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# Plant Parasitic Nematodes Classification using Pre-trained CNN Models: ResNet50 and VGG16

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## Abstract

Parasitic nematodes cause serious crop damage worldwide, resulting in significant financial losses. Approximately 0.01 % of these species have not yet been found, according to estimates from certain experts. Nematodes can be challenging to classify using conventional methods because most of them share similar morphological characteristics. In the past, nematodes could only be distinguished by their morphological qualities, which include body length, the orientation of their reproductive organs, and other physical attributes. The previously mentioned approach requires a great deal of labor and expertise, and it only uses expensive machinery and human skills to classify objects. DL-based methods have significantly improved and increased accuracy in recent years. These species were successfully classified using the DL algorithms ResNet50 and VGG16. Acrobeles, Acrobeloides, Aphelenchoides, Amplimerlinius, and Discolimus are the five species of nematodes that were employed. The provided dataset, which originally contained 1500 digital images of nematodes, is further increased to 5000 images by the use of data augmentation techniques such as zooming, flipping, shearing, and other processes. ResNet50 and VGG16, two pre-trained CNN models, have been enhanced to better categorize these species. The accuracy rates of the VGG16 and ResNet50 models are 95.87 % and 98.02 %, respectively.

*Keywords*: Nematode; Transfer Learning; Deep Learning; ResNet50; VGG16.

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## 1.Introduction

Nematodes, members of the phylum Nematoda**,** are unsegmented, transparent, cylindrical invertebrates commonly referred to as roundworms. They represent one of the most abundant and diverse groups of organisms on Earth, with estimates suggesting the existence of up to one million species, though fewer than 0.01 % have been formally described to date [1]. Nematodes occupy a wide range of ecological niches, functioning either as free-living organisms-commonly found in soil, freshwater, deserts, and deep subsurface environments- or as parasites of plants and animals.

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Free-living nematodes, which mostly consume bacteria, fungi, algae, and decaying organic matter, play an important role in the ecology by regulating microbial populations and cycling nutrients. However, because of their toxicity, a number of parasitic species are of medical and agricultural significance. Numerous parasitic disorders in humans, such as trichuriasis [2], hookworm infection [3], angiostrongyliasis [4], helminthiases [5] and onchocerciasis [6]; are caused by nematodes. Plant-parasitic nematodes are a serious hazard to crop productivity and health in agricultural settings. Nematodes are both ecological regulators and pests, but they are still not well understood, especially when it comes to species diversity and functional characterisation [7].

Conventional identification uses culturing methods and microscopic inspection to look for biological, genetic, and physiological traits [8,9]. Anatomical characteristics like body length, reproductive organs, and the shape of the mouthparts and tail have historically been used to differentiate between nematodes. The anatomy of their stylet, which are piercing mouthparts utilized for eating, is a crucial diagnostic characteristic. However, precise classification—particularly among closely related species-remains challenging and prone to errors because of overlapping morphological traits and a lack of skilled taxonomists [10]. Large-scale sample studies make this problem worse. Furthermore, traditional morphological identification is costly, time-consuming, and dependent on specialized tools and human skill. It entails contrasting standardized taxonomic keys with observable structures. Experts frequently combine conventional morphological methods with molecular (DNA-based) techniques to increase accuracy [11].

Identifying nematodes is made easier with the help of artificial intelligence (AI) techniques, especially those that scan microscopic images. By automating and speeding up the classification process, these technologies drastically cut down on the time and effort typically involved with morphological and molecular identification methods. A subset of artificial intelligence, machine learning (ML) has been effectively used in a number of fields, such as speech recognition [12], healthcare [13], business forecasting [14], and agriculture [15]. A more sophisticated subset of machine learning (ML), deep learning (DL), has lately shown considerable gains in accuracy and performance, especially in the fields of pattern recognition and image-based classification [16–18].

DL techniques have produced state-of-the-art outcomes in microscopic image analysis for tasks like autonomous car vision systems [19], object recognition, and cell and tissue segmentation [20]. Widely used designs like ResNet, Inception, Xception, and VGG16 are examples of Convolutional Neural Networks (CNNs), which were created especially for image classification tasks and are very good at extracting visual patterns from small datasets. The ResNet50 and VGG16 architectures have been updated in this study to better identify five nematode species: Acrobeles, Acrobeloides, Aphelenchoides, Amplimerlinius, and Discolaimus.

Several deep learning (DL) techniques have been applied for the automatic classification of nematode species from microscopic images. Common steps in DL pipelines include image acquisition, preprocessing, feature extraction, and classification. For instance, Abade *et al.* [21] classified 3,063 images from five soybean nematode species using 13 CNN models, including their proposed NemaNet, which achieved 99.34 % accuracy. Similarly, Lu *et al.* [22] utilized the public I-Nema dataset with six CNN models, reporting an average accuracy of 79 %.

The parasitic nematodes known as entomopathogenic nematodes (EPNs) infect insects with bacteria that lead to illness in the insects. The usage of EPNs has been investigated as a possible substitute for chemical pesticides, which have the potential to contaminate the environment. Three distinct species of EPNs are included [23]: Steinernema feltiae, Heterorhabditis bacteriophora, and Steinernema carpocapsae. The utilisation of currently available state-of-the-art model architecture is applied to transfer learning. Thirteen CNN architectures, whether or not the weights are pre-trained, are available for use in the Keras deep learning library. For the dataset of juvenile nematodes, the model's mean validation accuracy was 88.28 %, and for dataset of adult nematodes, it was 69.45 %. Living organisms that live in the soil called entomopathogenic nematodes are commonly used to biologically control agricultural insect pests. With the development of easy methods for administering them with traditional sprayers, they are among the best substitutes for pesticides.

By using microscopic images of Acrobeles and Acrobeloides nematodes [24], to show the classification of plant parasitic nematodes. The dataset comprises 277 photos that are further enhanced by data augmentation methods such as shearing, zooming, and so forth. These species are categorised using InceptionV3, a deep learning approach. The author's training and testing accuracy are 99 % and 90 %, respectively. The quarantine nematode species *Globodera pallida* and *Globodera rostochiensis* have been classified using image-based Convolutional Neural Network (CNN) models [25]. The accuracy rate of the suggested CNN model was 71%.

For the classification of five nematode trophic groups—Xiphinema, Helicotylenchus, Heterorhabditis indica, Meloidogyne incognita, and Anguina tritici—a novel lightweight CNN model was recently developed [26]. This model's precision, recall, and F1-scores all surpassed 95 %, and its classification accuracy was 98.52 %. Notably, it was four times faster and five times lighter than traditional models, which made it appropriate for expert-independent, real-time applications. The model was implemented through a mobile application that underwent effective validation on unseen data by nematode experts.

These studies highlight the potential of CNNs in nematode image classification. However, most existing work focuses either on limited species or lacks a comparative evaluation of pre-trained models under identical dataset conditions. In this experimental study, ResNet50 and VGG16 model were used that automatically classified and extracted features from digital microscopic images of five nematode species: Acrobeles, Acrobeloides, Aphelenchoides, Amplimerlinius, and Discolimus. The CNN was developed using Python, the Tensorflow framework, and the Keras API.

Despite advancements in DL-based nematode classification, visual similarity, dataset size constraints, and generalization problems still pose difficulties for species-level discrimination. Additionally, there is a lack of research on hybrid techniques that combine the advantages of several CNN architectures. In order to categorize five nematode species—

Acrobeles, Acrobeloides, Aphelenchoides, Amplimerlinius, and Discolaimus—we provide a novel hybrid framework in this study that uses ResNet50 and VGG16 CNN models.

The study's primary goals are to: (i) use transfer learning to create and improve the ResNet50 and VGG16 models. (ii) compare the suggested method with cutting-edge methods on the same dataset; (iii) assess their classification performance on an enhanced I-Nema dataset.

The remainder of this paper is structured as follows: Section 2 describes the dataset, materials, and proposed methodology; Section 3 presents experimental results and discussion; and Section 4 concludes the study with future directions.

## 2. Materials and Methodology

### 2.1. *Dataset and preprocessing*

The "I-Nema" state-of-the-art dataset comprises five plant parasitic nematode (PPN) species—Acrobeles, Acrobeloides, Aphelenchoides, Amplimerlinius, and Discolimus—has the highest damage relevance for crops. This publication presents the dataset to intentionally enhance the amount of our training data, data augmentation techniques like as flipping, shearing, zooming, and other procedures were used. Following that, there are 5000 photos in the final dataset, with 1000 photos for every species of nematode. After that, it was divided into 80:20 ratios, with 3750 shots making up the training set and 1250 photos making up the test set.

### 2.2. *Transfer learning*

CNN requires a large amount of processing power, a large dataset, and training time. Transfer learning is an option for solving this issue. In order to classify nematode species, ResNet50 and VGG16 models are applied. Below is a more detailed explanation of the selection criteria that were employed.

#### 2.2.1. *ResNet50*

For image recognition applications, ResNet-50 is a deep convolutional neural network. Convolutional, pooling, and fully connected layers make up its total of fifty layers. Residual Network, or ResNet for short, is an acronym that stresses the use of residual connections or "shortcuts" that omit one or more levels. These shortcuts reduce the vanishing gradient problem, allowing for considerably deeper network training. ResNet-50 is well known for its strong performance in computer vision tasks, as demonstrated by its outcomes in the ImageNet competition. It combines 1×1, 3×3, and 7×7 convolutions with more than 23 million parameters to produce a potent and computationally effective image. The ResNet50 model's architecture is depicted below in Fig. 1.

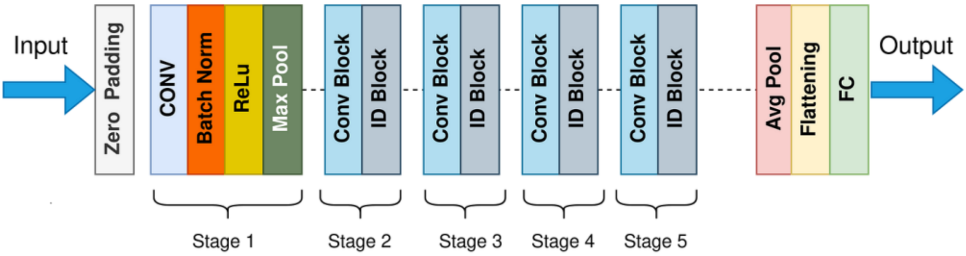


Fig. 1. Architecture of ResNet50.

### 2.2.2. *VGG16*

A straightforward and well-liked convolutional neural network architecture called VGG16 (Visual Geometry Group) is used in the ImageNet project, a sizable visual database project that is used to create software for visual object recognition. The idea of Very Deep Convolutional Networks for Large-Scale Image Recognition was first up by A. Zisserman and K. Simonyan of the University of Oxford. Sixteen convolutional layers are present. VGG16 is frequently utilized straight out of the box for a variety of applications because it is freely available online. The VGG16 architecture is displayed in Fig. 2.

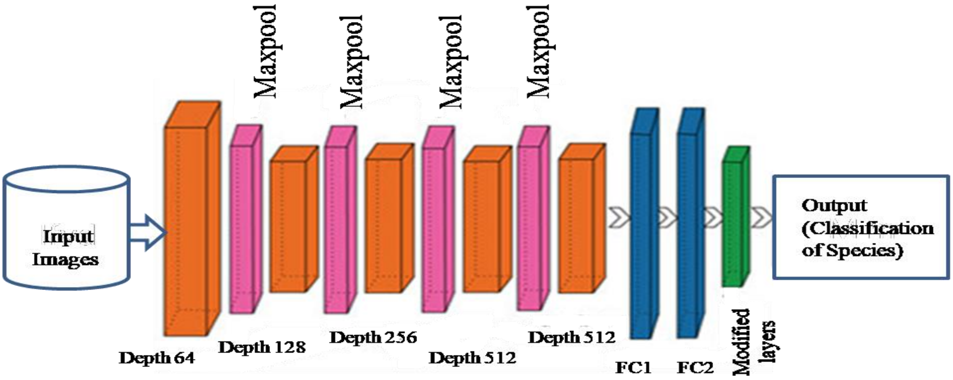


Fig. 2. Architecture of VGG16.

Deep learning models are widely used for prediction, however they have certain drawbacks, such as overfitting, incorrect categorization, and incorrect predictions for low-quality microscopic pictures. For the purpose of classifying nematodes, the unique hybrid model ResNet50 with VGG16 is suggested.

### 2.3. *Proposed technique*

Fig. 3 shows the flowchart of the proposed methodology. First, the provided image undergoes preprocessing. Preprocessing includes increasing the image count by employing data augmentation and scaling each image to 299 by 299 pixels. Following this, VGG16 and ResNet50, two widely used pre-trained CNN models, were employed for evaluation.

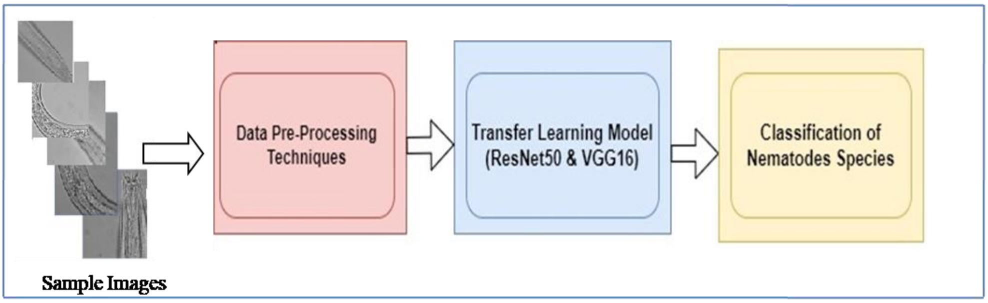


Fig. 3. Proposed methodology.

On the "ImageNet" dataset, the ResNet50 picture categorization system achieves accuracy scores higher than 80 %. Convolutions, concatenations, drops, average pooling, maximum pooling, and fully connected layers are the essential elements of the model. This approach often performs batch normalization on the inputs used for activation. SoftMax is employed in the computation of loss.

In contrast, the modified VGG16 that is offered consists of five blocks: two convolutional layers with Max Pooling and a Relu activation function make up the first two blocks, followed by three other blocks. Each block contains three convolutional layers using Max Pooling and a Relu activation function. Two blocks and an adaptive average pooling come after these blocks. A ReLu activation function, a dropout layer, and a linear layer are present in every block. Finally, a linear layer is used to predict the class of species. This model underwent 50 epochs of adjustment. The loss function is optimized by the "Adam optimizer," also referred to as the Adaptive Moment Estimation. The chosen model is trained using the cross-entropy loss function.

## 3. Results and Discussion

In this work, photographs of five different species of nematodes are used to train two CNN models—the ResNet50 and the VGG16 model-through transfer learning. For feature extraction, data from the ImageNet dataset was utilized. These characteristics were then given to classification layers so they could be categorized. These layers are made up of softmax and fully-connected layers. Moreover, the fully-connected layer size is maintained in all models. Since our task involves five classes, the Softmax layer generates five probabilities. One of the primary problems with applying transfer learning with little datasets is model overfitting.

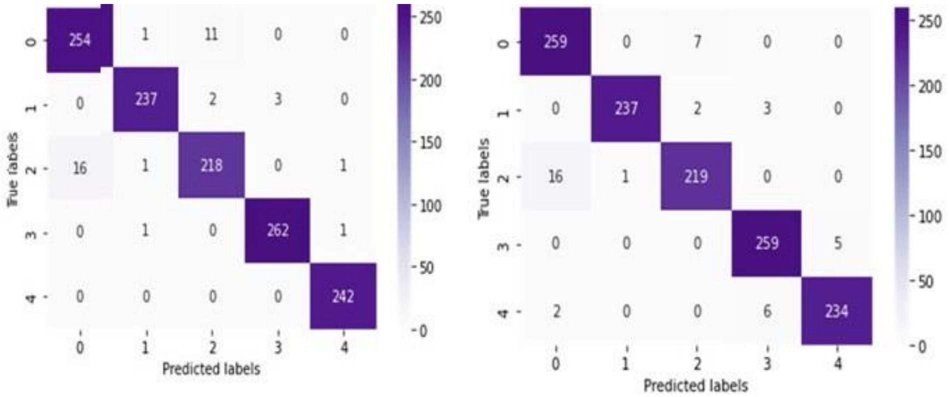
To avoid overfitting, a dropout with a value of 0.5 has been added before fully connected layers. Both models were trained for 50 epochs at a learning rate of 0.001 using the Adam optimizer. Moreover, Relu and Categorical-crossentropy, respectively, are the activation and loss functions that have been used. Python has been used in conjunction with the Tensorflow and Keras inbuilt libraries to develop CNN models. Through random dataset division, the suggested system's performance was examined, with 20 % of the dataset used for testing and 80 % for training. There are 1250 photos in the test set and 3750 images in the training set.

Augmentation techniques such as flipping, shearing, zooming, and so on have been applied to training data in order to provide CNN architecture with a variety of visual input. [27,28]. The performance of the classification model was assessed using a confusion matrix. This table compares the actual and expected values to provide a summary of the prediction findings. Typically, the matrix is arranged squarely, with each row denoting an instance in the real class and each column denoting instances in the projected class.

The elements of a confusion matrix for a binary classification task are explained as follows:
*True Positives (TP):* The total number of positive predictions made with accuracy.
*True Negatives (TN):* The quantity of cases that were accurately forecast as negative.
*False Positives (FP):* The quantity of cases that were erroneously counted as positive.
*False Negatives (FN)***:** The quantity of cases that were erroneously counted as negative.

Four metrics have been used to evaluate model performance: F-score, Accuracy, Recall, and Precision**.**
***Accuracy:*** The ratio of correctly predicted instances to the total instances.
Accuracy = (TP+TN)/(TP+TN+FN+FP)
***Precision:*** The ratio of correctly predicted positive instances to the total predicted positives.
Precision = TP/(TP+FP)
***Recall (Sensitivity or True Positive Rate):*** The ratio of correctly predicted positive instances to all actual positives.
Recall = TP/(TP+FN)
***F1 Score:*** The harmonic mean of precision and recall, providing a balance between the two.
F1Score = 2×Precision×Recall/(Precision + Recall)

Fig. 4 presents the confusion matrices for the VGG16 and ResNet50 models, illustrating the number of correct and incorrect predictions made by each model. The labels 0, 1, 2, 3, and 4 represent the nematode genera *Acrobeles*, *Acrobeloides*, *Aphelenchoides*, *Amplimerlinius*, and *Discolaimus*, respectively. The experimental data obtained with both models is shown in Table 1. The outcomes showed that the ResNet50 model performed better than the VGG16 model, with an accuracy of 98.02 %. Fig. 5 shows the plotted curves of training and validation accuracy over the epochs. The curves show that there is no over-fitting because the training accuracy is higher and comparable to the validation accuracy.



| True labels \ Predicted labels | 0 | 1 | 2 | 3 | 4 |
|---|---|---|---|---|---|
| 0 | 254 | 1 | 11 | 0 | 0 |
| 1 | 0 | 237 | 2 | 3 | 0 |
| 2 | 16 | 1 | 218 | 0 | 1 |
| 3 | 0 | 1 | 0 | 262 | 1 |
| 4 | 0 | 0 | 0 | 0 | 242 |

| True labels \ Predicted labels | 0 | 1 | 2 | 3 | 4 |
|---|---|---|---|---|---|
| 0 | 259 | 0 | 7 | 0 | 0 |
| 1 | 0 | 237 | 2 | 3 | 0 |
| 2 | 16 | 1 | 219 | 0 | 0 |
| 3 | 0 | 0 | 0 | 259 | 5 |
| 4 | 2 | 0 | 0 | 6 | 234 |

Fig. 4. Confusion matrix (a) ResNet50 and (b) VGG16.

Table 1. Classification results of InceptionV3 and VGG16.

| CNN Model | Acc. (%) | Prec. | Recall | F1score |
|---|---|---|---|---|
| ResNet50 | 98.02 | 0.98 | 0.98 | 0.98 |
| VGG16 | 95.87 | 0.96 | 0.95 | 0.9 |

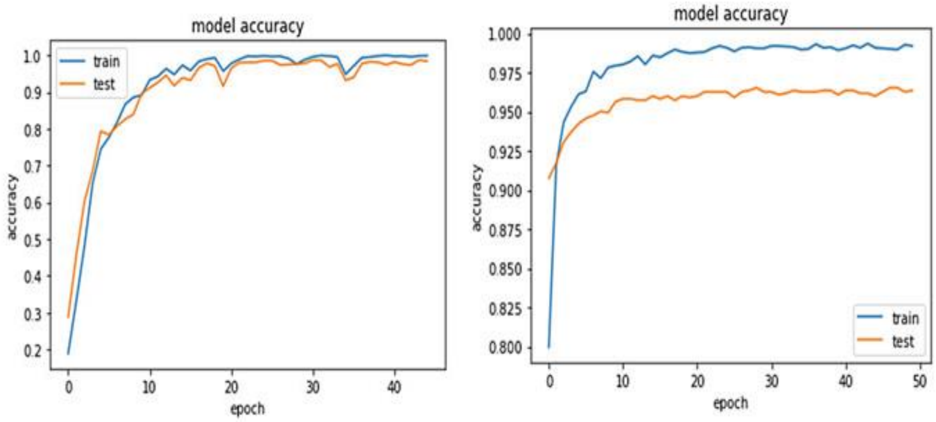


Fig. 5. Accuracy curves. (a) ResNet50 and (b) VGG16.

### 3.1. *Comparative analysis*

To improve the accuracy of nematode identification and classification, various researchers have proposed various architectures and techniques. Table 2 compares the current technique with our proposed technique. When compared to the existing state-of-the-art approaches, the proposed model achieved good accuracy. However, due to variations in model parameters and the use of different datasets, it is not possible to definitively determine which model performs better. Further evaluation can be conducted using additional performance metrics.

Table 2. Comparison of the proposed model with existing work.

| References | Technique used | Species/Dataset | Performance metrics |
|---|---|---|---|
| [29] | CNN | PPN<br>(44 nematode images) | Acc.=88 % |
| [30] | SVM | C. elegans | Acc.=94.8 % |
| [31] | SVM | Sugarbeet nematodes (Heteroderaschachtii)<br>Part 1 contains 47 images with overall 435 nematode cysts. Part 2 consists of 85 images with overall 1038 nematode cysts | Precision= 87 % and Recall= 84 % |
| [22] | CNN (AlexNet, VGG-16, VGG-19, ResNet-34, ResNet-50 and ResNet-101) | PPN<br>(2769 images were collected) | Acc. 79:0 % |
| Our Purposed Model | ResNet50 & VGG16 | PPN (5 Species) | ResNet50=98 %<br>VGG16=95 % |

## 4. Conclusion and Future Scope

Acrobeles, Acrobeloides, Aphelenchoides, Amplimerlinius, and Discolimus are the only five nematode species that are automatically categorized in this research utilizing the transfer learning method of ResNet50 and VGG16. 1500 microscopic photos of five PPN species were used in this study from the "I-Nema" public dataset. The number of photos was raised to 5000 by utilizing a variety of data augmentation techniques, such as flipping, shearing, zooming, and more. To classify these species, two cutting-edge DL models, VGG16 and InceptionV3, have been enhanced. The two different pre-trained CNN models were compared. Regarding classification results, it has been observed that the ResNet50 model performs better than other VGG16 models. The VGG16 model has an accuracy of 95.87 %, whereas the Inception V3 model has an accuracy of 98.02 %.

It is clear that compared to other previous approaches, our suggested method has yielded better outcomes. However, the study only examines five distinct nematode species. In our upcoming job, we will need to enhance its performance. In actuality, concatenation or combination of deep learning models may lead to better categorization results. Furthermore, the investigation's dataset was extremely small. The experiment will be conducted on a proprietary core dataset, with plans to include additional species and expand the dataset in future work. This research and the accompanying benchmark are expected to be valuable to scholars from related domains for advancing their own studies.

## Data availability

In this experimental paper we use secondary dataset set named as I-Nema dataset. And we select only five species out of them. https://github.com/xuequanlu/I-Nema

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