A relation network for plant disease detection based on fewshot learning

S. Hemalatha¹, Jai Jaganath Babu Jayachandran²

¹Department of Artificial Intelligence and Machine Learning, Rajalakshmi Engineering College, Chennai, India ²Department of Biomedical Engineering, Chennai Institute of Technology, Chennai, India

Article Info

Article history:

Received Oct 22, 2023 Revised Apr 7, 2024 Accepted Apr 17, 2024

Keywords:

Classification
Detection
Fewshot learning
Plant disease
Relation network

ABSTRACT

Accurate and timely disease detection remains a critical challenge in plant health management. Conventional methods often struggle to effectively differentiate between healthy and diseased plants, leading to compromised agricultural productivity and food security. In response to this pressing issue, this paper presents an innovative solution in the form of a novel few-shot learning (FSL) classifier, based on relation network (RN) specifically designed for precise plant disease detection from limited image samples. Leveraging inherent relationships between samples, the proposed relation network for plant disease classification (RN-PDC) enhances the detection performance by capturing intricate patterns within the data. Through comprehensive evaluation on a public image data subset, RN-PDC achieves exceptional detection accuracies of 0.9984 and 0.9967 in binary and multiclass classifications, respectively. This advancement holds great promise for revolutionizing disease diagnosis in the field of plant health, ultimately fostering more productive and sustainable agricultural practices.

This is an open access article under the CC BY-SA license.



4499

Corresponding Author:

S. Hemalatha

Department of Artificial Intelligence and Machine Learning, Rajalakshmi Engineering College

Chennai, 602 105, India Email: hemaaptc@gmail.com

1. INTRODUCTION

Plant diseases constitute a substantial menace to both global food security and the sustainability of agricultural practices [1]. Accurate and prompt identification of these diseases is critical in managing outbreaks and safeguarding agricultural output [2], [3]. However, conventional approaches to plant disease detection frequently hinge upon visual assessments conducted by human experts. While these methods have historically played a role, they are encumbered by subjectivity, prolonged processing times, and an inherent difficulty in achieving scalability [4]. In recent years, a remarkable avenue for revolutionizing disease detection in the agricultural domain has emerged with the ascent of deep learning techniques [5], [6]. These methodologies offer the potential to automate and expedite the process of disease identification. By leveraging the computational prowess of neural networks, these approaches can discern intricate patterns and subtle anomalies within plant images that might elude human observers. This technological leap forward offers a promising solution to the challenges posed by traditional detection methods.

Recent advancements in plant disease management have witnessed the application of various deep learning models beyond the conventional deep belief networks (DBNs) convolutional neural networks (CNNs) [7]. These models include recurrent neural networks (RNNs) for capturing temporal disease progression [8], long short-term memory (LSTM) networks for handling sequences [9], attention mechanisms for focused feature extraction, capsule networks for intricate pattern recognition, and transfer learning for adapting

pre-trained models to the domain [10]. Additionally, generative adversarial networks (GANs) aid in data augmentation [11], graph convolutional networks (GCNs) [12] leverage spatial relationships, and ensemble models enhance robustness [13]. These diverse models collectively signify the ongoing exploration of innovative strategies to enhance the accuracy and efficacy of automated plant disease detection. Evidential studies underline the proficiency of these models in achieving elevated accuracy rates while categorizing images of plant leaves afflicted by diseases and pests, ultimately contributing to more effective disease control and promoting sustainable agricultural practices.

Nevertheless, the effective deployment of deep learning models often hinges on the availability of substantial labeled data for training, an aspect that poses challenges within the realm of plant diseases, given the rarity and diversity of datasets in this context. Herein lies the significance of few-shot learning (FSL), an ingenious machine learning paradigm that empowers models to extrapolate insights from a limited pool of examples [14], [15]. This approach has garnered noteworthy achievements across diverse computer vision domains [16], thereby rendering it an enticing strategy to confront the data scarcity conundrum embedded in plant disease detection. By harnessing the principles of FSL, the limitations imposed by inadequate data resources can be mitigated, potentially ushering in a new era of precision in identifying and managing plant diseases.

In FSL paradigm, relation network (RN) [17], [18] emerge as a distinctive and promising approach. RNs constitute a neural network architecture tailored to harness the potency of relationships within data, facilitating enhanced generalization from limited examples. At their core, RNs seek to capture the intricate interplay between instances, exploiting the fine-grained associations present within few-shot tasks. This is accomplished through the integration of a dedicated relation module within the network architecture, enabling the model to understand the relative significance and relevance of different data points. RNs can offer a potent solution for enhancing plant disease classification accuracy by leveraging inherent data relationships, especially in scenarios with limited labeled examples. Through a dedicated relation module, RNs surpass the limitations of conventional deep learning models by discerning subtle associations between instances, thus bolstering disease identification robustness. Notably, RNs' application in this context remains relatively unexplored, underscoring the untapped potential for advancing plant disease detection. This research proposes the relation network for plant disease classification (RN-PDC) harnessing the potential of RNs to bridge data gaps for accurate classification, promising precision and adaptability in agricultural disease detection. The contributions of this study include the following:

- RN-PDC, a novel detection model, the first of its kind for plant disease detection
- An extendable framework which can be customized to new species and diseases.

This paper is structured as follows an exhaustive examination of FSL models pertinent to plant disease detection is furnished in section 2. The underlying methods employed in this research are described in section 3. Section 4 introduces the problem addressed in this research, RN-PDC architecture and the details of implementation. Section 5 presents experimental results and their interpretation, demonstrating the framework's efficacy. Finally, section 6 summarizes the research findings and proposes future research directions.

2. RELATED WORKS

FSL has demonstrated compelling outcomes in smart agriculture, encompassing tasks like the plant disease detection and classification, differentiation of plant leaves, and even plant counting. The timely identification of plant diseases holds pivotal importance in averting potential outbreaks and mitigating their adverse impact on crops. A FSL based framework for plant leaf classification utilizing a Siamese network was introduced by Wang and Wang [19]. This approach effectively trains a model to accurately classify new images using a limited number of labeled samples. The Siamese network's unique architecture enables it to understand the similarities between different instances, allowing the model to differentiate between plant leaf categories even with minimal training data. Li and Chao [20] introduced a pioneering approach for plant disease recognition through a semi-supervised FSL framework. Their method intelligently combines labeled and unlabeled data, capitalizing the strengths of both paradigms to boost accuracy in disease recognition models. By effectively utilizing limited labeled data and harnessing the power of FSL, their approach demonstrates a valuable strategy to overcome data scarcity challenges in plant disease recognition.

Janarthan *et al.* [21] devised a FSL model for citrus disease classification, centered on deep metric learning, even in the presence of sparse data. Their innovative model effectively leverages a limited number of labeled samples alongside an extensive pool of unlabeled samples. By harnessing this amalgamation, the model learns a deep distance metric capable of quantifying image similarities, thus enabling accurate citrus plant disease classifications. Ng *et al.* [22] pioneered the application of FSL to fruit ripeness classification. By efficiently harnessing the FSL paradigm, their approach not only addresses data scarcity challenges but also

holds potential for optimizing fruit quality assessment and post-harvest management in the agriculture and food industries.

In their study, Afifi *et al.* [23] utilized three pre-trained CNN architectures based on residual leaning such as ResNet variants, to establish baseline models. These were supplemented by a Triplet network and a deep adversarial metric learning (DAML) mechanism. The models underwent training on a comprehensive dataset and were subsequently fine-tuned to discern emerging plant pathologies captured in smaller image datasets. Evaluation encompassed the models' effectiveness in simultaneously identifying disease and plant species, as well as solely recognizing the disease, irrespective of the specific plant. Amidst FSL methods, embedding learning or metric learning stands out, addressing classification via efficient data comparison. This significance is particularly pronounced in the domain of recognizing plant diseases and pests, where data scarcity prevails. In this context, Tassis and Krohling [24] assesses FSL's prowess in biotic stress detection and severity estimation of stress in coffee leaves.

Li and Yang [25] introduced a novel few-shot recognition approach for cotton pests, implemented on an embedded terminal, to counter the limitations of existing techniques. This method leverages minimal raw training data to overcome shortcomings. The study incorporates metric learning for few-shot cotton pest detection and deploys field-programmable gate array (FPGA) chip-based terminal realization. Results showcased the method's efficacy in identifying cotton pests using a sparse training dataset. Nuthalapati and Tunga [26] introduced a novel approach catering to multi-domain FSL in agricultural contexts. The researchers innovatively incorporated transformers into plant disease recognition, presenting a multi-domain FSL framework adept at identifying various pests, plants, and their respective diseases.

Innovative approaches to the improvement of plant leaf disease recognition using FSL are explored in recent works, highlighting the potential for the enhancement of agricultural diagnostics through artificial intelligence. An enhanced FSL framework, specifically tailored for the recognition of plant leaf diseases, is introduced by Wu [27], showcasing the ability to learn from limited data. The concept is extended by Hepsağ [28], who employs a transfer learning approach within a FSL framework, with efficiency in plant disease identification being emphasized. This suggests a growing interest in the leverage of pre-existing knowledge to boost performance in scenarios with sparse training samples. Further innovation is contributed by Wang *et al.* [29], who integrate cross-domain self-supervised learning with a teacher-student network, focusing on the utility of multiple crops to facilitate learning across different domains, thereby addressing the challenge of domain specificity in plant disease recognition.

A supervised contrastive learning based few-shot plant disease recognition algorithm is proposed by Mu *et al.* [30], a method that enhances model performance by focusing on the learning of distinct features among limited examples. Hu *et al.* [31] presented the boosted min-size Sinkhorn (BMS) algorithm designed to enhance FSL by optimizing feature distributions from backbone architectures. The authors demonstrate that BMS significantly outperforms traditional methods like K-Means through extensive experiments, particularly in scenarios with limited labeled samples. Additionally, the study confirms BMS's generalization capabilities across various backbone models, establishing its effectiveness regardless of the architecture used.

Collectively, these studies underscore a dynamic shift towards the exploitation of FSL and its synergies with transfer learning, self-supervised learning, and contrastive learning techniques to address the critical challenge of accurately identifying plant diseases with minimal labeled data. Such advancements are potentially revolutionizing precision agriculture by making it more data-efficient and adaptable to diverse conditions. Generally, RNs excel in capturing intricate relationships and semantic associations within data, making them suitable for nuanced plant disease classification. Their ability to generate meaningful embeddings, considering contextual cues can compensate for data scarcity. RN based models can offer a robust solution by incorporating semantic understanding, contextual awareness, and data efficiency, promising enhanced accuracy and generalization in plant disease detection. This research strives to build a robust plant disease detection model based on a RN framework.

3. METHODS

This study employs a RN to construct a classifier model dedicated to identifying plant diseases. The RN embodies a FSL approach, utilizing a neural network structure designed to discern the relationships between data samples and their corresponding labels. It features an assembly of primary classifiers, each with its own relation module. These classifiers function by extracting insights from the embeddings of data samples and their labels. This involves computing pairwise relationships between sample-label pairs through the relation module. Subsequently, these relationships contribute to the computation of a weighted sum of embeddings, ultimately forming the conclusive representation of each sample. This intricate process enables the model to adeptly capture intricate relationships existing between samples and labels, fostering generalization even with minimal labeled instances. The schematic of the base classifier is depicted in

Figure 1. Given two pairs of inputs (x_1, y_1) and (x_2, y_2) , for the query input x', the target label y' is computed as in (1), where f learns the relationships between the samples and the query.

$$y' = \sum_{i=1}^{2} w_i \cdot f(x', (x_i, y_i))$$
 (1)

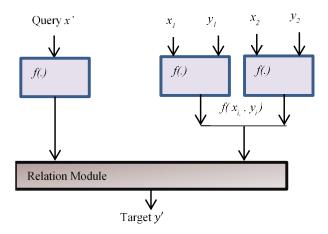


Figure 1. RN architecture

4. PROPOSED RELATION NETWORK FOR PLANT DISEASE CLASSIFICATION

This section presents details of implementation of the proposed RN-PDC model. Initially, it gives a mathematical formulation of the plant disease detection model. Further, it presents the RN-PDC architecture and its components. This section also gives a description of the training and testing datasets employed in this research. Finally, it describes the methodology employed in training the model.

4.1. Problem definition

The plant disease detection problem can be formulated as a multiclass classification task as below. Let X represent the set of N input images of plant leaves, where $x_i \in X$ is an individual image. Each image x_i is associated with a label y_i from a set of C possible classes $Y = \{1, 2, ..., C\}$. The objective is to learn a classifier f that maps each input image x_i to its corresponding class label y_i as in (2). The plant disease detection problem can be defined as finding the optimal classifier f^* that minimizes the classification error as in (3), where $\mathbb{I}(\cdot)$ is the indicator function, and $f(x_i)$ is the predicted class label for image x_i . The objective is to find a model f^* to predict the correct class label for a given plant leaf image, enabling accurate detection and classification of plant diseases.

$$f: X \to Y$$
 (2)

$$f^* = \arg\min_{f} \frac{1}{N} \sum_{i=1}^{N} \mathbb{I}\left(f(x_i) \neq y_i\right)$$
(3)

4.2. Proposed relation network for plant disease classification architecture

The proposed RN-PDC is implemented as in Figure 2 which comprises the embedding, base learning and meta learning layers. Initially, the support and query subsets are constructed from the training dataset by episodic sample selection. The RN-PDC model is built as a multiclass classifier which learns to discern multiple classes by learning the relationships between the support and query subsets. The components of the RN-PDC are described.

The method for selecting samples in the proposed system for detecting plant diseases establishes support and query sets for each episode of training. This component of the layer chooses a predefined number of samples for the support set and a single sample for the query set from each class within the training data, thus creating an episode. The support set serves the purpose of teaching the system about the relationships between samples and their labels, while the query set is used to evaluate how well the model can generalize when presented with new samples, based on a limited set of labeled examples. The embedding layer is a generally a CNN that contains multiple layers, including convolutional, pooling, and activation layers. It is designed to learn intricate features in a hierarchical manner from the input image data of support and query

sets. The output of the CNN is a collection of embeddings that represent each image in both sets. These embeddings efficiently capture important features like edges, shapes, and textures, which are pivotal for solving classification problems. This research employs the pre-trained VGG16 in creating the image embeddings. The base learning layer receives embeddings from the support set and utilizes a set of base classifiers to learn parameters for predicting labels of new samples. Its primary goal is to develop a shared representation of the support set, enabling classification in FSL scenarios. This is achieved by training a CNN or similar deep learning architecture on the support set embeddings. The CNN typically comprises convolutional, pooling, and fully connected layers, which employ filters to extract features from the embeddings and create a classification-ready representation for new samples. During the training phase, the CNN adjusts its parameters to reduce the classification error with the support set. For the base classifiers in this study, a pre-trained version of SqueezeNet is utilized.

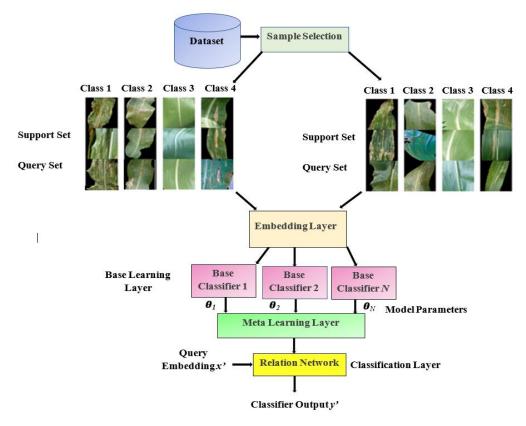


Figure 2. RN-PDC architecture

The meta learning layer leverages the parameters derived from the base learning layer to assemble the RN. It achieves proficiency in the RN by iteratively refining the base classifier's model parameters. This refinement process is directed towards bolstering the model's proficiency in categorizing new instances based on their resemblance to instances within the support set. Such an approach equips the model with the agility to swiftly adjust to unfamiliar tasks using a minimal number of examples. This quality is particularly beneficial for FSL applications, as it allows the model to efficiently generalize to new, unseen situations. The classification layer contains the RN and is responsible for predicting the label of the query sample. It produces a probability distribution over all classes, assigning a probability score to each class. To convert the RN's output into a concrete prediction, the softmax function is typically applied. This function normalizes the output scores, ensuring that each class probability lies between 0 and 1, and the sum of all probabilities equals 1. The predicted class for the query sample is then determined by selecting the class with the highest probability score.

4.3. Dataset and details of implementation

In this study, the RN-PDC model is put through training and evaluation on the subset of data pertaining to Corn diseases from the Plant Village dataset. The distribution of the training and testing data is given in

Table 1. The model is developed and assessed using the Matlab 2023 platform, operating on an i7 processor with 32 GB of RAM, coupled with an NVIDIA GeForce GTX 1080 Ti graphics processing unit.

Table 1. Dataset description

Image Class	Size of training dataset	Size of testing dataset
Common Rust	3816	952
Grey Leaf Spot	1644	408
Healthy	3720	928
Northern Leaf Blight	3152	788
UnHealthy	8612	2148

4.4. Model training

The classifier model suggested is configured to identify plant diseases using a training dataset. The training process unfolds across several episodes, as detailed below. The model undergoes training in a series of episodes in the following manner.

- 1. Initialization: Initialize the parameters of the RN-PDC model: θ for the feature extraction module and ϕ for the relation module.
- 2. Episode Iteration: For each training episode (S, Q):
 - a. Support set preparation:
 - i. Sample C classes from the training data: $C = \{c_1, c_2, ..., c_C\}$.
 - ii. For each class c_i , sample K labeled examples: $S = \{(x_1, y_1), (x_2, y_2), \dots, (x_K, y_K)\}$
 - iii. Extract features using the feature extraction module: $f_{\theta}(x)$ for $x \in S$
 - b. Query set preparation:
 - i. Sample N unlabeled images: $Q = q_1, q_2, ..., q_N$.
 - ii. Extract features for query set images: $f_{\theta}(q)$ for $q \in Q$.
 - c. Relation learning:
 - i. Compute pairwise relationships: $f_{\theta}(q)$ for $q \in Q$
 - ii. Calculate weighted sum of embeddings:

$$z_q = \sum_{x \in S} r_{\phi}(f_{\theta}(x), f_{\theta}(q)) \cdot f_{\theta}(x)$$
 for $q \in$

d. Loss calculation: Compute the loss, where y_q is the true label of q.

$$L = \sum_{q \in Q} CrossEntropy(z_q, y_q)$$

- e. Gradient descent: Update parameters θ and ϕ using gradient descent: $\theta \leftarrow \theta \alpha \nabla_{\theta} L$, where α is the learning rate.
- 3. Iterative improvement: Repeat the episode iteration process for a predefined number of episodes to improve the generalization of the model from a smaller dataset.

5. EXPERIMENTAL RESULTS AND DISCUSSIONS

This section details the experimental setup, performance evaluation, and interpretation of results for the proposed FSL based RN-PDC model for plant disease detection. It explains the experiment configuration, performance metrics (accuracy, inference speed, model size), and compares the RN-PDC model against existing methods. The results analysis highlights the model's advancements and discusses its superior accuracy in detecting plant diseases with limited data.

5.1. Experimental setup

The proposed RN-PDC is implemented with the VGG16 and the squeezeNet. This classifier model is implemented with the hyperparameters. The proposed RN-PDC utilizes two pre-trained models, VGG16 and SqueezeNet. The classifier model is constructed with specific hyperparameters as shown in Table 2. The model is set to run for a maximum of 100 epochs, and each epoch consists of episodes. The number of episodes is varied during training, with values of 100, 75, and 50 used. The model adopts a learning rate set to 0.001 and utilizes adaptive moment estimation (ADAM) for optimization to boost performance. To avert overtraining, L2 regularization is implemented with a value of 0.001. Training ceases upon achieving a reduction in validation loss, confirming efficient training that doesn't overlearn from the training dataset. By combining

these hyperparameters and employing the VGG16 and SqueezeNet models, the proposed RN-PDC aims to achieve accurate and efficient plant disease classification.

Table '	2. 1	RN-	PDC	hyper	parameters

rusic 2. It (I B c ii) perparameters			
Parameter	Values		
Maximum epochs	100		
No. of episodes	100,75,50		
Learning rate	0.001		
Optimization	ADAM		
L2 regularization parameter	0.001		
Stopping criterion	Validation loss		

5.2. Performance evaluation

The model's effectiveness is gauged using metrics such as Accuracy (Acc), Sensitivity (Sn), Specificity (Sp), Precision (Pre), F1 score, and Matthew's correlation coefficient (MCC). These measurements are calculated based on the true positive (TP), true negative (TN), false positive (FP), and false negative (FN) outcomes recorded when testing the RN-PDC against the test dataset. The performance indicators are presented in Table 3.

Table 3. Performance metrics

rusic s. r cirormance metrics			
Metrics	Classification		
	Binary	Multiclass	
Acc	0.9984	0.9967	
Sn	0.9989	0.9968	
Sp	0.9989	0.9981	
Pre	0.9965	0.9957	
F1	0.9973	0.9966	
MCC	0.9961	0.9955	

It is seen that the model achieves consistently high values for all the metrics, exhibiting the best performance for binary classification. The accurate predictions of the RN-PDC, balanced classification of positive and negative samples, and effective handling of diverse classes indicate its potential as a valuable tool for plant disease management and classification tasks. Further, the confusion matrices are shown in Figures 3 and 4 for binary and multiclass classifications respectively, depicting how well the RN-PDC model categorizes instances across different classes, shedding light on its strengths in accurately classifying plant diseases in both scenarios. It is seen that the model is capable of discerning the healthy and unhealthy cases with a good degree of accuracy compared to the detection of individual classes. This degradation in multiclass classification is attributed to the class imbalances and it demonstrates the need for balanced datasets for reducing the misclassifications.

The receiver operating characteristics (ROC) curves are depicted in Figure 5 with the optimal operating points. It is seen that the best area under the curve (AUC) is obtained for binary classification, in alignment with the objective metrics. This resonates harmoniously with the objective metrics evaluated earlier, reinforcing the notion of RN-PDC's superior performance over its counterparts.

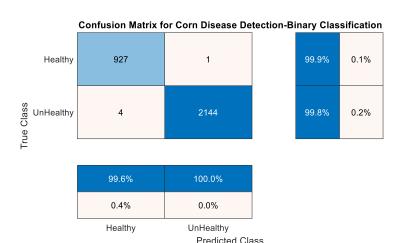
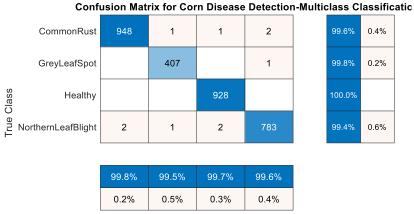


Figure 3. Confusion matrix for binary classification



CommonRusteyLeafSpot HealthyorthernLeafBlight
Predicted Class

Figure 4. Confusion matrix for multiclass classification

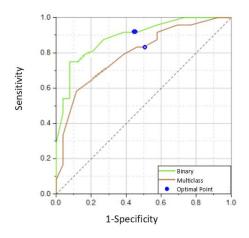


Figure 5. Receiver operating characteristics curves

Furthermore, within Table 4, there is a comprehensive illustration of the performance evaluation contrasting RN-PDC against the current leading methodologies across diverse objective metrics. Notably, these outcomes underscore RN-PDC's remarkable superiority. It's distinctly outperforming the established models and yielding substantial advancements in performance.

Table 4. Performance comparison with state of the art

FSL Approach	Acc (multiclass)	Inference time (ms)	Model size (M)
Semi-supervised FSL [20] (2021)	0.9485	31.5	42
Deep metric learning [21] (2020)	0.8479	37.8	46.2
DAML [23] (2020)	0.7581	45.36	50.82
Embedded learning [24] (2022)	0.6777	54.43	55.9
Multi domain FSL [26] (2021)	0.6059	65.32	61.49
Enhanced FSL [27] (2023)	0.9049	34.05	50.07
Transfer learning based FSL [28] (2023)	0.8973	32.80	49.73
Cross domain FSL [29] (2024)	0.8906	32.58	48.44
Contrastive learning based FSL [30] (2024)	0.8830	32.32	47.10
RN-PDC (Proposed)	0.9967	21	12.1

This table showcases a comparison across different FSL methodologies, emphasizing multiclass accuracy, inference time, and model size as key metrics. The proposed RN-PDC method stands out significantly, offering the highest accuracy (0.9967), the shortest inference time (21 ms), and the smallest model size (12.1 M). This superiority suggests that RN-PDC not only excels in learning from limited data but also in operational efficiency and model compactness. Metric learning methods, which rely on learning

distance metrics to classify instances, show good accuracy but are outperformed by RN-PDC. These approaches, despite their effectiveness, tend to have longer inference times and larger models, indicating a trade-off between accuracy and efficiency. DAML and embedded learning, focusing on domain adaptation and embedding spaces respectively, demonstrate varying degrees of success in handling FSL challenges. However, their relatively lower accuracies and larger model sizes compared to RN-PDC highlight the limitations of their methodologies in optimizing all three metrics simultaneously. Multi domain and enhanced FSL approaches aim to improve FSL performance by integrating knowledge from multiple domains or enhancing feature learning mechanisms. Yet, their efficiencies and accuracies are not on par with RN-PDC, underscoring the innovative edge of the RN-PDC methodology.

Transfer learning based FSL and cross domain FSL methods attempt to leverage pre-existing models or knowledge across different domains to improve FSL outcomes. While they show promise in reducing model sizes and improving inference times, their accuracies still fall short of RN-PDC's benchmark. Contrastive learning based FSL, focusing on learning robust representations by contrasting positive and negative samples, marks a step towards more efficient and compact models. Nevertheless, the RN-PDC model excels by offering an improved equilibrium among accuracy, efficiency, and compactness of the model. The exceptional efficacy of the RN-PDC approach in FSL is largely due to its novel employment of RN, markedly boosting its precision, operational efficiency, and size efficiency. This method achieves the highest accuracy, shortest inference time, and smallest model size among the evaluated approaches, highlighting the effectiveness of RN in optimizing FSL tasks. By focusing on the relational context between data points, RN-PDC efficiently extracts and utilizes deep features, leading to superior performance across critical metrics. This approach demonstrates the potential of RN to revolutionize FSL methodologies by providing a balanced and effective solution to the challenges of learning from limited data.

6. CONCLUSION

This paper introduces a novel FSL classifier for plant disease detection called the RN-PDC which exploits the relationships between samples to enhance the classification performance. This model captures the intricate relationships between the samples and the target classes for classification of healthy and unhealthy cases, and distinguishing three kinds of plant diseases and healthy plants. This model is trained and tested on the corn image data subset achieving high detection accuracies of 0.9984 and 0.9967 under binary and multiclass classifications respectively. Such progress promises widespread applicability and has the potential to significantly improve the accuracy and efficiency of disease diagnosis within the field of plant health. The RN-PDC model can be extended to new plant species and pathologies by retraining it with such technology stands to offer considerable benefits to not only plant health professionals but also the overall well-being of crops, fostering a more productive and sustainable agricultural landscape.

REFERENCES

- S. Savary, L. Willocquet, S. J. Pethybridge, P. Esker, N. McRoberts, and A. Nelson, "The global burden of pathogens and pests on major food crops," *Nature Ecology and Evolution*, vol. 3, no. 3, pp. 430–439, 2019, doi: 10.1038/s41559-018-0793-y.
- [2] A. Singh, B. Ganapathysubramanian, A. K. Singh, and S. Sarkar, "Machine learning for high-throughput stress phenotyping in plants," *Trends in Plant Science*, vol. 21, no. 2, pp. 110–124, 2016, doi: 10.1016/j.tplants.2015.10.015.
- [3] R. W. Mwangi, M. Mustafa, K. Charles, I. W. Wagara, and N. Kappel, "Selected emerging and reemerging plant pathogens affecting the food basket: A threat to food security," *Journal of Agriculture and Food Research*, vol. 14, 2023, doi: 10.1016/j.jafr.2023.100827.
- [4] A. K. Rath and J. K. Meher, "Disease detection in infected plant leaf by computational method," Archives of Phytopathology and Plant Protection, vol. 52, no. 19–20, pp. 1348–1358, 2019, doi: 10.1080/03235408.2019.1708546.
- [5] S. P. Mohanty, D. P. Hughes, and M. Salathé, "Using deep learning for image-based plant disease detection," Frontiers in Plant Science, vol. 7, 2016, doi: 10.3389/fpls.2016.01419.
- [6] A. Ahmad, A. E. Gamal, and D. Saraswat, "Toward generalization of deep learning-based plant disease identification under controlled and field conditions," *IEEE Access*, vol. 11, pp. 9042–9057, 2023, doi: 10.1109/ACCESS.2023.3240100.
- [7] M. Jung *et al.*, "Construction of deep learning-based disease detection model in plants," *Scientific Reports*, vol. 13, no. 1, 2023, doi: 10.1038/s41598-023-34549-2.
- [8] D. Garg and M. Alam, "Integration of convolutional neural networks and recurrent neural networks for foliar disease classification in apple trees," *International Journal of Advanced Computer Science and Applications*, vol. 13, no. 4, pp. 357–367, 2022, doi: 10.14569/IJACSA.2022.0130442.
- [9] M. Turkoglu, D. Hanbay, and A. Sengur, "Multi-model LSTM-based convolutional neural networks for detection of apple diseases and pests," *Journal of Ambient Intelligence and Humanized Computing*, vol. 13, no. 7, pp. 3335–3345, 2022, doi: 10.1007/s12652-019-01591-w.
- [10] A. Sagar and D. Jacob, "On using transfer learning for plant disease detection," bioRxiv, vol. 1, pp. 1-8, 2021, doi: 10.1101/2020.05.22.110957
- [11] Y. Zhang, S. Wa, L. Zhang, and C. Lv, "Automatic plant disease detection based on tranvolution detection network with GAN modules using leaf images," Frontiers in Plant Science, vol. 13, 2022, doi: 10.3389/fpls.2022.875693.
- [12] R. Vora, S. Nayak, S. Phate, D. Shah, and S. C. Shrawne, "Node embeddings in graph convolutional networks for plant disease detection," 2022 4th International Conference on Advances in Computing, Communication Control and Networking, ICAC3N 2022,

- pp. 506-511, 2022, doi: 10.1109/ICAC3N56670.2022.10074040.
- S. Vallabhajosyula, V. Sistla, and V. K. K. Kolli, "Transfer learning-based deep ensemble neural network for plant leaf disease detection," Journal of Plant Diseases and Protection, vol. 129, no. 3, pp. 545-558, 2022, doi: 10.1007/s41348-021-00465-8.
- Y. Wang, Q. Yao, J. T. Kwok, and L. M. Ni, "Generalizing from a few examples: a survey on few-shot learning," ACM Computing Surveys, vol. 53, no. 3, 2020, doi: 10.1145/3386252.
- [15] M. Ochal, M. Patacchiola, J. Vazquez, A. Storkey, and S. Wang, "Few-shot learning with class imbalance," IEEE Transactions on Artificial Intelligence, vol. 4, no. 5, pp. 1348–1358, 2023, doi: 10.1109/TAI.2023.3298303.
- [16] D. Wertheimer and B. Hariharan, "Few-shot learning with localization in realistic settings," Proceedings of the IEEE Computer Society Conference on Computer Vision and Pattern Recognition, vol. 2019-June, pp. 6551-6560, 2019, doi: 10.1109/CVPR.2019.00672.
- F. Sung, Y. Yang, L. Zhang, T. Xiang, P. H. S. Torr, and T. M. Hospedales, "Learning to compare: relation network for few-shot learning," Proceedings of the IEEE Computer Society Conference on Computer Vision and Pattern Recognition, pp. 1199-1208, 2018, doi: 10.1109/CVPR.2018.00131.
- [18] Z. Wu, Y. Li, L. Guo, and K. Jia, "PARN: position-aware relation networks for few-shot learning," Proceedings of the IEEE International Conference on Computer Vision, vol. 2019-Octob, pp. 6658-6666, 2019, doi: 10.1109/ICCV.2019.00676.
- [19] B. Wang and D. Wang, "Plant leaves classification: A few-shot learning method based on siamese network," IEEE Access, vol. 7, pp. 151754–151763, 2019, doi: 10.1109/ACCESS.2019.2947510. Y. Li and X. Chao, "Semi-supervised few-shot learning approach for plant diseases recognition," *Plant Methods*, vol. 17, no. 1,
- 2021. doi: 10.1186/s13007-021-00770-1.
- [21] S. Janarthan, S. Thuseethan, S. Rajasegarar, Q. Lyu, Y. Zheng, and J. Yearwood, "Deep metric learning based citrus disease classification with sparse data," IEEE Access, vol. 8, pp. 162588-162600, 2020, doi: 10.1109/ACCESS.2020.3021487.
- [22] H. F. Ng, J. J. Lo, C. Y. Lin, H. K. Tan, J. H. Chuah, and K. H. Leung, "Fruit ripeness classification with few-shot learning," Proceedings of the 11th International Conference on Robotics, Vision, Signal Processing and Power Applications, pp. 715–720, 2022, doi: 10.1007/978-981-16-8129-5_109.
- A. Afifi, A. Alhumam, and A. Abdelwahab, "Convolutional neural network for automatic identification of plant diseases with limited data," Plants, vol. 10, no. 1, pp. 1-16, 2021, doi: 10.3390/plants10010028.
- [24] L. M. Tassis and R. A. Krohling, "Few-shot learning for biotic stress classification of coffee leaves," Artificial Intelligence in Agriculture, vol. 6, pp. 55-67, 2022, doi: 10.1016/j.aiia.2022.04.001.
- Y. Li and J. Yang, "Few-shot cotton pest recognition and terminal realization," Computers and Electronics in Agriculture, vol. 169, 2020, doi: 10.1016/j.compag.2020.105240.
- [26] S. V. Nuthalapati and A. Tunga, "Multi-domain few-shot learning and dataset for agricultural applications," The IEEE International Conference on Computer Vision, vol. 2021-Octob, pp. 1399-1408, 2021, doi: 10.1109/ICCVW54120.2021.00161.
- W. Wu, "Enhanced few-shot learning for plant leaf diseases recognition," Journal of Computing and Electronic Information Management, vol. 11, no. 3, pp. 26-28, 2023, doi: 10.54097/jceim.v11i3.06.
- [28] P. U. Hepsag, "Efficient plant disease identification using few-shot learning: a transfer learning approach," Multimedia Tools and Applications, 2023, doi: 10.1007/s11042-023-17824-2.
- G. Wang, Y. Wang, J. Zhang, X. Wang, and Z. Pan, "Cross-domain self-supervised few-shot learning via multiple crops with teacher-student network," Engineering Applications of Artificial Intelligence, vol. 132, 2024, doi: 10.1016/j.engappai.2024.107892.
- J. Mu, Q. Feng, J. Yang, J. Zhang, and S. Yang, "Few-shot disease recognition algorithm based on supervised contrastive learning," Frontiers in Plant Science, vol. 15, 2024, doi: 10.3389/fpls.2024.1341831.
- [31] Y. Hu, S. Pateux, and V. Gripon, "Squeezing backbone feature distributions to the max for efficient few-shot learning," Algorithms, vol. 15, no. 5, 2022, doi: 10.3390/a15050147.

BIOGRAPHIES OF AUTHORS



S. Hemalatha D 🖫 🚾 🕻 is an Assistant Professor in the Department of Artificial Intelligence & Machine Learning at Rajalakshmi Engineering College. She earned her B.E. in Computer Science and Engineering from Adhiparasakthi Engineering College, Madras University in 2000, and her M.E. in Computer Science and Engineering from Anna University, Chennai in 2011. With over 21 years of teaching experience in both undergraduate and postgraduate programs, her expertise includes AI, machine learning, data science, and data mining. Throughout her career, she has contributed to various reputable institutions, enriching the field of computer engineering with her extensive knowledge and experience. She can be contacted at email: hemaaptc@gmail.com.



Jai Jaganath Babu Javachandran 🗓 🐰 🚾 🗘 is currently an Associate Professor at the Department of Biomedical Engineering, Chennai Institute of Technology, Chennai. He obtained his Ph.D. at Pondicherry University, Pondicherry, in 2018. He did his M.E. Degree in Medical Electronics from Anna University, Chennai, in 2007, and Bachelor degree in Electronics and Communication Engineering from the University of Madras, Chennai. His areas of interest are bio-signals, medical image processing, sensor networks, and smart antennas. He can be contacted at email: jaijaganathbabuj@citchennai.net.