The input image size is 256 x 256 pixels, which was obtained with a resizing stage for efficiency. After that, a rescale operation was performed to scale the image related to the given ratio (1/255) to preserve the same distribution throughout the image by protecting the key features in the images. In this way, the pre-processing operation converted each pixel value in the range 0-255 to values in the range 0-1.

2.2. Proposed method

This section describes and explains the proposed methodology for the classification of potato leaf diseases. The idea of detecting such diseases in plants is to identify unordinary or sick parts of the leaves which are used as images to feed the method.

The proposed deep-learning-based model has numerous advantages. Firstly, since the detection of leaf disease systems could have a significantly important role in the early stages. If the disease is quickly diagnosed, it can help to prevent the disease from spreading. In addition, such a system could provide benefits to farmers who do not have any information, or knowledge about such diseases and their possible impact on plants. The proposed model could be used to detect the disease and learn how to act, preserve, and improve crop health conditions.

The proposed model was designed specifically to perform accurate classification of plant leaf diseases related to potato leaves and to execute operations sufficiently and accurately. The CNN architecture can automatically characterize the local features. With the architecture, patterns and relationships in images can be captured effectively through the algorithm. Furthermore, CNNs can extract unique patterns and features from each image and learn by improving every cycle round using mathematical operations and features like convolutional and pooling layers. These allow CNN architecture to gain the ability to recognize patterns and features, and execute complex issues efficiently. Such capabilities in CNN architecture allows models to execute prediction operations with high accuracies and produce better results than conational models in most cases.

The general structure of the proposed approach is illustrated in Figure 3. The initial step is to prepare a dataset to feed the deep learning algorithm as input. The plant leaf disease dataset includes different disease images and their labels as directories. Pre-processing is performed to improve the quality of extracting the needed segments or features from the input images. Different operations can be performed for images like rescaling and resizing. Pre-processing operations are important since they can affect the model's classification performance directly. Afterward, the dataset is divided into training, validation, and testing sets. The next step is the training process in which the inputs are fed to the CNN architecture and trained to evaluate a set of weights that will result in a prediction with the trained labels. After that, the performance of the model is evaluated according to various criteria such as accuracy, precision, recall, and f-score. Finally, the class label of the given test image is obtained as an output from the deep learning model which is evaluated with the achieved probability scores for each label.

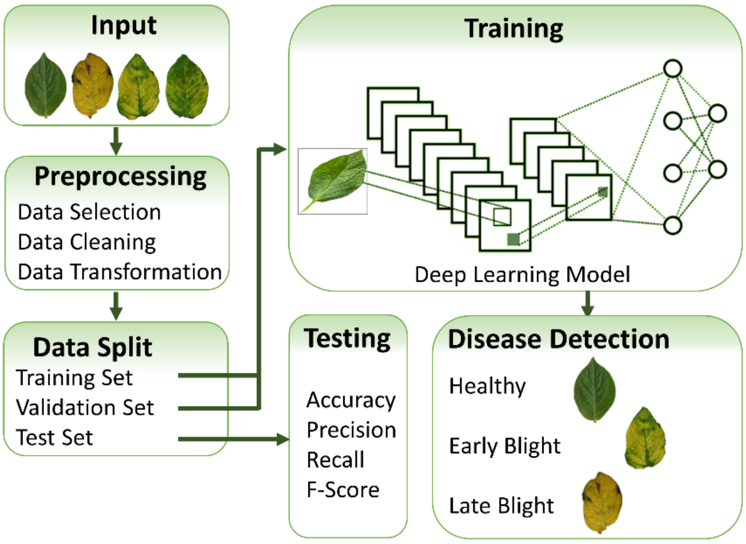

Figure 3- The proposed method: an overview of the general structure

Figure 4 represents the architecture of the proposed model based on the CNN structure. CNN is a type of deep neural network, mostly used to analyze images and videos. The convolution layer uses filters that perform convolution operations which is the dot product of two matrices. One of the matrices is the kernel which is a set of parameters, whereas another matrix is the input that is converted to an array. The pooling operation is simple in that there is a two-dimensional filter over each feature by sliding on them and creating an array with a smaller portion that contains the features extracted from the Conv2D layer. Pooling layers are useful in reducing the number of parameters to be learned and simultaneously decrease the computational complexity of the network. The fully connected input layer, called flatten, takes the output from the last layer and performs a flattening operation to turn it into a single vector. After the flattening operation is completed, the output is fed to the neural network and applies weights to predict the class label. In the end, it gives the final probabilities for each label.

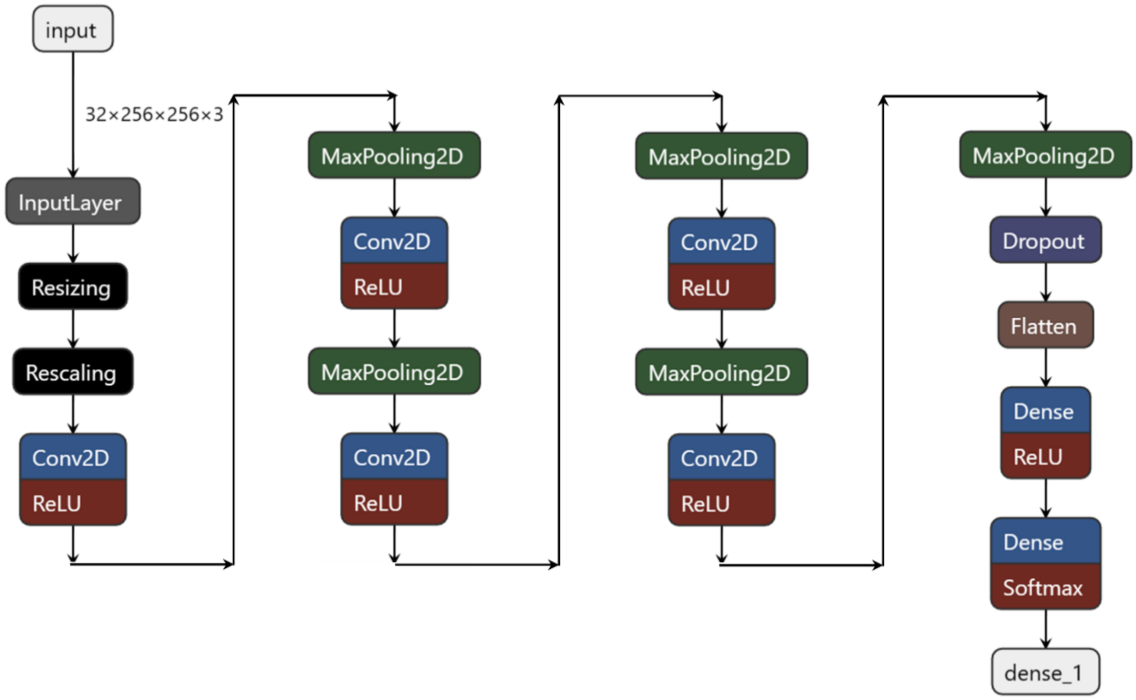

Figure 4- Proposed CNN architecture for potato plant leaf disease detection and classification

The proposed method includes the steps described below.

1. Reading input images from the dataset.

2. Pre-processing images using resize and rescale operations to preserve standards between images.

3. Dividing the data into a training dataset, a testing dataset, and a validation dataset.

4. Applying filters to input images, extracting key features through convolution operations which are performed with Conv2D and Rectified Linear Unit (ReLU) in Figure 4.

5. Reducing the computational complexity of the network while preserving important features which is represented as MaxPooling2D in Figure 4.

6. After convolution and pooling operations are performed, dropout functionality is executed to prevent overfitting to force the model to learn independent features by setting randomly a portion of the input units to zero.

7. After the dropout operation, the feature maps are flattened and transformed into one-dimensional vectors. Then, those vectors are connected to fully connected layers. These layers classify the learned features by mapping the extracted features to the labeled outputs.

8. The final step involves performing classification based on the outputs from the fully connected layers with the usage of the softmax activation function at the end of the proposed model as a layer. This function calculates the probabilities for each class. The sum of the predicted probabilities needs to be in the range of 0 to 1. The class that has the highest probability is labeled as the predicted result which is done using dense_1 in Figure 4.

9. After the model is created, with the usage of testing and validation datasets, performance metrics are calculated to identify the effectiveness and reliability of the proposed model. The classification metrics could be accuracy, precision, recall, and f-score.

Accuracy is the proportion of correct results (either true positive or true negative) in a testing set. It is calculated using the following equation:

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

Where; the parameters TP (True Positives), TN (True Negatives), FP (False Positives), and FN (False Negatives) are the metrics to calculate specificity, sensitivity, and accuracy in performance measurement. TP is used to present the number of correctly predicted positive classes. TN is the result of correctly predicted negative classes. FP is the number of cases predicted positive when they are negative. Finally, FN represents the number of cases predicted as negative when the results should be positive.

Precision is the accuracy of positive predictions with the proportion of correctly predicted positive classes out of the total classes positively predicted. The calculation formula is as follows:

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

Recall (sensitivity) represents correctly predicted positive classes divided by the total actual positive classes. It is calculated using the following equation:

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

The f-score is a metric that is used in classification problems that measure the model performance using correctly predicted positive classes (recall) with the accuracy of positive predictions (precision). The calculation formula is as follows:

$$Fscore = \frac{2 * (Precision * Recall)}{(Precision + Recall)}$$

Macro-averages represent the average across all classes. The performance metric (e.g., precision, recall, or f-score) take place separately for each class. For weighted-averages, the metric is also calculated separately for each class and weighted by the class usage frequencies.

3. Results and Discussion

In this section, the overall achieved prediction accuracies are presented. The proposed CNN model was trained and tested using the potato leaf images dataset. The data is divided into three groups: training, validation, and testing. The training set with 0.8, the testing set with 0.1, and the validation set with 0.1 split ratio are evaluated.

The proposed model obtained 96.82% accuracy and 8.76% loss in training, and 99.48% accuracy and 4.55% loss in the validation dataset. In the testing dataset, the model achieved 98.28% accuracy and 6.44% loss for potato leaf disease classification. Figure 5 and Figure 6 show the ranges of the model indicator that emphasize the effectiveness of the proposed model. Figure 5 represents the accuracy of the proposed model on both the training and testing datasets throughout 15 epochs. It is clear that the model performance increases as the number of epochs increases. Figure 6 shows the loss plot for the proposed model on the training and testing sets for 15 epochs. In general, the model provides low-loss values with increasing epochs.

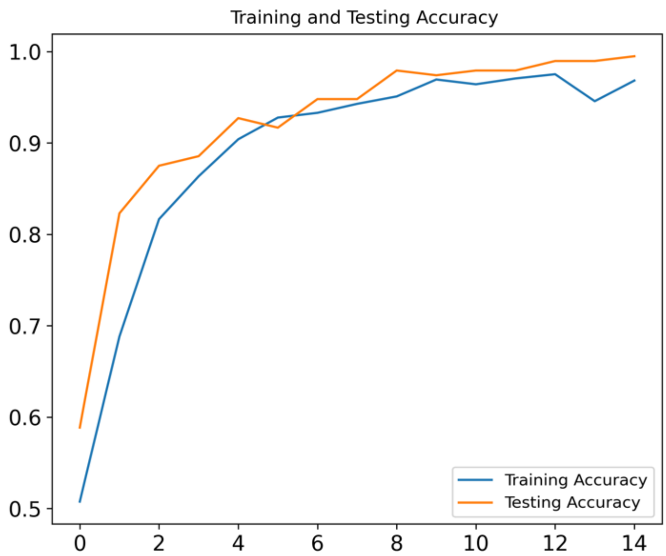

Figure 5- Training & testing accuracy graph of the proposed model

Figure 6- Training & testing loss graph of the proposed model

Table 1 shows the performance of the proposed model using precision, recall, and f-score results for potato diseases. The macro-averages and weighted-averages range between 0.946 and 0.985, which are very close to 1, meaning that the method does return few errors.

Table 1- The performance of the proposed model for each class in terms of precision, recall, and f-score metrics

Potato Leaf Disease	***Precision***	***Recall***	***F-score***
Early Blight	1.000000	0.972727	0.986175
Late Blight	0.955357	1.000000	0.977169
Healthy	1.000000	0.866667	0.928571
Macro Average	0.985119	0.946465	0.963972
Weighted Average	0.979410	0.978448	0.978297

Table 2 represents the confusion matrix of potato diseases which represents the proposed CNN algorithm performance over the validation dataset. It visualizes the predicted true positive, false negative, false positive, and true negative values for each class label. High diagonal elements of the confusion matrix (102, 115, and 12) for each class, with low non-diagonal elements, confirmed the high performance and robustness of the machine learning model for predicting plant leaf diseases. According to the matrix, the proposed model produced only 3 incorrect outputs out of 232 predictions.

Table 2- Confusion matrix of the proposed model for all potato diseases

	Early Blight	*Late Blight*	*Healthy*
Early Blight	102	0	0
Late Blight	1	115	2
Healthy	0	0	12

Figure 7 shows samples that were taken from the dataset randomly and labeled with actual and predicted labels using the proposed model for potato leaves. As can be seen, the constructed model usually had no difficulty in identifying potato leaf diseases. For example, the first sample leaf image was labeled correctly with a 99.96% probability.

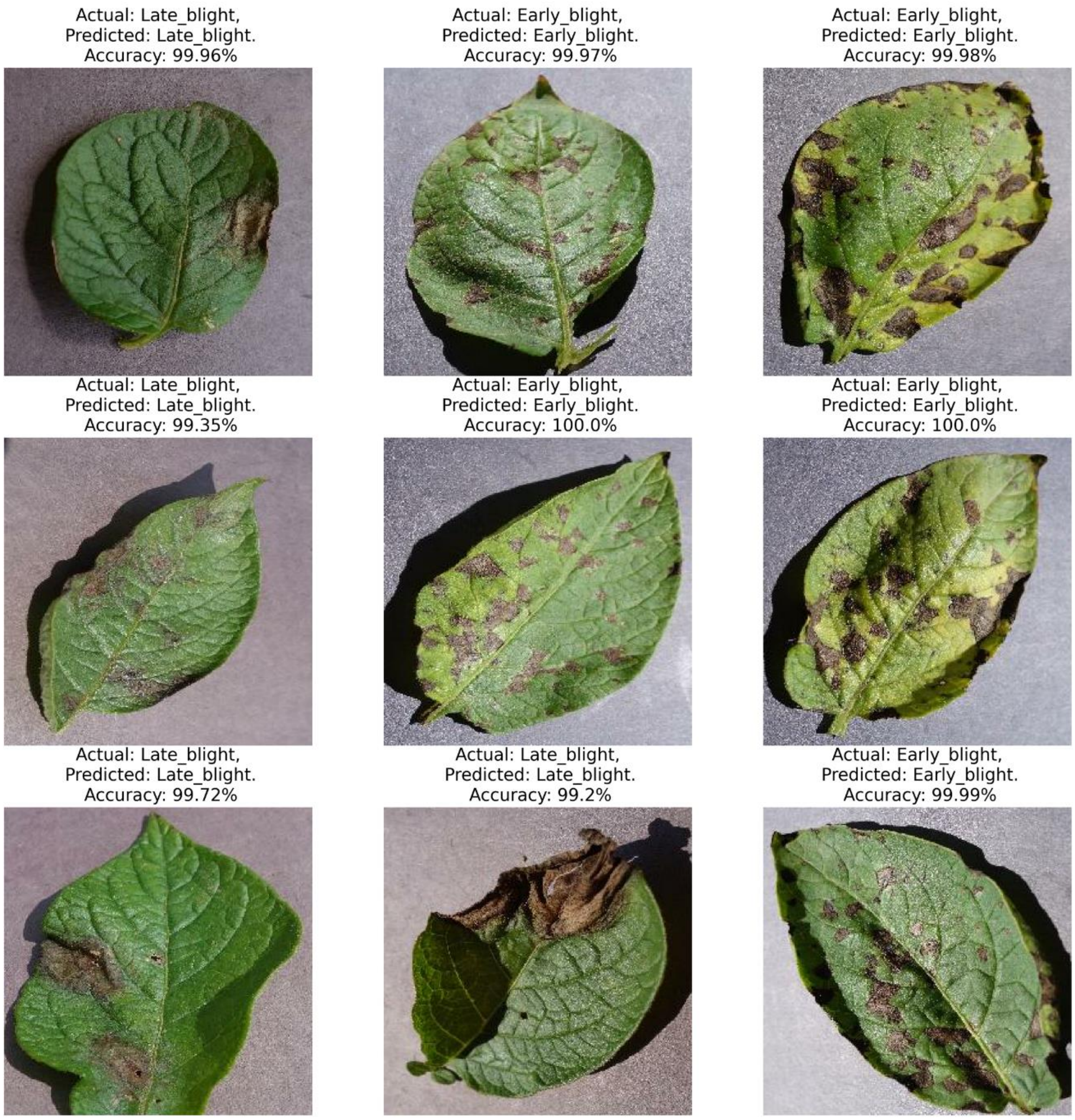

Figure 7- Sample prediction results for potato leaf images

Table 3 shows the results of previously designed models for the detection of potato plant leaf diseases. Based on the table, it is clear that the proposed model achieved a higher performance (98.28%) than the state-of-the-art models (89.67%) on the same dataset and same plant type on average. Consequently, the model demonstrated its superiority over the other models with an average of 8.6% improvement. For example, it performed better than RF (92%) (Swetha & Jayaram 2019), DT (91%) (Iqbal & Talukder 2020), KNN (86.40%) (Sharma et al. 2021), and LR (74.80%) (Kurmi & Gangwar 2022). As observed in Table 3, SVM is the most frequently used methodology. As seen in Table 3, the proposed model outperformed SVM-based models. Compared to the deep learning models such as Google Network (GoogleNet) (92.33%) (Nanehkaran et al. 2023), dense network (DenseNet-121) (95.00%) (Ahmed & Yadav 2023), efficient DenseNet (97.20%) (Mahum et al. 2023), VGG (91.60%) (Kumar & Patel 2023), AlexNet (90.00%) (Wagle & Harikrishnan 2021), and ResNet-18 (95.81%) (He et al. 2022), the proposed model achieved the highest accuracy.

In addition to the accuracy indicator, the precision, recall, and f-score values were also compared. Sharma et al. (2021) obtained the results of approximately 0.899 for all the metrics using the SVM method. Islam et al. (2017) achieved 0.9500 for all these metrics using the SVM method. Mathew et al. (2022) achieved values of 0.9205 and 0.9200 for precision and recall, respectively, from their model. In another study (Aurangzeb et al. 2020), the results of these measures were obtained using Cubic SVM with precision (0.9433) and recall (0.8530) values. The precision value was recorded as 0.9160 by Sanjeev et al. (2020). Jeyalakshmi & Radha (2020) recorded precision (0.9679), recall (0.9702), and f-sore (0.9689) values using the SVM method. Mukherjee (2020) measured and obtained precision, recall, and f-score as 0.5655, 0.4562, and 0.5050, respectively. When precision, recall, and f-score metrics are considered, the proposed model in this study performed better than the previous studies by obtaining 0.9794, 0.9784, and 0.9783, respectively.

Table 3- Comparison of the proposed model compared to the state-of-the-art models on the potato leaf image dataset

Reference	***Year***	***Method***	***Accuracy (%)***
Ahmed & Yadav	2023	DenseNet-121	95.00
Mahum et al.	2023	DenseNet-201	96.03
		Efficient DenseNet	97.20
Nanehkaran et al.	2023	AlexNet	90.00
		GoogleNet	92.33
		ZFNet	89.33
		CNN	91.33
		Le Network (LeNet)	91.00
Bhagat & Kumar	2023	SVM	97.00
Kumar & Patel	2023	VGG	91.60
		RF	73.80
		Deep CNN	92.90
		First Scalable Neuromorphic Fault-Tolerant Context-Dependent Learning	94.00
		Dendritic Event-Based Processing	93.00
		Entropy-based Local Binary Pattern	90.00
		Hierarchical Deep Learning CNN	95.77
		Tree-CNN	86.50
		Radial Basis Function Neural Network	86.50
Mathew et al.	2022	SVM	83.00
		Voting (SVM + KNN + DT)	92.00
Sarker et al.	2022	CNN	93.00
		ResNet50	97.00
		VGG19	84.00
Shwetha & Sneha	2022	Backpropagation Neural Network	92.00
		SVM	95.00
		VGG19 + LR	97.80
Moharekar et al.	2022	CNN	94.60
He et al.	2022	ResNet-18	95.81
		Disease Image Recognition based on Bilinear Residual Networks	96.05
Monowar et al.	2022	Bootstrap Your Own Latent	88.30
		Simple Siamese	86.10
		Cross Iterative Kernel K-means enhanced with Image Classification and Similarity Measurements	82.50
		Deep CNN	89.90
Kurmi & Gangwar	2022	Bag-of-visual-words (BoW) + Fisher Vectors (FV) + Hand-Crafted Feature (HCF) + SVM	91.90
		BoW + FV + HCF + LR	89.60
		BoW + FV + HCF + Multi-Layer Perceptron	87.10
Rozaqi et al.	2021	VGG16	95.00
		CNN - Sederhana	80.00
		Inception-V3	78.00
		ResNet-50	78.00
Wagle & Harikrishnan	2021	SVM	95.83
		AlexNet	90.00
Ghosh & Roy	2021	CNN	87.47
Kaur & Devendran	2021	Scale-Invariant Feature Transform (SIFT) + Ensemble	88.23
		Law's Mask + Gabor + Ensemble	95.66
		Law's Mask + SIFT + Gabor + Ensemble	93.16
		Gabor + Ensemble	84.23
Saeed et al.	2021	CNN	91.67
Sharma et al.	2021	SVM	92.90
		KNN	86.40
		DT	78.70
Guo et al.	2021	GhostNet	97.17
Ismail et al.	2020	Linear SVM	90.00
		Quadratic SVM	88.00
		Cubic SVM	91.30
		Boosted Tree	94.70
		Deep Learning	90.40
Tiwari et al.	2020	VGG19	97.80
Aurangzeb et al.	2020	Cubic SVM	94.50
		LDA	92.70
		Ensemble Tree	92.60

Table 3 (Continue) - Comparison of the proposed model compared to the state-of-the-art models on the potato leaf image dataset

Reference	*Year*	*Method*	*Accuracy (%)*
Singh & Kaur	2020	K-Means + SVM	95.99
Mukherjee	2020	SVM + Fuzzy Logic	91.59
Iqbal & Talukder	2020	LR	94.00
		RF	97.00
		KNN	91.00
		NB	84.00
		DT	91.00
		LDA	78.00
Jeyalakshmi & Radha	2020	NB	88.67
		KNN	94.00
		SVM	96.83
Chaitanya & Yasudha	2020	CNN	94.84
Ahmad et al.	2020	Local Binary Pattern	92.50
		Directional Local Quinary Patterns	96.20
		Local Ternary Patterns	90.60
Jasim & Al-Tuwaijari	2020	CNN	97.20
Sanjeev et al.	2020	Feed Forward Neural Network	96.50
Singh & Kaur	2019	Gray-Level Co-Occurrence Matrix + KNN	97.00
Swetha & Jayaram	2019	RF	92.00
		SVM	94.00
		DT	91.00
		KNN	89.00
		LR	16.00
		NB	85.00
Pardede et al.	2018	SVM - Linear	87.01
		SVM - Radial Basis Function	83.99
		SVM - Polynomial (Order 2)	83.06
		SVM - Polynomial (Order 3)	79.58
Islam et al.	2017	SVM	95.00
Oppenheim & Shani	2017	VGG16	96.00
Patil et al.	2017	Neural Networks	92.00
		RF	79.00
		SVM	84.00
Aparajita et al.	2017	Segmentation Methodology	96.00
Average			*89.67*
Proposed Model		**Convolutional Neural Network**	**98.28**

In a deep learning study, there are two main types of uncertainty: model uncertainty and data uncertainty. Model uncertainty (MU) includes the uncertainty in network architecture design that could yield a high performance. Data uncertainty (DU) typically refers to incorrect, incomplete, or unknown samples in input data that cause uncertainty in the corresponding output. In this study, the MU was assessed by using various metrics, including accuracy, precision, recall, and f-score; the MU was measured using the Wilcoxon statistical test. The differences between the results of various CNN architectures given in Table 3 and the result of the proposed CNN architecture were evaluated in a pairwise comparison manner. The p-value (0.03781e-4) obtained by the Wilcoxon test indicates that the proposed CNN architecture is proper for making an accurate prediction since the p-value is smaller than the significance threshold (0.05). In the point of data uncertainty, the proposed model was tested on a public and widely-used dataset in the literature. The information on data collection and its technical validation can be found in (Hughes & Salathe 2015).

4. Conclusions

The development of detection systems is crucial for achieving and performing stable, precise, and reliable predictions in agriculture. The detection of plant diseases can be achieved through the use of general image processing methods and with a deep learning algorithm that can be integrated at various stages of a plant's life cycle. The effort performed to analyze and identify diseases could be reduced and simplified with the usage of automation technologies in agriculture which, could provide a healthy and sustainable environment for plants and it could limit significant threats like extinction of various plant species.

The main findings of this study can be summarized as follows:

- The results of the experiments showed that the proposed model achieved 98.28% accuracy in potato leaves.
- On the testing dataset, the model obtained a 6.44% loss for potato leaf disease classification.
- The model presented in this study performed very well by achieving precision (0.9794), recall (0.9784), and f-score (0.9783) values.
- The CNN model reached a high accuracy in a number of epochs (15 iterations).
- According to the confusion matrix, the proposed model produced only 3 incorrect outputs out of 232 predictions over the validation dataset.
- When the results of the studies (89.67%) in the literature were compared, the performance was approximately 8.6% improved on average.

One limitation of this study is that itis capable of detecting only diseases that are labeled in the dataset used for the proposed model training which are named as healthy, early and late blight. Future studies could focus on gathering well-designed and easily processed datasets that include other diseases, and in this way, improve the performance of previously found methods. Another possible future study may also be the use of detection algorithms in mobile devices to assist people who do not have an opportunity to access such applications for their plants for early-stage support.

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