Transfer Learning using Hybrid Convolution and Attention Model for Nematode Identification in Soil Ecology

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ABSTRACT

Nematodes constitute a crucial component of soil ecosystems, contributing significantly to soil ecology. The ability to differentiate between non-parasitic and plant-parasitic species is a critical aspect of efficient crop management. However, manual identification methods are labor-intensive, time-consuming, and susceptible to errors. Recent developments in the realm of machine and deep learning have paved the way for their application in the field of nematode identification. This study implements a hybrid convolution and attention network, termed CoAtNet-0, which integrates a Convolutional Neural Network (CNN) and a transformer for the identification of nematode genera. The performance of this model is anticipated to be robust across various dataset sizes. The current investigation employed a combined dataset, comprising both a self-collected nematode dataset and a public dataset, to evaluate the performance of CoAtNet-0 under single and double data augmentation conditions. Furthermore, it explored the efficacy of the Adam, Stochastic Gradient Descent (SGD), and RMS optimizers to identify the most effective optimizer for the CoAtNet-0 model. Adam was selected due to its typically satisfactory performance, while SGD was chosen as it often delivers superior results in deep learning applications. RMSprop was utilized for performance comparison among adaptive optimizers devoid of momentum. Upon evaluation, it was determined that the highest performance was achieved by the CoAtNet-0 model using the SGD optimizer on the non-augmented dataset, delivering an accuracy of 97.22%. Thus, the selection of suitable data augmentation methods and an appropriate optimizer is instrumental in optimizing the performance of the CoAtNet-0 model for nematode identification.

1. INTRODUCTION

Nematodes serve as integral constituents of soil ecology, contributing significantly to the functionality of soil ecosystems. Alongside other soil-dwelling organisms, they partake in intricate food webs to perform key functions and deliver crucial ecological services, such as soil structure conservation [1, 2]. Their role in soil ecology is multifaceted, participating in various biological processes, including nitrogen cycling, and subsequently influencing plant cultivation. In the context of agricultural systems, soil nematodes play a diverse array of roles. Soil nematodes can be broadly classified into two categories: beneficial non-parasitic nematodes and detrimental plant-parasitic nematodes. A majority of soil nematode species are not plant parasites but instead, contribute positively to ecological processes. For instance, through microbial grazing, these non-parasitic nematodes can alter the microbial community, thereby modulating the rate of decomposition [3-5]. These non-parasitic nematode groups possess inherent systems that maintain and regulate the life balance of numerous organisms. Contrastingly, plant-parasitic nematodes pose a significant threat to agricultural productivity. These nematodes are implicated in the damage to plants and consequent global yield losses. Estimates suggest that plant-parasitic nematodes account for 12-14% of economic crop loss, equating to

approximately 125-173 billion USD [6-8]. However, due to a lack of awareness, particularly among farmers in underdeveloped countries, the actual extent of damage caused by plant-parasitic nematodes is likely underestimated [9].

Accurate identification of the contradictory behavior exhibited by these two types of nematodes is necessary to choose the best crop management strategy. The nematode identification process is complicated because of their small size, the enormous diversity of nematodes presents in a sample, and the need for specific morphological characteristics. Image-based identification is the technique that is the most employed and easiest to use [10]. The nematologist uses the visual inspection of the nematode microscopic pictures to carry out the currently used manual identification method. This procedure is labor-intensive and time-consuming, especially when working with numerous specimens.

Deep learning was proven to perform satisfactorily in several related studies regarding nematode classification from microscopic images. Convolutional neural networks (CNN) have also proven crucial for expediting nematode identification. A CNN is a type of multi-layer neural network that specializes in identifying, recognizing, and classifying objects in images, as well as detecting and segmenting them. This technique can automatically learn a hierarchy of features, which can then be utilized for classification [11]. CNN technique is adapted for handling massive quantities of data

and identifying various objects under challenging settings, such as objects in microscopic images.

A deep convolutional selective encoder architecture was created to recognize and count soybean cyst nematodes (SCN) in clutter-field images [12]. The suggested approach achieves results similar to the expert's; SCN achieved 92% and 95% accuracy in less and highly cluttered images, respectively. A new design integrating DenseNet121 and Inception Blocks was suggested by research [13] for identifying phytonematodes. The proposed method, employing the transfer learning technique, resulted in an accuracy rate of 98.99%.

A self-acquired, non-public dataset is used in research [14] to conduct nematode classification using an Xception deep learning model. However, model selection and training were constrained by hardware limitations. A variety of nematode genus produced by research [15] is now publicly available, and this dataset was used to train several deep-learning models. According to the authors, the ResNet family model exhibits the most astounding precision performance. To differentiate between non-parasitic and plant-parasitic nematodes, Faster Region-based Convolutional Neural Networks were employed by research [16] utilizing microscopic images. The technique produced an accuracy of up to 87.5%. Several deep-learning models were employed to identify self-acquired Indonesian plant-parasitic nematode identification. This study obtained the highest accuracy of more than 90% [17-19].

This study aims to enhance previous research on nematode identification by examining a novel hybrid convolutional and attention-based model named CoAtNet-0. The CoAtNet-0 model combines the CNN architecture with transformers to generate new building blocks and achieve state-of-the-art performance. This new model has the generalization capability of CNN and the high scalability of transformers [20]. CoAtNet-0 was selected for this study because it demonstrated exceptional performance in image classification when compared to other models in the ImageNet benchmark [21]. This study incorporated the datasets from studies [15, 17] and analyzed the performance of the CoAtNet-0 model with respect to both single and double-data augmentation. Five different image augmentation techniques, including noise addition, flipping (both horizontally and vertically), brightness change, blurring, and contrast adjustment, were selected. Moreover, this study also examined three optimizer functions, namely Adam, SGD, and RMSProp, during the training stage to determine the optimum optimizer for CoAtNet-0 in the nematode identification task.

2. METHOD

2.1 Research workflow

The research workflow for identifying nematodes using hybrid convolution and attention models is depicted in Figure 1. The self-collected nematode dataset [17] was combined with the public dataset from the study [15]. The acquired dataset is then preprocessed using several techniques. First, samples were cropped utilizing edge detection to eliminate space and lessen unnecessary information. Grayscale images of the samples were then created since classification only relies upon the nematode's morphological characteristics. Then, to fit the input size of the CoAtNet-0 model, each image is reduced to 224 by 224. Last, all images were then augmented using single and two augmentations before they were used as the input of the CoAtNet-0 model. The model's training process utilized several optimizer functions, namely Adam, SGD, and RMSProp optimizer. The result was then evaluated using several metric evaluations, such as test accuracy, mean class accuracy, F1 score, precision, and recall.
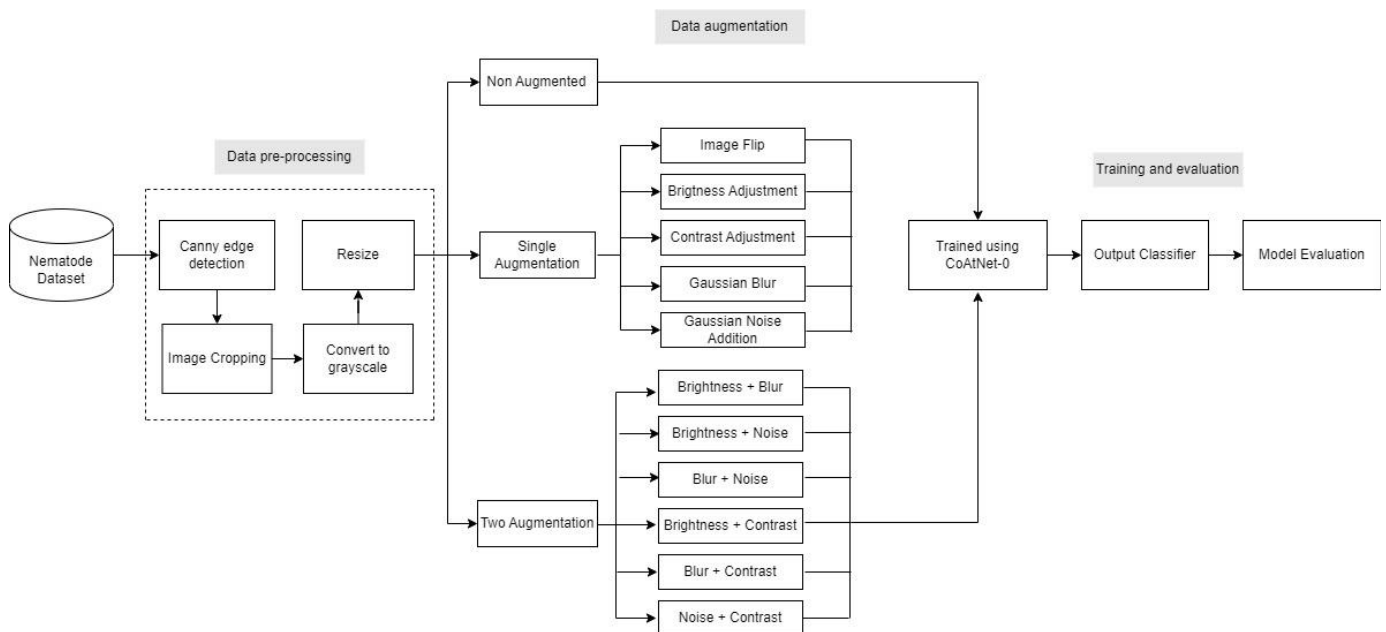
Figure 1. Research workflow

2.2 Nematode datasets

The nematode dataset was collected in the agricultural area of Indonesia. Each nematode genus was captured using an optical connection with a light microscope Olympus CX31 with a magnification of 40-1000 [22]. However, due to the limitation of the data, the self-collected dataset was combined with the public nematode dataset from the study [15] for this study. The dataset is divided into three parts, namely the training, validation, and test dataset, with a ratio of 80:10:10.

The nematode dataset has 26 classification classes with a total of 3595 Nematoda images, divided into 2876 data for training, 360 data for validation, and 359 data for testing. The distribution and sample of the nematode genus dataset used in this study are presented in Table 1. The sample image for each genus used in this study is given in Figure 2.

Table 1. Class distribution on the dataset

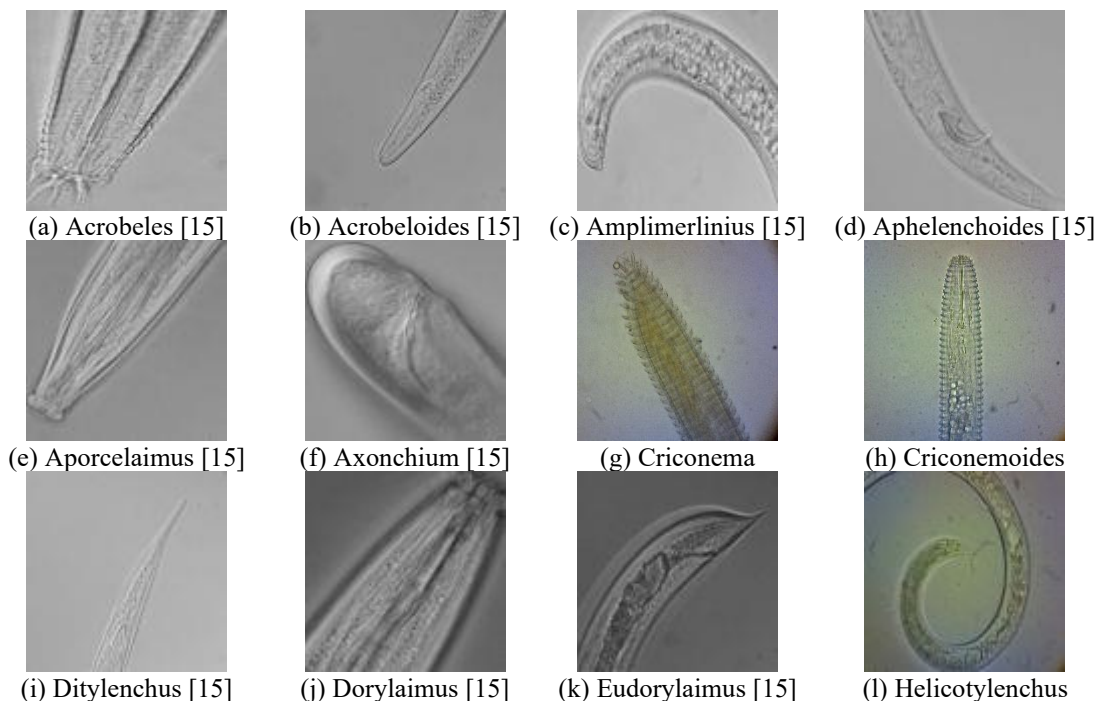| Nematode Genus	Number of Samples
Genus Acrobeles	71
Genus Acrobeloides	184
Genus Amplimerlinius	24
Genus Aphelenchoides	347
Genus Aporcelaimus	128
Genus Axonchium	170
Genus Criconema	3
Genus Criconemoides	103
Genus Ditylenchus	330
Genus Dorylaimus	38
Genus Eudorylaimus	86
Genus Helicotylenchus	213
Genus Hemicycliophora	6
Genus Hirschmanniella	130
Genus Hoplolaimus	151
Genus Meloidogyne	211
Genus Mesodorylaimus	96
Genus Miconchus	57
Genus Mylonchulus	139
Genus Panagrolaimus	327
Genus Pratylenchus	402
Genus Pristionchus	196
Genus Radopholus	12
Genus Rhabditis	81
Genus Trichodorus	30
Genus Xiphinema	60
Total	**3595**

2.3 CoAtNet-0 architecture

Convolutional models provide more powerful generalization and faster convergence speed, while transformer-based models have more capacity and might benefit from more extensive and more varied datasets. By combining the advantages of both architectures, CoAtNet, a hybrid model that incorporates both depthwise Convolution and self-Attention, can be unified using simple relative attention. The vertical stacking of convolution layers and attention layers in a principled way has also been found to be effective in improving generalization, capacity, and efficiency. The CoAtNet architecture comprises five stages arranged in a linear sequence. These stages include an ordinary convolutional layer (S0), First MBConv (S1), Second MBConv (S2), First Transformer (S3), and Second Transformer (S4). The CoAtNet model has five basic versions from CoAtNet-0 to CoAtNet-4 and three variations of CoAtNet-5 to CoAtNet-7 with variable block parameters [20]. Figure 3 depicts the CoAtNet-0 model implemented in this study. The CoAtNet-0 model which merges the CNN structure with transformers create novel building blocks and obtain state-of-the-art results on the ImageNet benchmark [21]. The outstanding performance of the CoAtNet model makes it an ideal choice for the feature extraction and classification of microscopic images of nematodes.

2.4 Data augmentation

The data augmentation is carried out on the dataset to increase the variation and prevent overfitting when carrying out the training process by performing various image transformation operations. The selected image transformation is flipping the image (vertically and horizontally), adding noise, blurring the image, changing the brightness, and changing the contrast. This image transformation type is commonly used to increase the variety of datasets in deep learning problems. Other augmentations, such as translations or affine transformations, are not chosen because some of their augmentation results will cover essential features, such as the head or tail of the nematode genus and can reduce the model's performance. The following implementation is employed in the data augmentation process.

(a) Acrobeles [15]   (b) Acrobeloides [15]   (c) Amplimerlinius [15]   (d) Aphelenchoides [15]

(e) Aporcelaimus [15]   (f) Axonchium [15]   (g) Criconema   (h) Criconemoides

(i) Ditylenchus [15]   (j) Dorylaimus [15]   (k) Eudorylaimus [15]   (l) Helicotylenchus

(m) Hemicycliophora   (n) Hirschmanniella   (o) Hoplolaimus   (p) Meloidogyne

(q) Mesodorylaimus [15]   (r) Miconchus [15]   (s) Mylonchulus [15]   (t) Panagrolaimus

(u) Pratylenchus   (v) Pristionchus [15]   (w) Radopholus   (x) Rhabditis [15]
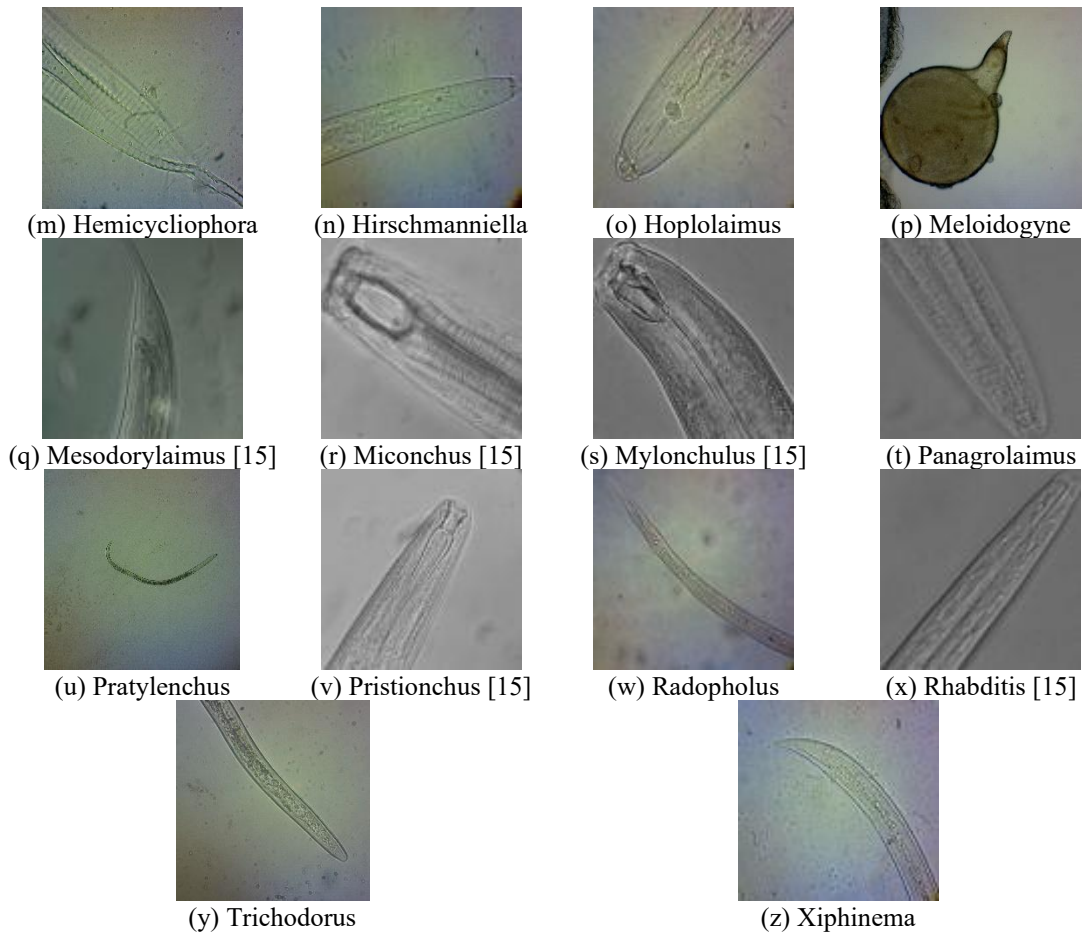
(y) Trichodorus   (z) Xiphinema

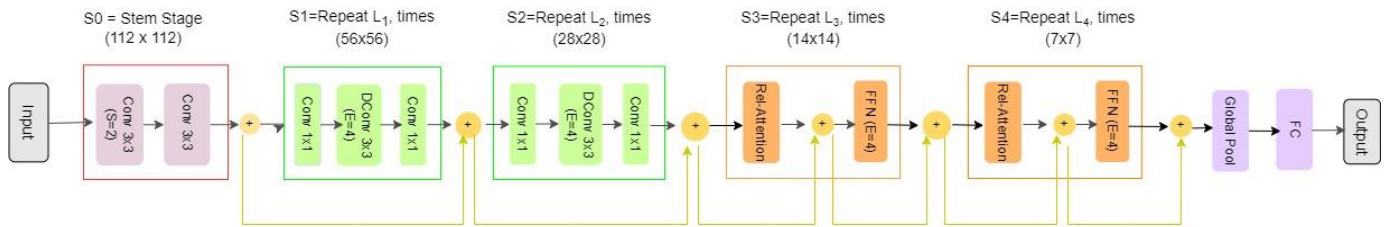**Figure 2.** Sample of nematode dataset

Figure 3. CoAtNet-0 architecture

- Image flipping is performed randomly for each data in the dataset with a 50% probability for each operation. The average distribution of the result is about 25% of the images with no flip, 25% horizontal flip, 25% vertical flip, and 25% of the images with both operations.
- Noise addition is utilized by generating random white Gaussian noise to images with a standard deviation of 0.15 and a mean value of 0, with a probability of 50% for each data.
- The process of blurring the image is utilized randomly with a probability of 50% using a 3 x 3 kernel size of Gaussian filter with a standard deviation of 1.
- Brightness adjustment is applied using a random increase in image brightness, ranging from 0-0.3. This transformation is applied to all the datasets.
- Changing the contrast is applied by randomly increasing the contrast, with a minimum factor of 0.3 and a maximum of 3. This transformation is applied to all the datasets.

The augmentation process is continued by combining two augmentation methods. The previous five augmentation methods determine the choice of augmentation combination. Depending on the model's performance against an augmentation method, that method may be excluded from the selection of the combination. All data augmentation is only applied to the training dataset.

2.5 Optimizer functions

In the training stage, three different optimizers were utilized to determine the optimum optimizer for the CoAtNet-0 model. This also eliminates the unfair advantage of the CoAtNet-0 model in cases where a hyperparameter perfectly matches the need for a certain model-dataset combination capable of achieving more remarkable performance. Adam, SGD, and RMSprop were three of the optimizers employed in the experiments. Adam was chosen because of its superb performance in contrast to other optimization methods and because it works well in practice [23]. SGD is utilized for depicting gradient descent optimizers and is frequently employed to create cutting-edge findings in deep-learning studies. Moreover, SGD can improve generalization

performance [24]. RMSProp was selected due to its satisfactory performance in non-convex and non-stationary issues [25].

2.6 Systems implementations

The CoAtNet-0 model was constructed and trained using TensorFlow and Keras, which were implemented with the Google Colab Pro version featuring specifications for a GPU in the form of an NVIDIA P100 or T4, a CPU in the form of Xeon Processing @2.3 GHz, and a maximum memory capacity of 25 GB, all based on availability. Each model is trained using identical hyperparameter settings as follows.

- SoftMax for dense layer and sparse cross-entropy for loss function
- Input size of 224 x 224 x 3, batch size of 32 and epoch of 100
- Learning rate of 0.001 for Adam and RMSprop and 0.01 for SGD

2.7 Metric evaluation

Several metrics evaluations will be used to assess the performance of the CoAtNet-0 model. The two main metrics that will be utilized are the metrics used by previous studies [15] namely the Test Accuracy and Mean Class Accuracy metrics. The Test Accuracy metric is used to calculate the accuracy of all images in the test dataset. The Mean Class Accuracy metric is used to measure the average classification accuracy of each genus in the dataset to assess whether the model can learn the morphological characteristics of each nematode genus. Other metrics that will be used are the F1-Score and the average of Precision and Recall. The F1-Score

metric is a classification scoring metric that is calculated by taking the symmetrical average of recall and precision, appropriate for use when the class in the dataset is unbalanced. The F1-Score average method applied in this study is a weighted average to obtain accuracy on unbalanced datasets. The formula for Test Accuracy, Mean Class Accuracy, F1-Score, Precision, and Recall are given in Eqs. (1)-(5).

$$Test\ Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \tag{1}$$

$$Mean\ Class\ Accuracy = \frac{1}{c}\sum_{i=1}^{c}\frac{1}{n_i}\sum_{j=1}^{n_i} a_j^i \tag{2}$$

$$Precision = \frac{TP}{TP+FP} \tag{3}$$

$$Recall = \frac{TP}{TP+FN} \tag{4}$$

$$F1\ score = \frac{2 \times Precision \times Recall}{Precision+Recall} \tag{5}$$

3. RESULT AND DISCUSSIONS

The CoAtNet-0 model implemented using single augmentation obtained the highest accuracy of 97.22% for non-augmented datasets using SGD as an optimizer. The lowest accuracy of 68.61% was acquired when CoAtNet-0 model trained using RMSprop optimizer and non-augmented dataset. The complete result of CoAtNet-0 for identifying nematode implemented using single augmentation is presented in Table 2.
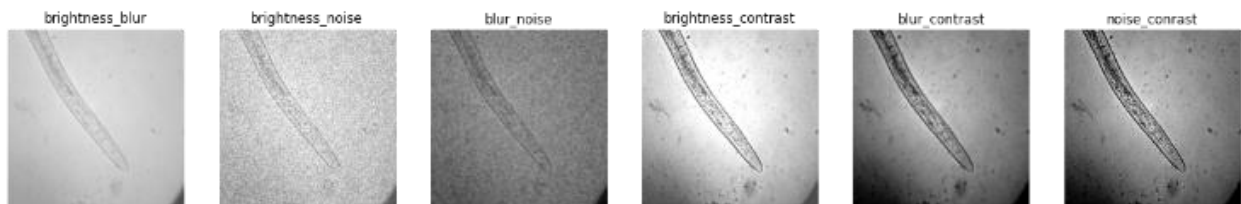

Figure 4. Example of genus trichodorus implemented using two augmentations

Table 2. CoAtNet-0 performance using single augmentation

Optimizer	Augmentation	Test Accuracy	Mean Class Accuracy	F1 Score	Precision	Recall
Adam	No Augmentation	90.00%	0.9065	0.8991	0.9069	0.9
	Flip	76.67%	0.7647	0.7667	0.7956	0.7667
	Brightness	80.00%	0.8232	0.8147	0.8739	0.8
	Contrast	81.67%	0.7981	0.8028	0.8415	0.8167
	Gaussian Blur	87.78%	0.8667	0.8829	0.8948	0.8778
	Gaussian Noise	82.78%	0.8148	0.8283	0.8545	0.8278
SGD	**No Augmentation**	**97.22%**	**0.9798**	**0.9722**	**0.9742**	**0.9722**
	Flip	91.67%	0.8485	0.9148	0.9226	0.9167
	Brightness	93.89%	0.9402	0.9393	0.9436	0.9389
	Contrast	93.89%	0.9461	0.9387	0.941	0.9389
	Gaussian Blur	93.61%	0.8923	0.9351	0.9382	0.9361
	Gaussian Noise	85.83%	0.8141	0.8557	0.8621	0.8583
RMSprop	No Augmentation	81.39%	0.8082	0.8148	0.8579	0.8139
	Flip	73.33%	0.6772	0.7223	0.775	0.7333
	Brightness	82.78%	0.7805	0.8239	0.8464	0.8278
	Contrast	68.61%	0.6897	0.6749	0.743	0.6861
	Gaussian Blur	83.89%	0.8168	0.8388	0.8793	0.8389
	Gaussian Noise	65.83%	0.666	0.6583	0.7501	0.6583

Table 3. CoAtNet-0 performance using combination of two augmentations

Optimizer	Augmentation	Test Accuracy	Mean Class Accuracy	F1 Score	Precision	Recall
	No Augmentation	90.00%	0.9065	0.8991	0.9069	0.9
	Brightness + Blur	87.22%	0.8565	0.8677	0.8903	0.8722
	Brightness + Noise	79.44%	0.8036	0.7947	0.8221	0.7944
ADAM	Blur + Noise	75.00%	0.6565	0.7603	0.8296	0.75
	Brightness + Contrast	85.28%	0.8628	0.8543	0.8786	0.8528
	Blur + Contrast	84.44%	0.7895	0.8453	0.8707	0.8444
	Noise + Contrast	74.44%	0.7116	0.7389	0.7952	0.7444
	No Augmentation	**97.22%**	**0.9798**	**0.9722**	**0.9742**	**0.9722**
	Brightness + Blur	95.00%	0.9058	0.9484	0.9515	0.95
	Brightness + Noise	83.89%	0.747	0.8338	0.8463	0.8389
SGD	Blur + Noise	84.44%	0.7489	0.837	0.8465	0.8444
	Brightness + Contrast	93.33%	0.8976	0.9338	0.943	0.9333
	Blur + Contrast	93.33%	0.9267	0.9334	0.9372	0.9333
	Noise + Contrast	81.39%	0.713	0.8126	0.8382	0.8139
	No Augmentation	81.39%	0.8082	0.8148	0.8579	0.8139
	Brightness + Blur	85.28%	0.8403	0.8517	0.8745	0.8528
	Brightness + Noise	73.89%	0.7144	0.7441	0.7962	0.7389
RMSprop	Blur + Noise	79.44%	0.7547	0.7929	0.8051	0.7944
	Brightness + Contrast	81.11%	0.7943	0.8087	0.8531	0.8111
	Blur + Contrast	73.61%	0.6978	0.727	0.7671	0.7361
	Noise + Contrast	61.39%	0.5994	0.6005	0.7168	0.6139
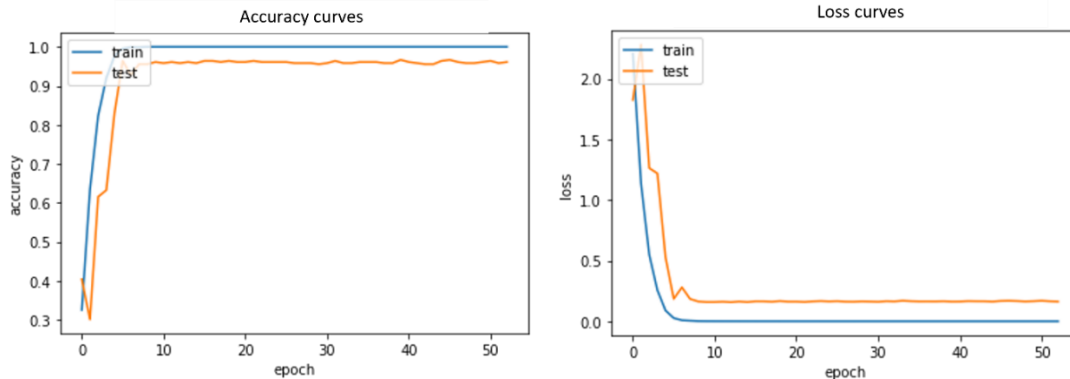
Figure 5. Learning curves of CoATNet-0 implemented using SGD optimizer on non-augmented dataset

To determine whether combining augmentation methods would enhance the model accuracy, two types of augmentation from previous methods were combined, excluding the flip method. This method was excluded because in most tests, the application of image-flip augmentation resulted in a decrease in model accuracy. Consequently, six new dataset variations were generated by combining four augmentation methods (brightness, contrast, blurring addition, and noise addition). An example of the results of applying two augmentations to Genus Trichodorus can be seen in Figure 4. Table 3 presents the results of CoAtNet-0 model performance with a combination of the two augmentations for.

The performance results of the CoAtNet-0 model with two augmentations produce the highest accuracy of 95% for the brightness and blur augmentation dataset implemented using the SGD optimizer. This result is still below the model's accuracy when trained with non-augmented dataset and utilized SGD optimizer, which is 97.22%. The dataset implemented noise and contrast augmentation using the RMSprop optimizer provided the least accuracy, amounting to 61.39%.

After observing the model performance results of various combinations of augmentations from Table 2 and Table 3, the dataset trained using SGD optimizer and non-augmented dataset resulted in the highest accuracy of 97.22%. Figure 5 shows the learning curve for the CoAtNet-0 model implemented using the SGD optimizer on a non-augmented dataset. This curve can be employed to monitor the learning process of the model and diagnose the behavior of a machine learning model. The learning curve indicated that the SGD optimizer provided good stability during the training of the nematode dataset. However, the model still experienced minor overfitting, owing to the limited number of datasets. This is likely because CoAtNet-0 has more capacity than is necessary for the problem.

The results of the highest-performing CoAtNet-0 confusion matrix are shown in Figure 6. From the confusion matrix, the majority of the classes were correctly predicted. However, there are some nematode genus that are mistakenly predicted, such as Acrobeloides, Axonchium, Pratylenchus, and Pristionchus, each of which has one mistakenly predicted image. Moreover, Genus Hirschmanniella, Meloidogyne, and Panagrolaimus are all resulted in two fault prediction. This may be due to the similarities between classes, along with the image, which is primarily black and white and is distinguished by only a combination of nematode morphological traits.
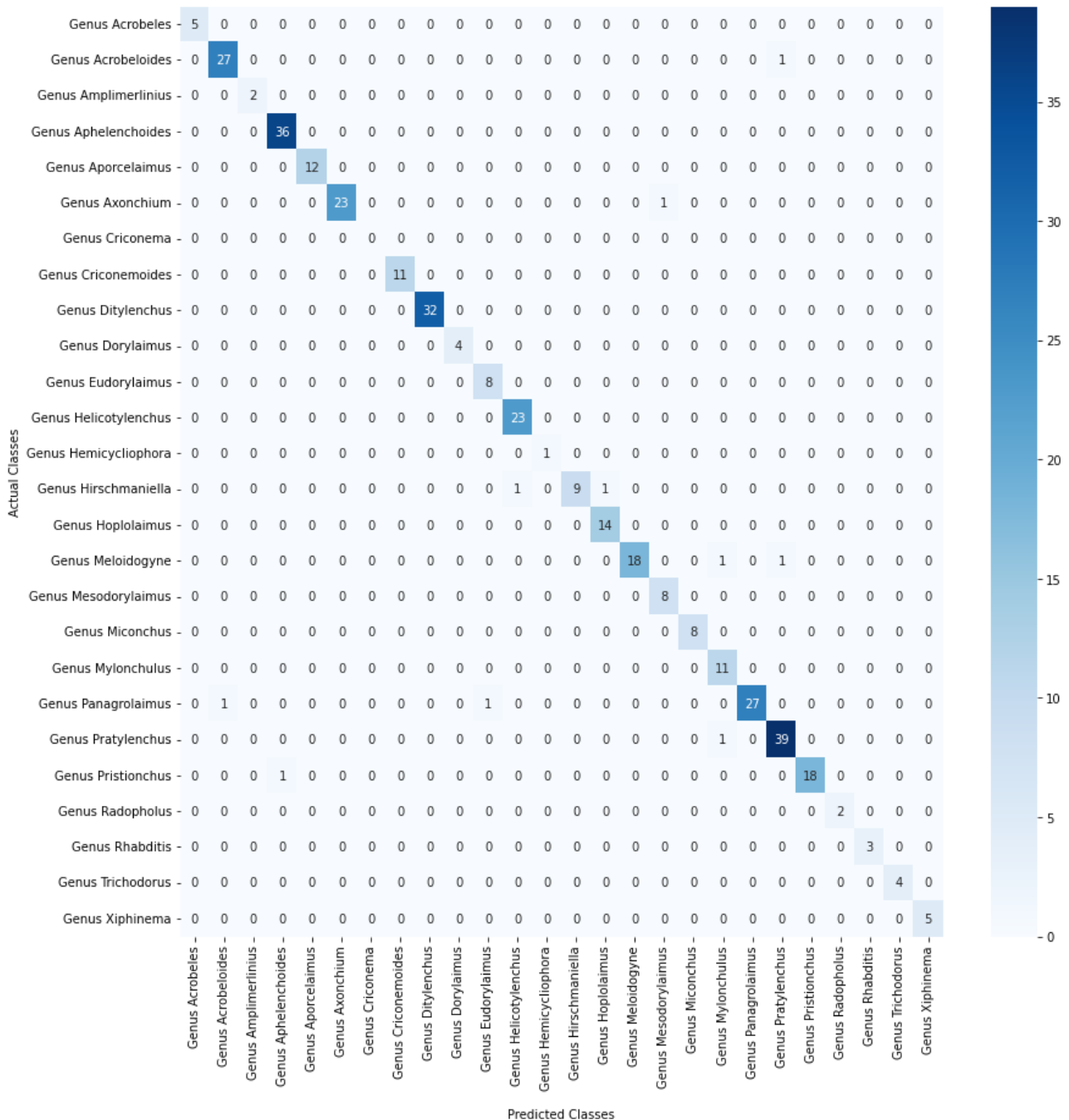
Figure 6. Confusion matrix result from CoAtNet-0 implemented using SGD Optimizer on non-augmented dataset

Incorporating more variations into the dataset through data augmentation does not always lead to improved performance. The selected augmentation techniques do not increase the variation of dataset in relation to the feature of each nematode genus characteristics. The model's capacity to discern the classification issues based on the feature of each nematode cannot be enhanced in this way. Furthermore, image transformation, in both single and two augmentations, can simultaneously cover the morphological features of the nematode to be analyzed, which can make the model more difficult to learn.

The results showed that the performance of CoAtNet-0 varied when different combinations of augmentation techniques and optimizers were used. It was found that specific augmentations are more effective when used with particular optimizers, which can lead to variations in performance. It was inferred from the results that the selection

of the augmentation and optimizer is crucial for achieving the best performance of the CoAtNet-0 model. However, future research is necessary to address other circumstances, such as developing more efficient and high-performance CNN architectures specialized for nematode microscopic images. Additionally, identifying nematodes under damaged conditions is important, as this study only utilized images of perfect condition nematodes.

4. CONCLUSIONS

Combining convolution and attention implemented using transfer learning of the CoAtNet-0 model for identifying nematode genus provides satisfactory results. The best model performance resulted from the CoAtNet-0 model utilizing SGD optimizer and trained with no augmentation. Using the

right optimizer is essential to getting the best performance from a model. The augmentation used must match contextually on the dataset used. Adding variations to the dataset using data augmentation only sometimes increases performance. If the model's performance on the non-augmented dataset is inferior, augmentation can help improve the model. However, in high-performance models, such as the CoAtNet-0 model on non-augmented datasets, the change in accuracy varies. In some cases, two image transformations cover the features to be studied in the Nematode genus. Regarding nematode morphology, the amount of variety in each genus's features is not noticeably increased by the augmentation applied. Simultaneous use of two augmentations also does not guarantee an improvement of the CoAtNet-0 model's performance as it might obscure the most significant features of nematode images, making it more challenging for the model to learn. Moreover, given the minor overfitting indication from the learning curves, it is likely that the CoAtNet-0 model has more capacity than necessary to accurately extract and classify nematodes. From the overall results, it was concluded that the selection of the augmentation and optimizer is crucial for achieving the best performance of the CoAtNet-0 model in nematode identification tasks. Further research should be conducted to develop or implement a more efficient model for nematode classification. The results of this research, which can be incorporated into a more user-friendly platform, can be used to support and assist nematologists in identifying both non-parasitic and plant-parasitic nematodes.

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REFERENCES

[1] Ridall, A., Ingels, J. (2021). Suitability of free-living marine nematodes as bioindicators: Status and future considerations. Frontiers in Marine Science, 8: 685327. https://doi.org/10.3389/fmars.2021.685327

[2] Moura, G.S., Franzener, G. (2017). Biodiversity of nematodes biological indicators of soil quality in the agroecosystems. Arquivos do Instituto Biológico, 84: 1-8. https://doi.org/10.1590/1808-1657000142015

[3] Neher, D.A. (2001). Role of nematodes in soil health and their use as indicators. Journal of Nematology, 33(4): 161-168.

[4] Neher, D.A. (2010). Ecology of plant and free-living nematodes in natural and agricultural soil. Annual Review of Phytopathology, 48(1): 371-394. https://doi.org/10.1146/annurev-phyto-073009-114439

[5] Du Preez, G., Daneel, M., De Goede, R., Du Toit, M.J., Ferris, H., Fourie, H., Schmidt, J.H. (2022). Nematode-based indices in soil ecology: Application, utility, and future directions. Soil Biology and Biochemistry, 169: 108640. https://doi.org/10.1016/j.soilbio.2022.108640

[6] Singh, S., Singh, B., Singh, A.P. (2015). Nematodes: A threat to sustainability of agriculture. Procedia Environmental Sciences, 29: 215-216. https://doi.org/10.1016/j.proenv.2015.07.270

[7] Mesa-Valle, C.M., Garrido-Cardenas, J.A., Cebrian-Carmona, J., Talavera, M., Manzano-Agugliaro, F. (2020). Global research on plant nematodes. Agronomy, 10(8): 1148. https://doi.org/10.3390/agronomy10081148

[8] Gamalero, E., Glick, B.R. (2020). The use of plant growth-promoting bacteria to prevent nematode damage to plants. Biology, 9(11): 381. https://doi.org/10.3390/biology9110381

[9] Jones, J.T., Haegeman, A., Danchin, E.G.J., Gaur, H.S., Helder, J., Jones, M.G.K., Perry, R.N. (2013). Top 10 plant-parasitic nematodes in molecular plant pathology. Molecular Plant Pathology, 14(9): 946-961. https://doi.org/10.1111/mpp.12057

[10] Bogale, M., Baniya, A., DiGennaro, P. (2020). Nematode identification techniques and recent advances. Plants, 9(10): 1260. https://doi.org/10.3390/plants9101260

[11] Taye, M.M. (2023). Theoretical understanding of convolutional neural network: Concepts, architectures, applications, future directions. Computation, 11(3): 52. https://doi.org/10.3390/computation11030052

[12] Akintayo, A., Tylka, G.L., Singh, A.K., Ganapathysubramanian, B., Singh, A., Sarkar, S. (2018). A deep learning framework to discern and count microscopic nematode eggs. Scientific Reports, 8(1): 9145. https://doi.org/10.1038/s41598-018-27272-w

[13] Abade, A., Porto, L.F., Ferreira, P.A., de Barros Vidal, F. (2022). NemaNet: A convolutional neural network model for identification of soybean nematodes. Biosystems Engineering, 213: 39-62. https://doi.org/10.1016/j.biosystemseng.2021.11.016

[14] Uhlemann, J., Cawley, O., Kakouli-Duarte, T. (2020). Nematode identification using artificial neural networks. In International Conference on Deep Learning Theory and Applications, pp. 13-22. https://doi.org/10.5220/0009776600130022

[15] Lu, X., Wang, Y., Fung, S., Qing, X. (2021). I-nema: A biological image dataset for nematode recognition. arXiv preprint, arXiv: 2103.08335. https://doi.org/10.48550/arXiv.2103.08335

[16] Angeline, N., Shabrina, N.H., Indarti, S. (2023). Faster region-based convolutional neural network for plant-parasitic and non-parasitic nematode detection. Indonesia Journal of Electrical Engineering and Computer Science, 30(1): 316-324. http://doi.org/10.11591/ijeecs.v30.i1.pp316-324

[17] Shabrina, N.H., Lika, R.A., Indarti, S. (2023). Deep learning models for automatic identification of plant-parasitic nematode. Artificial Intelligence in Agriculture, 7: 1-12. https://doi.org/10.1016/j.aiia.2022.12.002

[18] Shabrina, N.H., Indarti, S., Lika, R.A., Maharani, R. (2023). A comparative analysis of convolutional neural networks approaches for phytoparasitic nematode identification. Communications in Mathematical Biology and Neuroscience, 2023: 65. https://doi.org/10.28919/cmbn/7993

[19] Shabrina, N.H., Lika, R.A., Indarti, S. (2023). The effect of data augmentation and optimization technique on the performance of efficientNetV2 for plant-parasitic nematode identification. In 2023 IEEE International Conference on Industry 4.0, Artificial Intelligence, and Communications Technology (IAICT), BALI, Indonesia, pp. 190-195. https://doi.org/10.1109/IAICT59002.2023.10205661

[20] Dai, Z., Liu, H., Le, Q.V., Tan, M. (2021). CoAtNet: Marrying convolution and attention for all data sizes. Advances in Neural Information Processing Systems, 34:

3965-3977.

[21] Stojnic, R., Taylor, R., Kardas, M., Elvis, Cucurull, G. (2022). Image classification on imagenet. https://paperswithcode.com/sota/image-classification-on-imagenet.

[22] Mutala'liah, M., Indarti, S., Wibowo, A. (2018). The prevalence and species of root-knot nematode which infect on potato seed in Central Java, Indonesia. Biodiversitas Journal of Biological Diversity, 20(1): 11-16. https://doi.org/10.13057/biodiv/d200102

[23] Kingma, D.P., Ba, J. (2014). Adam: A method for stochastic optimization. arXiv preprint, arXiv:1412.6980. https://doi.org/10.48550/arXiv.1412.6980

[24] Zhou, P., Feng, J., Ma, C., Xiong, C., Hoi, S.C.H. (2020). Towards theoretically understanding why Sgd generalizes better than Adam in deep learning. Advances in Neural Information Processing Systems, 33: 21285-21296.

[25] Sun, S., Cao, Z., Zhu, H., Zhao, J. (2019). A survey of optimization methods from a machine learning perspective. IEEE Transactions on Cybernetics, 50(8): 3668-3681. https://doi.org/10.1109/TCYB.2019.2950779