

REGION-BASED FULLY DEEP CONVOLUTIONAL NEURAL NETWORKS ENHANCED WITH CARNIVOROUS PLANT ALGORITHM FOR PLANT DISEASE DETECTION AND CLASSIFICATION

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ABSTRACT

The pace of agricultural production is one of the most critical factors determining a nation's overall economic well-being. Diagnosing symptoms at an earlier stage can significantly reduce the spread of infectious diseases, increasing agricultural productivity. This research aims to advance agricultural technology and eventually boost agricultural productivity and financial outcomes by providing an effective approach for early detection and management of plant diseases. The automated detection of plant diseases is essential to plant monitoring since plant diseases are one of the most significant challenges faced in agriculture. This research proposes a method for recognizing and categorizing plant illnesses using region-based fully deep convolutional neural networks (RFDCNN). This method also utilizes Carnivorous Plant Algorithm (CPA) to enhance the average, mean precision of the results obtained using RFDCNN architecture and feature extraction. 230 plant disease leaf images like potato, Strawberry, pepper, peach, Squash, citrus, tomato, cherry, etc., from a farm field were gathered for this plant disease classification, along with a dataset of plant villages. According to the findings of the experiments, the RFDCNN-CPA deep learning framework that was suggested is able of accurately and efficiently classifying the many different varieties of plant leaves. The end results demonstrated that the RFDCNN-CPA obtained a higher accuracy rate of 97.92%, precision analysis of 95.82%, an f-score of 90.52%, and an overall execution time of 0.42ms.

Keywords: *Agriculture, Deep Learning, Plant Disease Detection and Classification, Region-based Fully Deep Convolutional Neural Networks, Computer Vision*

1. INTRODUCTION

The development and increased production of agricultural plants depend on early disease detection and treatment [1]. Manually tracking plant diseases will be an inaccurate and difficult task [2]. Farmers find it a challenging and expensive task to find subject experts to monitor plant diseases. To detect plant diseases, it became necessary to keep vigilant on the fields of crops constantly [3]. Researchers are currently proposing several approaches [4] to discover involuntary houseplant diseases using AI methods that require less human labor. A deep convolutional neural network (DCNN) is one popular method for classifying images [5]. We use the convolutional, pooling, and fully connected layers of the DCNN to learn structures from exercise information [6]. Transfer learning applies a previously trained neural network to a new task

using a different dataset. The most frequently used transfer learning algorithms for image classification are Inception-v3, MobileNet, DenseNet, VGG16, and ResNet [7].

The DCNN algorithm can effectively train more data [8]. Data augmentation methods use a variety of data transformation techniques to generate new images from existing datasets [9, 10]. Deep convolutional generative adversarial networks (DCGAN), neural style transfer (NST), or fundamental image modification (BIM) are common techniques for data augmentation [11]. Some of the most commonly used BIM techniques are symmetrical transformations, flipping, scaling, filling, rotation, cropping, and translation. Using training data, the DCGAN neural network generates a new set of visuals [12]. Two DCNNs, the discriminator DCNN and the generator DCNN, are combined to form the GAN data generator. The

discriminator network classifies both the initial and newly generated images from the DCNN generator. The DCNN generator produces new images that resemble the training set. Researchers identify DCGAN as one of the best image augmentation methods for processing medical images [13].

Moreover, DCNNs require appropriate hyperparameter values to enhance their classification performance. Hyperparameters are the essential training variables that can impact how effectively deep learning techniques work. DCNNs' most frequently used hyperparameters are the dropout value, activation function, filter size, epochs, loss function, mini-batch size, and learning rate. Selecting the correct hyperparameter value when solving a severe learning problem can be challenging. Hyperparameter tuning techniques [14] help find the ideal hyperparameter values for the DCNNs. The two most widely used methods for improving deep learning parameters are grid search and random search [15].

One of the earliest contemporary methods for using CNN to complete image detection tasks was the region-based convolutional neural network (RCNN) [16]. Limited research has been conducted on applying deep learning (DL) techniques to carry out this complex agricultural operation in the context of identifying plant diseases. To increase the mean average precision, the authors annotated images of tomato leaves [17].

The proposed study implements a deep learning-based method to recognize and categorize plant diseases using images of leaves taken at various resolutions. We created a reliable method for classifying plant diseases using region-based intense convolutional neural networks (RFDCNN). The Carnivorous Plant Algorithm (CPA) is adopted to improve mean average precision and feature extraction. The experiment's findings demonstrate that the suggested RFDCNN-CPA deep learning model can accurately and quickly categorize a variety of plant leaf diseases types.

The remaining sections of this paper is prepared as: Section 2 presents a list of related works, and Section 3 provides a wide explanation of the suggested model. Section 4 provides an example of how well our framework performs in detection. In Section 5, we conclude our discussion.

2. LITERATURE SURVEY

Dhaka et al. presented the foundational framework of the CNN model to diagnose plant diseases. [18]. Furthermore, preprocessing methods and performance metrics were studied to evaluate the framework's performance. Nagaraju et al. [19] also reviewed earlier studies to identify the foremost datasets, preprocessing methods, and deep learning strategies for different leaves. They examined and evaluated eighty-four plant disease detection research methods. They discovered that many DL techniques have restrictions when analyzing the images and stated that the effectiveness of the framework depends on appropriate preprocessing methods. Lu et al. [20] published an analysis of the organization of houseplant illnesses using CNN. They assessed the key issues with various CNN models for different plant diseases and the effectiveness of DL criteria. They identified that more investigation with larger datasets was essential to obtaining a more satisfying outcome.

Golani et al. [21] conducted a study of hyperspectral data for the identification of leaf illnesses. They have highlighted both the present issues and potential directions and proved neural network methods were effective for crop protection with various hyperspectral sensors in the plant leaves. Bangari et al. proposed a study of leaf disease identification on potato leaves using CNN architecture [22]. They determined that convolutional neural networks are better for leaf disease detection after reviewing numerous papers.

Toda et al. [23] examined the neural and its intermediate layer knowledge with computer vision techniques along with a CNN model to detect plant diseases. They demonstrated that neural networks could precisely capture the textures and colors of illness abnormalities upon diagnostic tests. CNN presents the probability of accessing the data recorder visually. The findings imply that, although visualization approaches offer a way of analyzing, humans are always most important in their interpretation, as in the instance of fusing computer-generated results with expertise in plant study.

Tassis et al. [24] used an integrated framework of multiple convolutional neural networks to computerize identity detection and pest recognition models. The coffee tree leaf images taken from iPhones are used as a dataset for the framework.

Hashed-out R-CNN is utilized to classify data, PSPNet, UNet, and ResNet are utilized for image segmentation and training. The author is not very concentrated on the preprocessing of the data. Esgario et al. [25] developed an Android app that identifies various leaf diseases in coffee leaves. Infections and illnesses have a substantial impact on agricultural yield and quality. Early detection of symptoms can considerably minimize the spread of

infectious diseases, enhancing agricultural productivity. Because leaf diseases are considered the most severe concern in agriculture, computerized diagnosis of plant infections is critical and essential in plant monitoring. A plant's leaves reflect the majority of disease symptoms. Hence, the proposed work presents a deep learning-based framework for recognizing and classifying plant ailments that utilizes leaf images of various resolutions.

Table 1: Comparison of Current Methods

Researcher	Year	Aim	Method	Performance	Advantages
Le VNT et al. [26]	2020	A technique to identify and categorise crop and weed disease	k-FLBPCM framework and SVM were employed.	Accuracy 98.63%	The method increased the classification accuracy for plants with comparable morphological textures.
Agarwal M et al. [27]	2020	To recognise and categorise the disease affecting the tomato crop, use a CNN-based architecture.	A CNN based method was presented.	Accuracy 91.2%	The method is effective in terms of computation.
Turkoglu M et al. [28]	2021	To identify plant disease and to suggest pest control	An ensemble CNN, SVM classifier, GoogleNet, AlexNet, ResNet50, DenseNet201, and ResNet101.	Accuracy 97.56%	Plant disease classification is resistant to minor variations in the work.
Karthik et al. [29]	2020	To find disease in tomato leaves using DL.	CNN-based framework utilizing a residual network	Accuracy 98%	The project can withstand noisy samples.
Zhang Y, et al. [30]	2020	To extract features and utilize a Faster-RCNN method with a deep residual framework rather than the VGG16 model.	Faster-RCNN model	mAP 97.18%	The research is resistant to noise and distortions in alleged samples.
Pantazi XE et al. [31]	2019	To analyse geographies and develop classifiers for automatic detection of disease in various plant species	LBP algorithm and the SVM classifier.	Accuracy 95%	The model has increased generalizability.
Oo YM et al. [32]	2018	To detect leaf diseases and categorize using image processing.	The SVM and the GLCM and LBP descriptors were used	Accuracy 98.2%	The framework can identify the diseased plant portion from the suspected samples if there are significant light variations.

The design of an enhanced region-based CNN algorithm for the detection, localization, and classification of tomato leaf disease is the focus of this research, which found a classification accuracy of 96.4% after 300 epochs. Loss represents the average cross-entropy of each epoch during the training process [33]. To construct the ensemble classifiers, a variety of preparation, feature extraction, and classification techniques were implemented. We determined the most effective ensemble classifiers by comparing the performance of these numerous ensemble techniques. Two databases, Plant Village and Taiwan tomato leaves,

were utilized to evaluate the accuracy and dependability of the proposed method in both controlled laboratory environments and real-world scenarios [34]. To optimize the denseNet-121 architecture for the efficient implementation of the mutation-based Henry Gas Solubility Optimization (MHGSO) algorithm, the hyperparameters have been adjusted. The principal objective of optimizing hyperparameters for a convolutional neural network (CNN) is to reduce the network's computational complexity and error rate. This stage facilitates the achievement of a higher level of accuracy by the MHGSO-optimized DenseNet-121 architecture

when categorizing diverse plant images from the Plant Village dataset [35]. Mitra et al. proposed a deep learning method for categorizing several varieties of succulent tomato plants using the CNN model. After completing 15 epochs, the model achieved 89% accuracy on the dataset. However, this is insufficient for model optimization to get better results [36].

Building reliable disease detection algorithms requires ensuring the consistency and quality of the collected data. To build a reliable and quality dataset, issues like image quality, variation in plant appearance, and unequal data distribution among several illnesses must be addressed. Many existing models focus on the detection of a single disease or single plant. The methodology entails promptly interceding the region of interest within the collected images. Existing studies rarely consider the occlusion concern. The proposed study overcomes these research gap by implementing the hybrid deep learning models and a balanced database dataset.

The proposed system is implemented to optimize the hyperparameters of plant disease

detection and classification systems while enhancing their precision, resiliency, and effectiveness through the integration of the CPA and the RFD-CNNs' capabilities in disease localization and spatial feature extraction.

3. PROPOSED SYSTEM

The proposed RFDCNN-CPA model's architecture discusses training techniques, experimental requirements, and data collection. The architecture of the proposed method for plant leaf disease detection is depicted in Figure 1. The Carnivorous Plant Algorithm is an attempt to improve the average mean precision. We develop the RFDCNN-CPA model using TensorFlow 2.9.1, NumPy 1.19.2, Matplotlib 3.5.2, and OpenCV 4.5.5 libraries in Python 3.7. Data preparation, pre-processing, model creation, and disease detection tasks are carried out with an Intel Core i7 CPU, which holds a random-access memory of sixteen gigabytes on an HP Z240 workstation. The NVidia DGX-1 is used as a deep learning server station. We trained and evaluated the proposed RFDCNN-CPA using contemporary methods.

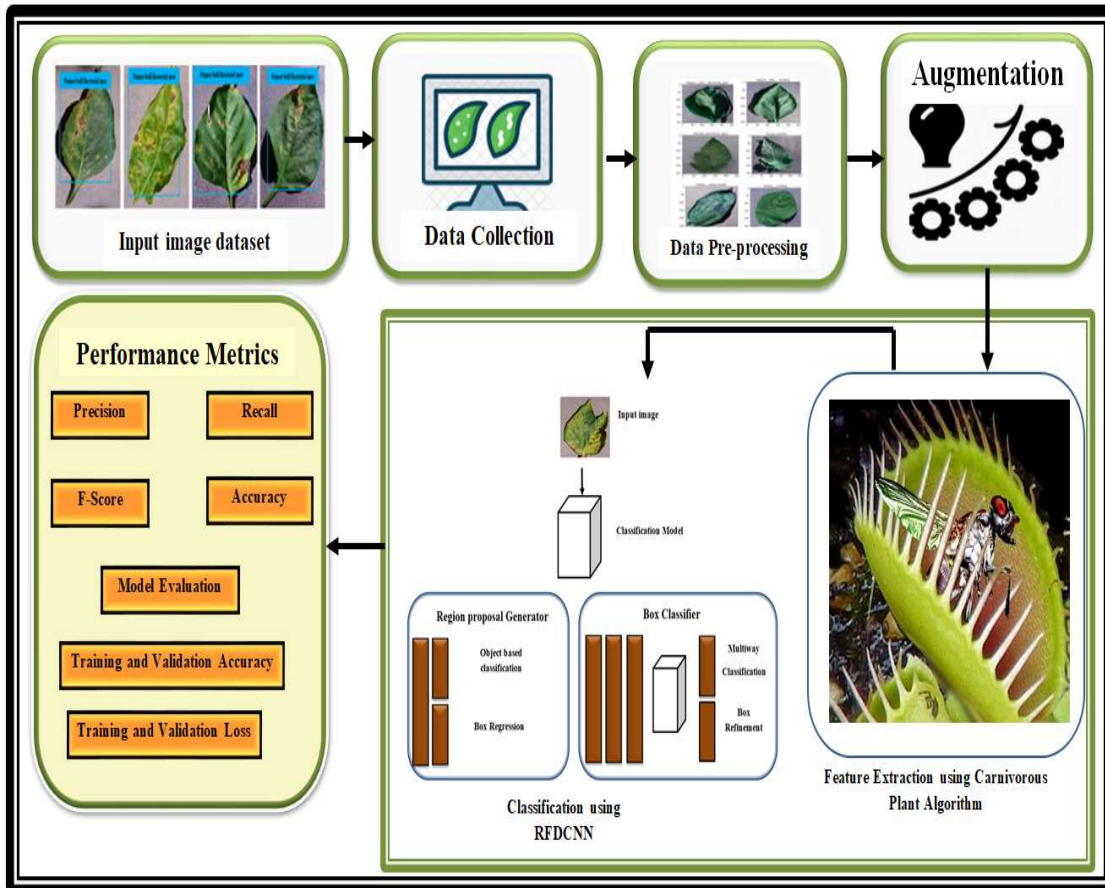


Figure 1: Proposed method of RFDCNN-CPA method

the deep learning server accelerates deep neural network training by combining eight Tesla P100 GPUs and eight Xeon E5-2694 Version 4 CPUs. The following subsections provide more information on the various steps of plant disease detection, including dataset preparation and preprocessing.

3.1 Rusts

A group of plant diseases known as rusts is brought on by the Pucciniales family of fungi. The genus *Puccinia* encompasses more than half of the 7,000 rust species, distributed among 168 rust genera. Rust fungi are extremely specific plant diseases with a variety of distinguishing characteristics. The numerous rust fungi harm a wide variety of plants, as shown in Fig 2 and 3.



Figure 2: Rust Leaves

Though each species has an extremely constrained spectrum of hosts and is unable to multiply on unhosted plants, Many rust fungi are difficult to grow in pure culture as well. At certain stages of its life cycle, one kind of rust fungus has the potential to spread infection to two distinct plant hosts. It can also make up to five different structures that produce spores, such as the aecia, spermogonia, telia, uredinia, and basidia, which are all different in how they look and how they work inside.

The host range of every kind of spore is rather constrained, and it typically affects one particular plant species. The rust fungus can individually infect still-living plants. A spore that touches a plant's surface germinates, infects its host, and produces disease. Certain plant sections only become contaminated, including petioles, leaves, young shoots, fruits, stems, etc.

A severe rust infection can cause a plant to seem stunted, yellow chlorotic, or exhibit other signs like fruiting rust bodies. Rust fungi develop inside infected plant parts and produce fruiting rust bodies

that release spores, either internally or, more frequently, externally, on the surfaces of the infected components. The plant may exhibit abnormalities such as witch's broom, stunted growth, galls, stem canker, or hypertrophy of the infected plant sections as a result of some rust species' recurring systemic infections. Rusts get their name from the coatings of rust-colored, brown, or powdery spores that are typically seen on plants shells. The anti-wheat rust holiday Robigalia, which occurs on April 25, has ancient origins.

Rust leaves

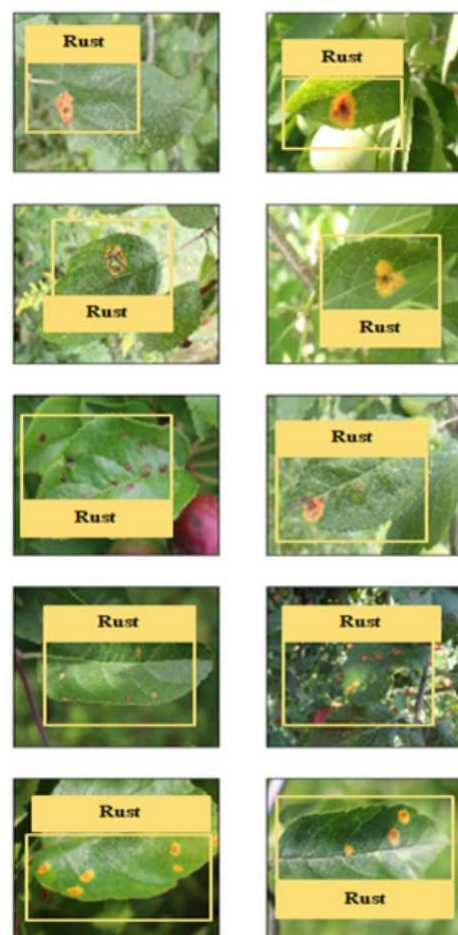


Figure 3: Rust Leaves sample images

3.2 Powdery

Powdery mildew is a fungus illness that can affect many different types of plants. Infections with powdery mildew are produced by different types of fungal species that belong to the order Erysiphales. Powdery mildew has several distinct traits, making it one of the simpler plant diseases to recognize. The

stems and leaves of diseased plants have powdery white patches on them, as shown in figure 4, and more sample images in figure 5.



Figure 4: Powdery leaves

Lower leaves are the most susceptible to mildew, yet it can develop on any portion of the plant above ground. The illness intensifies, leading to the development of numerous asexual spores that enlarge and multiply the spots. Depending on the plant's length, the mildew can also travel to the top and bottom of the plant. The optimum conditions for the growth of powdery mildew are moderate temperatures and high humidity.

The spread of the disease discovers the perfect temperate habitat, wet, in greenhouses. Because powdery mildew can survive in a greenhouse, it damages agricultural and horticultural practices. We control the disease by utilizing bio-organic treatments, chemical approaches, and genetic resistance. Understanding powdery mildew and its treatment is essential since the ensuing illness can significantly reduce vital agricultural yields.

3.3 Data Collection

We evaluate the proposed technique's detection and classification performance using the PlantVillage dataset. The PlantVillage dataset includes 54,366 images of plant leaves from 14 different plant species, with 26 classifications for damaged plants and 12 categories for healthy plants, as shown in Figure 6. We gathered 230 plant disease leaf images from a farm field, including cherry, strawberry, squash, peach, citrus, orange, and corn, for this plant disease classification, along with the plantVillages dataset.

Additionally, 44 different plant species leaves were gathered for this classification of leaf diseases. With the Plantvillage dataset, trials for all 14 crop species, including potato, tomato, grape, and apple, are included. The Plantvillage database trials vary in

Powdery leaves

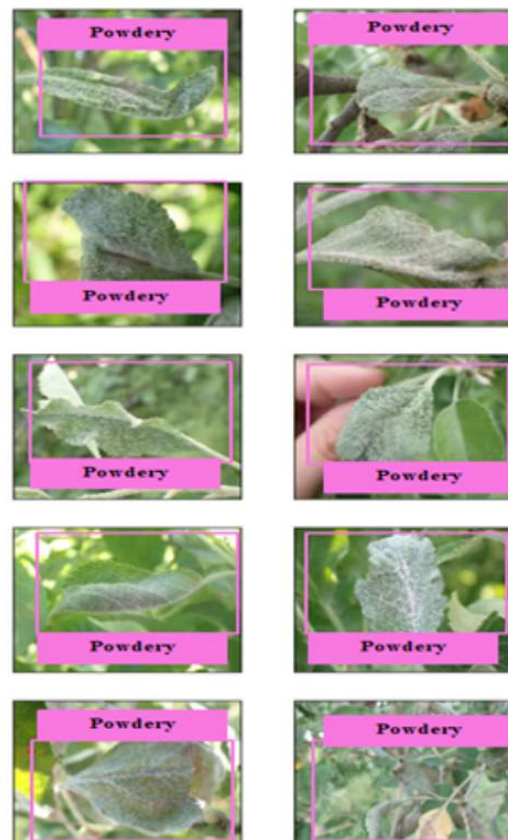


Figure 5: Powdery Leaves sample image

size, colour, light, angle, blur, noise, and other factors. We performed many tests on the collected database, which contains various categories of plants and their ailments, to assess the stability of the proposed method.

3.4 Data Pre-processing and Augmentation

Images are reduced in size to 224 x 224 and converted from BGR to RGB using the pre-process input function because Python, by default, expects BGR input. This prevents data leakage issues (R, G, and B). By using a technique called "data augmentation," it is possible to significantly broaden the range of readily available data for training models without actively gathering new data. The concept of the Keras Image Data Generator is utilized to enhance the data (zoom range, flip horizontally, resize, and rotation range) which is represented in figure 6.

3.5 Utilizing the Carnivorous Plant Algorithm for Feature Extraction

Carnivorous plants detain and consume wildlife to obtain nutrients, unlike most plant life that gets its nutrients through photosynthesis.

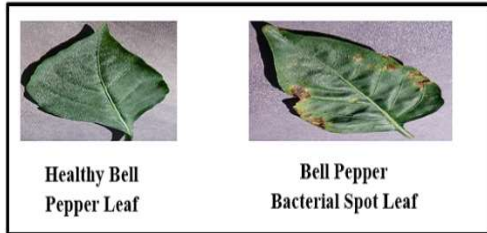
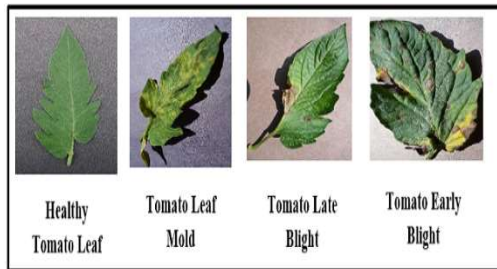
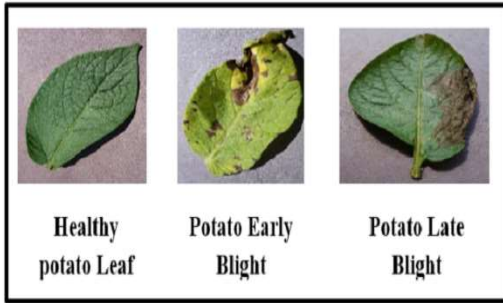


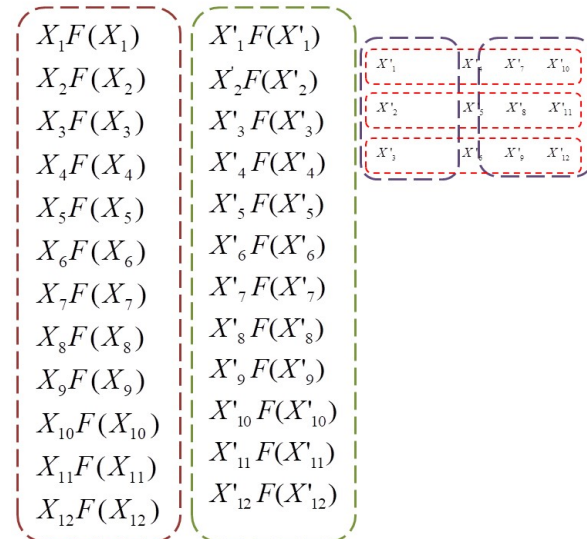
Figure 6: Plant disease classification example images

To survive in hostile environments devoid of the nutrients needed for growth and reproduction, they frequently attract flies, frogs, lesser lizards, animals, and other small wildlife with their shade or emissions. These tiny organisms add extra nitrogen and phosphorus to the diet. The development of the CPA, a meta-heuristic procedure, involved simulating every step of carnivorous plant predation, from luring prey to catching and consuming it. The algorithm comprises four stages: grouping and classification, growth, reproduction, and recombination. The following is a description of the details.

3.5.1. Grouping and classification

The general population includes n CPAs. Individuals are ranked in the population from most minor to largest based on their suitability standards for the minimization problem. Because $n_1 > n$ and n_1 is divisible by n , the bottom n_1 individuals are considered prey, whereas the top n are considered carnivorous plants. Each group consists of n individuals, one of which is a carnivorous plant, and n prey. The group includes the digit n . The best prey, then the second-best prey, and so on until the best prey is drawn to the best carnivorous plants, are attracted to the best carnivorous plant. The best carnivorous plant will initially draw in the best prey ($N+1$), followed by the second-best ($N+2$), and so on, until the best carnivorous plant ($N+1$) marks the best effect.

An example of the grouping process is shown in Fig. 7, where the population size is $nn = 12$, the number of carnivorous plants is $n = 3$, and the



number of prey is $n_1 = 9$, and before sorting, $X = (X_1, X_2, \dots, X_{12})$, and after sorting, $X_0 = (X_0 1, X_0 2, \dots, X_0 12)$, the objective ($X_0 12$).

Figure 7: The CPA grouping procedure at size 12

3.5.2. Growing stage

Some prey were drawn to the scent of the carnivorous plant, but others eluded it or managed to flee. As a result, the CPA now includes an attraction probability (γ). If $\gamma (\gamma = 0.8)$ is larger than the arbitrary quantity λ (λ is produced in the variety $[0, 1]$) the insectivorous houseplant is successful in luring

the prey to grow, and the following model can be expressed:

$$newxp_i = p_{iv} + \alpha \otimes (xp_i - p_{iv}) \quad (1)$$

$$\alpha = gr * rand \quad (2)$$

where \otimes denotes multiplying the variables in two vectors at the same position, xp_i is the carnivorous plant in group i , p_{iv} is the v th prey in group i . $rand$ is the random vector in the range $[0,1]$, and gr is the growth rate, which is normally equal to 2. The following is a possible way to express the prey's growth model.: If is γ less than λ , either the prey escaped the trap or the plant failed to draw the prey to it:

$$newp_{ij} = p_{iv} + \alpha \otimes (p_{iu} - p_{iv}) \quad (3)$$

$$= \begin{cases} gr * randf(p_{iu}) < f(p_{iv}) \\ 1 - gr * randf(p_{iv}) < f(p_{iu}) \end{cases} \quad (4)$$

where p_{iu} and p_{iv} stand for multiplying variables within two vectors at the same position, and P and v^{th} stand for the group's p_{iv} and prey, respectively. The fitness values of the v^{th} and p_{iu} prey in the group are $f(p_{iu})$ and $f(v^{th})$, respectively (p_{iu}). The $[0, 1]$ range of the random vector $rand$.

3.5.3. Phase of reproduction

It is possible to summarize the mathematical model: The reproduction process is only allowable on the best omnivorous herb.

$$newxp_i = \begin{cases} xp_1 + \beta \otimes (xp_j - xp_i)(f(xp_j) < f(xp_i)) \\ xp_1 + \beta \otimes (xp_j - xp_i)(f(xp_j) < f(xp_j)) \end{cases} \quad (5)$$

$$\beta = \mu * rand \quad (6)$$

Groups i and j 's carnivorous plants are referred to as xp_j and xp_i , respectively. On average, the generative rate is equal to 1.8. Groups i and j carnivorous plants have fitness values of $f(xp_j)$ and $f(xp_i)$, respectively. The ideal member of the population is xp_1 .

3.5.4 Phase one of recombination

First, a new population is produced by mating newly created individuals with members of a preexisting population. Second, we ranked the new population members from small to significant based on their fitness scores. Pick the top n people to keep the population size constant with the previous population. Recombination allows for the selection of fitter individuals for the next generation.

3.6. Region-based Fully Deep Convolutional Neural Networks (RFDCNN)

The only variance between RFDCNN network and the Faster-RCNN is that after region of interest (ROI) pooling, convolutional layers are removed [37]. After ROI pooling, the region suggestions produce the similar score maps for the regular elective. Due to the lack of a learnable layer after the ROI, this DL architecture is also less complex than models like the Faster RCNN, which significantly reduces computation time. Fig. 8 illustrates the fundamental design of the RFDCNN architecture and the associated feature extractor and proposal generator.

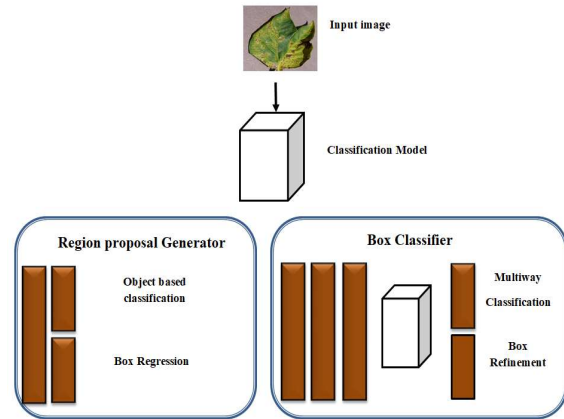


Figure 8: Region-based Fully Deep Convolutional Network's structure (RFDCNN)

4. RESULTS AND DISCUSSION

4.1. Performance Metrics

TP stands for exact data labels, accurately anticipated, in contrast to the real data. FP refers to any negative data labels that were incorrectly predicted and allocated to the incorrect category of image labels. The symbol TN denotes predicted negative sample data sets. FN represents inaccurately predicted positive labels. The various parameters that were calculated using the following formulas can be used for evaluation:

$$Precision = \frac{TP}{TP+FP} \quad (9)$$

$$Recall = \frac{TP}{TP+FN} \quad (10)$$

$$F - Score = 2 * \frac{precision*recall}{precision+recall} \quad (11)$$

$$Accuracy = \frac{TP+T}{TP+TN+FP+F} \tag{12}$$

Confusion matrices are also used to precisely evaluate data that includes predictions as well as ground truth labels. The diagonal elements, which have an inverse relationship with the overall accuracy of the trained model, stand in for the true positives. Each cross-validation fold has a unique confusion matrix.

4.1.1. Precision

A precision comparison of the RFDCNN-CPA technique with other existing approaches shown in Fig. 9 and Tab. 2. The graph shows the precise improvement in performance achieved by the proposed deep learning method. The CNN, RCNN, ANN, SVM, and DT models have precision values of 84.927%, 87.426%, 82.043%, 78.526%, and 88.635% with data 100, but the RFDCNN-CPA model has a precision value of 91.763%. The RFDCNN-CPA model has been shown to perform well with a range of data sizes.

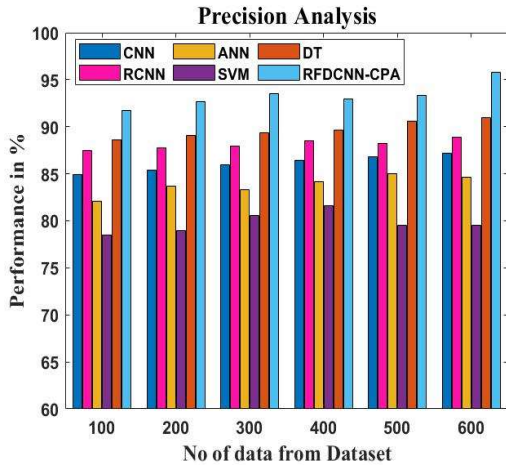


Figure 9: Precision Analysis for RFDCNN-CPA method with existing systems

Table 2: Precision Analysis for RFDCNN-CPA method with existing systems

No of data from dataset	CNN	RCN N	ANN	SVM	DT	RFD CNN - CPA
100	84.92	87.42	82.04	78.52	88.63	91.76
200	85.43	87.72	83.65	78.97	89.09	92.63
300	85.98	87.92	83.28	80.53	89.32	93.54

400	86.39	88.53	84.19	81.63	89.64	92.95
500	86.83	88.24	85.03	79.53	90.62	93.32
600	87.22	88.92	84.63	79.53	90.98	95.82

4.1.2. Recall

A comparative recall analysis of the RFDCNN-CPA methodology with other existing methods is shown in Fig. 10 and Table 3. The recall performance of the deep learning technique is good, as the graph illustrates. The RFDCNN-CPA model has been shown to operate optimally over a range of data sizes. The RFDCNN-CPA has a recall value of 97.938% under 600 observations, whereas the CNN, RCNN, ANN, SVM, and DT models have recall values of 84.526%, 91.653%, 92.936%, 88.736%, and 86.927%, respectively

Table 3: Recall Analysis for RFDCNN-CPA method with existing systems

No of data from dataset	CNN	RCN N	ANN	SVM	DT	RFD CNN - CPA
100	82.43	89.42	91.43	87.32	84.98	93.76
200	83.84	89.67	92.03	87.64	85.42	93.65
300	82.94	89.92	91.73	87.91	86.98	94.02
400	83.53	90.43	92.74	88.01	86.32	95.62
500	84.02	90.82	93.76	88.35	85.72	96.56
600	84.52	91.65	92.93	88.73	86.92	97.93

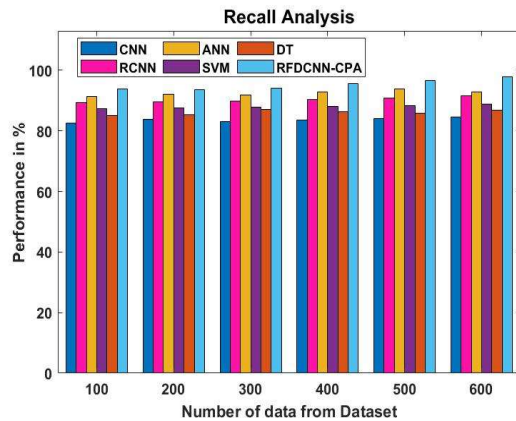


Figure 10: Recall Analysis for RFDCNN-CPA method with existing systems

4.1.3. F-Score

A comparative f-score analysis of the RFDCNN-CPA technique with other current approaches is presented in Fig. 11 and Table 4. The figure shows that f-score performance has improved as a result of the deep learning technique.

Table 4: F-Score Analysis for RFDCNN-CPA method with existing systems

No of data from dataset	CNN	RCN N	ANN	SVM	DT	RFD CNN - CPA
100	69.63	83.04	75.53	71.83	79.63	85.63
200	69.53	83.64	76.92	72.73	80.43	85.76
300	70.09	83.82	77.43	72.93	81.53	86.33
400	71.72	84.32	76.32	73.53	81.83	87.92
500	70.53	84.92	78.43	73.82	82.63	89.43
600	70.83	84.64	79.63	74.02	82.93	90.52

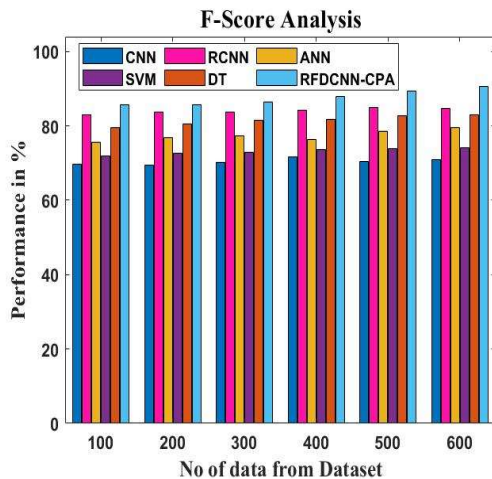


Figure 11: F-Score Analysis for RFDCNN-CPA method with existing systems

For instance, the RFDCNN-CPA model's f-score for data 100 is 85.636%, while the CNN, RCNN, ANN, SVM, and DT models have f-scores of 69.635%, 83.049%, 75.536%, 71.837%, and 79.635%, respectively. The RFDCNN-CPA model has proved its best performance with various data sizes.

4.1.4. Accuracy

Figure 12 and Table 5 compare the accuracy of the RFDCNN-CPA methodology with different strategies. The graph shows that accuracy and performance have increased with the deep learning approach. Thus, with data 100, the accuracy value for RFDCNN-CPA is 96.032%, while the accuracy values for the CNN, RCNN, ANN, SVM, and DT models are 92.746%, 87.324%, 85.735%, 89.637%, and 94.536%, respectively.

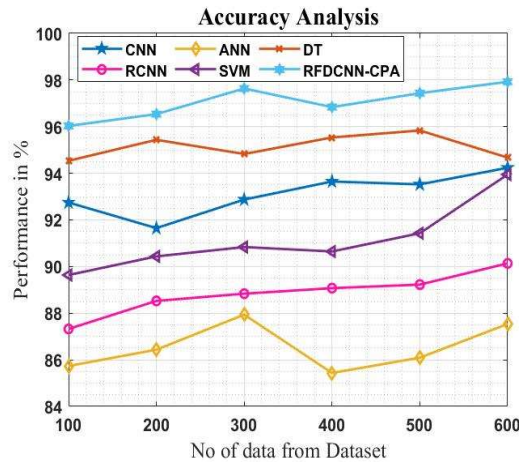


Figure 12: Accuracy Analysis for RFDCNN-CPA method with existing systems

Table 5: Accuracy Analysis for RFDCNN-CPA method with existing systems

No of data from dataset	CNN	RCN N	ANN	SVM	DT	RFD CNN - CPA
100	92.74	87.32	85.73	89.63	94.53	96.03
200	91.64	88.52	86.43	90.43	95.43	96.53
300	92.87	88.83	87.93	90.83	94.82	97.63
400	93.64	89.07	85.43	90.64	95.53	96.83
500	93.52	89.22	86.09	91.42	95.83	97.43
600	94.23	90.13	87.53	93.94	94.67	97.92

4.1.5. Execution Time

The execution time analysis of the RFDCNN-CPA methodology using existing techniques is presented in Table 6 and Fig. 13. The data demonstrates that the RFDCNN-CPA

method has done better than the other approaches in every way. The RFDCNN-CPA approach, for instance, took just 0.0345 ms to execute with 100 pieces of data, but the other techniques that are currently in use, such as CNN, RCNN, ANN, SVM, and DT, had execution durations of 0.0943 ms, 0.0832 ms, 0.0743 ms, 0.0604 ms, and 0.0472 ms, respectively.

Table 6: Execution Time Analysis for RFDCNN-CPA method with existing systems

No of data from dataset	CNN	RCNN	ANN	SVM	DT	RFDCNN-CPA
100	0.094	0.083	0.074	0.060	0.047	0.034
200	0.095	0.080	0.070	0.06	0.049	0.032
300	0.096	0.082	0.072	0.067	0.050	0.036
400	0.090	0.083	0.078	0.065	0.051	0.038
500	0.092	0.084	0.080	0.062	0.055	0.040
600	0.094	0.083	0.083	0.062	0.058	0.042

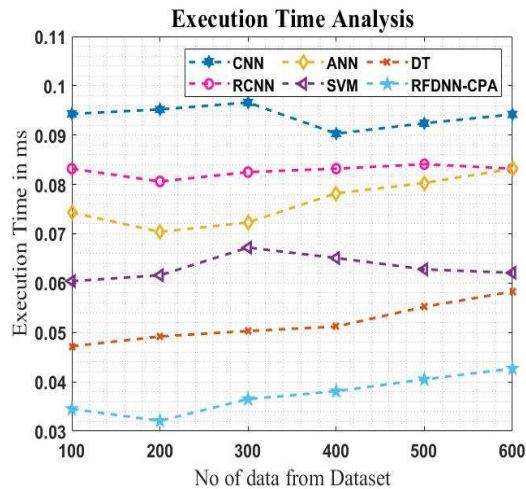


Figure 13: Execution Time Analysis for RFDCNN-CPA method with existing systems

The results of the studies validate the effectiveness of the RFDCNN-CPA deep learning architecture to address plant disease identification issues. The proposed system demonstrated remarkable accuracy and precision in classifying different plant diseases, with the Carnivorous Plant Algorithm (CPA) and advanced deep learning techniques. The high

precision rate, precision analysis, and f-score of the RFDCNN-CPA framework, as demonstrated by plant images, show its dependability in accurately identifying and categorising plant diseases. Moreover, the extremely fast execution time of the proposed technique emphasizes its computing efficiency and makes it suitable for real-time applications in agricultural contexts.

5. CONCLUSION

Plant diseases present a considerable threat to worldwide food security as they result in considerable reductions in crop productivity and have economic ramifications for agricultural practitioners and sectors. For the implementation of effective disease classification, timely and precise detection and categorization of plant diseases are critical. We developed a dependable plant disease classification system utilizing region-based convolutional neural networks with the Carnivorous Plant Algorithm (RFDCNN-CPA) to identify leaf diseases that promote the development of healthy plants and to classify diseases. To efficiently optimize the hyperparameters of the RFD-CNN model, implement the Carnivorous Plant Algorithm. Through the implementation of an automated hyperparameter tuning procedure, the research endeavors to enhance the detection system's overall performance and efficacy. The current methodologies attain an accuracy range of 87.535% to 94.674%. The accuracy of the proposed model, however, is 97.925%. In the future, it is anticipated that deep learning will be used to evaluate the severity and probability of plant diseases. Additionally, plant stems, fruits, and flowers will be examined for disease presence, along with plant leaves.

Data Availability

The manuscript data set can be freely downloaded from <https://www.kaggle.com/datasets>.

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Conflicts of Interest

There are no competing interests, according to the authors. The authors alone are responsible for the writing and content of this article.

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