Deep Learning Based Classification of Microscopic Fungi for Agriculture Application

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Abstract. Plant diseases are one of the significant reasons that lead to the destruction of crops and plants. These diseases are caused by bacteria, virus, algae, fungi, etc. Among these diseases, fungi causes the major diseases in plants and crops. This article aims to collect the novel dataset of fungi infected leaves of two different fruit plants. To take pictures of the fungus at a microscopic scale, these leaves are carefully grown and examined under a microscope with a 40X objective. By utilizing the machine learning classifiers and deep learning architectures We develop and examine the models on the collected novel dataset. Using 5 fold cross validation experimental results showed the high recognition accuracy of 97.52% for the ResNet-50 model.

Keywords: Fungi · Leaf diseases · Microscopic images · Machine learning · Deep learning · ResNet-50

1 Introduction

Plant diseases are one of the most significant reasons that lead to the destruction of crops and plant. These diseases may be caused by environmental condition, deficiency of nutrient, due to bacteria, virus or fungi. Among the many diseases, fungi cause the major diseases to plants and crops. India being an agriculture country and almost more than half percent of our agriculture provides the majority of the revenue to the inhabitants; it is the need of an hour to identify these diseases at early stage.

The diseases may occur at any part or through the entire crop or plant. Different fungi or bacteria cause different types of the diseases to the plant. Traditional method of identifying these diseases is through knowledge of the domain expert or with the help of farmers. Identifying of these diseases sometimes may lead to the wrong assumption of the diseases and which may lead to usage of wrong fertilizers or chemicals to the plant. The manual method of identifying diseases is tiresome, expensive and time consuming. Hence the need arise to work on automated identification of fungi affected diseases of plants.

Classifying the diseases through visible symptoms of the diseases is done by most of the researchers. Authors in [1–10] have worked on leaf identification of diseases

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using machine learning (ML) and deep learning (DL) models. [11–15] have worked on feature extraction of the leaf diseases and these features are used to classify the diseases according to the respective categories using machine learning classifiers. The authors in [16] have worked on new method of classifying the leaf diseases by extracting the features from DL model and classifying these images using ML models. This reduces the time complexity of the models.

Microscopic level of fungi classification is done by authors in [17–21]. In such case, the fungi are acquired by tainted food, soil, human body, airborne fungus, etc. Our goal is to recognise fungus at the molecular level by developing a novel fungus dataset of spores and hyphae of fungi. We are the first of our type to focus on plant leaf diseases caused by fungus of fruit plants.

We have considered two fungi infected fruit plants leaves. Anthracanose of mango leaf is caused by fungi Colletotrichum Gloeosporioides (CG) and Leaf spot of Custard apple is caused by fungi Cylindrocladium Colhounii (CC). The dataset consist of 602 images of which are divided into four classes which include spores of Colletotrichum gloeosporioides, hypahe of Colletotrichum gloeosporioides, spores of Cylindrocladium colhounii and hyphae of Cylindrocladium colhounii.

The remainder of the article is divided into two sections: Sect. 2 describes the literature review, preparation of dataset is given in Sect. 3, Sect. 4 gives the overview of dataset, The anticipated technique is described in Sect. 5 utilizing several models and classifiers., experimental results are summed up in Sect. 6, Sect. 7 evaluates the results, Sect. 8 sums up the conclusions and Sect. 9 gives the future scope of our work.

2 Literature Survey

Machine learning techniques are used in a variety of fields, but feature engineering is still the most difficult challenge to solve. With the advent of deep neural networks, promising outcomes for plant pathology are now available without the need for time-consuming feature engineering. Deep neural networks improve visual recognition accuracy considerably. This section describes the many deep learning techniques used by researchers to identify plant diseases. S. Gayathri et al. [22] proposed a CNN based LeNet architecture for leaf diseases classification of Tea leaves, as India is the highest consumer of tea. The dataset of tea leaves consists of three different categories of diseased leaves. And using their proposed approach they got a good result of 90.23%. Maeda-Gutiérrez et al. [23] classified the leaves of tomato plant which is obtained from the Plant village dataset. Their work focused on the fine tuning of the CNN models such as AlexNet, GoogleNet, ResNet 18, Inception V3 and ResNet 50 models. The results from the GoogleNet model obtained are significant with AUC of 99.12%.

Rangarajan et al. [24] studied the Plant village dataset of tomato leaves which has six different class labels. They used the deep learning models of AlexNet and VGG 16 network to train on different hyper parameters. They analyzed the different hyper parameters of the models like weight, bias of learning rate and mini batch size of the models. Mosin Hasan et al. [25] implemented drone based precision farming using CNN to classify the tomato leaves. They used their own dataset and utilized the inception model of Google for training the model. They obtained good accuracy of 99% and the model

performed well. Md. Rasel Howl al. [26] studied the guava plant from Bangladesh and created their own dataset of Guava with four different classes. They developed their own customized Deep-CNN. The experimental results show an average accuracy of 98.74% on the test set. R. Sujatha et al. [27] compared the ML and DL models using the leaves of citrus dataset. They used different techniques and analyzed the result on the dataset. The results of trials show that DL models performed well when compared to the ML techniques.

Table 1. Survey of Microscopic Image Identification and Classification

Sl. No.	Name	Utilized database	Utilized technique	Category's	Obtained accuracy
1	Muhammad Waseem Tahir et al, [17]	Private dataset of fungal spores	CNN's unique architectural style	5 different classes of fungi	94.8%
2	Anuruk Prommakhot etal, [18]	Private dataset of fungal spores	CNN's unique architectural style	2 different classes of fungi	98.03%
3	Lin Liu et al, [19]	Private dataset of fungal spores	ANN architecture	One class	Model gives good result
4	Bartosz Zieliński et al, [20]	Digital Images of Fungus Species database	Deep Neural Network (DNN) and Bag of words	10 different classes of fungi	DNN gave good recognition accuracy
5	Robert Kerwin C. Billones et al, [21]	Own aspergillus dataset	Customized CNN architecture	9 different classes of fungi	94.31%

Table 2. Overview of the dataset

Sl. No.	Class labels	Training Images	Testing Images	Total images
1	Spores of Cylindrocladium colhounii (CC)	122	30	152
2	Spores of Colletotrichum gloeosporioides (CG)	180	46	226
3	Hyphae of Cylindrocladium colhounii (CC)	104	26	130
4	Hyphae of Colletotrichum gloeosporioides (CG)	74	20	94
Total Images				**602**

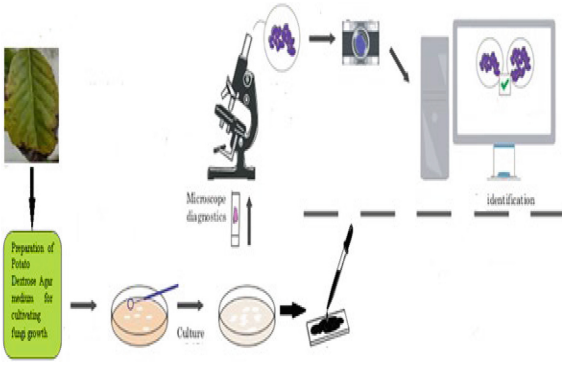

Fig. 1. Flowchart for the proposed method of identifying the spores and hyphae of fungi.

Table 1 summarizes the identification of microscopic images of fungus that are found on human bodies, polluted soil, or food sources. Fungi identification of plant leaf diseases at microscopic level is not addressed.

For the purpose of categorizing the fungus, authors developed a custom designed convolutional neural network. We experiment on transfer learning of DL models such as Alex-Net, SqueezeNet and ResNet50 model. We also evaluate the dataset using the hybrid approach in [16] such as CNN-KNN, CNN-LDA and CNN-SVM. Fivefold cross validation is utilized for all the models to get the optimized results.

3 Preparation of Novel Dataset

In this section, we describe the method utilized to obtain the microscopic images of fungi from plant leaf. The Fig. 1 shows the proposed method for identifying and classifying the spores and hyphae of fungi.

The infected leaf of mango/custard apple is taken and washed thoroughly with distilled water and kept aside. A Potato Dextrose Agar (PDA) medium is prepared and kept in Autoclave for 15min at 121' C. After Autoclave the mixtures is dispensed from the flask of around 10ml- 15ml in Petri dish and incubate the infected leaf in the PDA medium. Allow the fungus on the medium to grow for two days. Using the sterile needle transfer the mycelia mat from the Petri dish to a sterile slide. Observe this slide under 40X objective lens. These are captured using 12Mega pixel camera and this dataset consists of 602 images in total.

4 Overview of Dataset

We have developed a novel fungus database. The database is collected from Dept. of Microbiology, Gulbarga University, Kalaburagi, Karnataka, India. The database is developed from anthracnose disease of mango plant and leaf spot disease of custard apple plant. These are again divided into four different classes, which is on the basis of number of days passed on observation. Fungus spores are observed after 2 days of incubating

Fig. 2. Anthracanose of mango

Fig. 3. Leaf spot of Custard apple

with the infected leaf on the PDA medium. And after 5 days we see the fungal hyphae grown on the medium. This observation is classified into four classes, which are spores of Colletotrichum gloeosporioides, hyphae of Colletotrichum gloeosporioides, spores of Cylindrocladium colhounii and hyphae of Cylindrocladium colhounii. These total counts to 602 images. The novel dataset is not publicly available yet. Below Table 3 shows the summary of the database, Fig. 2 and 3 shows the leaf diseases of mango and custard apple plant caused by fungi. Figure 4, 5, 6 and 7 shows the microscopic images of these four respective classes.

5 Methods/Models Used

Image processing techniques often do not deliver state of the art results in the field of biological sciences like the fungal disease [17]. To detect the microscopic fungi, we employ the Convolution Neural Network (CNN) architecture, which provides the state of the art results. And to establish the novelty and credibility of our novel dataset, we employ different Machine Learning (ML) techniques, Deep Learning (DL) models. The hybrid approach of machine learning and deep learning technique described in [16] is also implemented to evaluate the performance of our novel dataset.

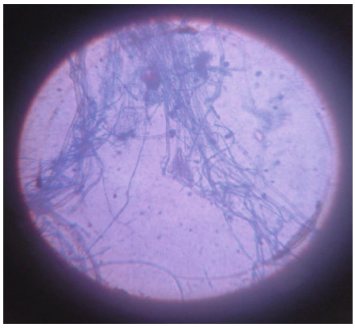

Fig. 4. Hyphae of Cylindrocladium colhounii

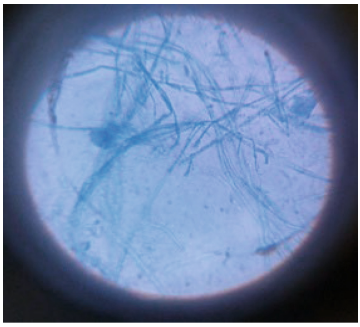

Fig. 5. Hyphae of Colletotrichum gloeosporioides

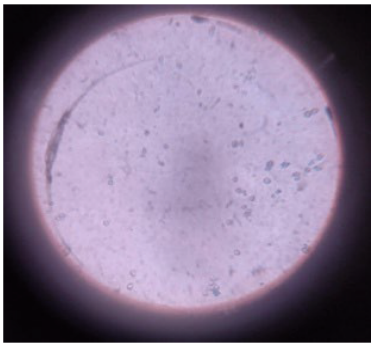

Fig. 6. Spores of Cylindrocladium colhounii

The authors in [17–21] have worked on own customized CNN architectures. We aim to work on transfer learning of Deep learning models such as AlexNet [28], SqueezeNet [29] and ResNet50 [30] model. These models are already trained on thousands of images of different categories. The architectures used are shown in Fig. 8 , 9 and 10 respectively.

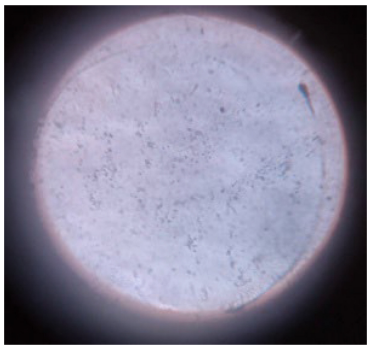

Fig. 7. Spores of Colletotrichum gloeosporioides

Fig. 8. Overview of AlexNet architectur

Fig. 9. Overview of SqueezeNet architecture

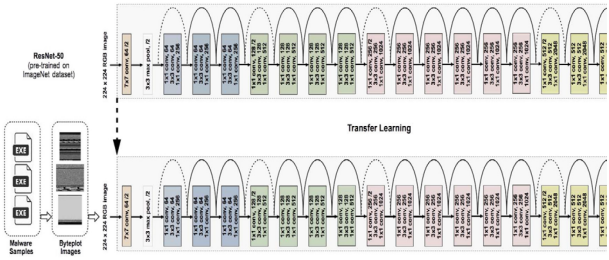

Fig. 10. Overview of ResNet50 architecture. Reprinted from "Malicious software classification using transfer learning of resnet-50 deep neural network" by Rezende, Edmar, Guilherme Ruppert, Tiago Carvalho, Fabio Ramos, and Paulo De Geus, 2017, 16th IEEE International Conference on Machine Learning and Applications (ICMLA).

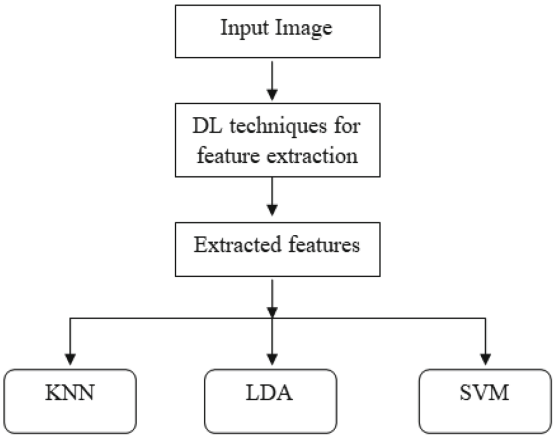

Fig. 11. Hybrid approach using ML and DL technique.

Table 3. Domain Details

Environment	Parameters
OS	Windows 10 Pro
CPU	Intel® Core™ i7–2620 with 2.70GHz
RAM	12GB
Hard Disk	1 TB

In the hybrid approach, the features are collected from Customized CNN architecture which has 5 layers. The collected features are stored and used for classification using machine learning classifiers. We use three machine learning classifiers which are K Nearest Neighbor (KNN), Linear Discriminant Analysis (LDA) and Support Vector Machine (SVM). The below Fig. 11 shows the flow chart for hybrid approach.

The deep learning models are trained on the same execution environment and same hyper-parameters, to compare the models effectively. The Table 3 shows the Domain Details utilized (Table 4).

6 Results of the Experiment

In this part, we assess the hybrid approach's experimental findings and the Deep learning models. For training and testing purpose, the database is divided as 80:20 split. Where 80% of data is given for training and the rest is used for validation purpose. The learning rate of the models is kept at 0.0001. 5 fold cross validation is used to optimize the accuracy and all the models are trained for 25 epochs. Below Table 5, 6, 7, 8 and 9 shows the identification accuracy of class-level recognition for Alex-Net, Squeeze-Net, ResNet50, CNN- KNN, CNN- LDA and CNN- SVM.

Confusion matrix for all the models is given below from Table 10, 11, 12, 13, 14 and 15.

Figure 12 shows the comparative analysis of models.

The derived performance metrics for each model are displayed in Table 16.

From Table 16 it is evident that ResNet50 model gave good recognition accuracy of 97.52% compared to the other models on the collected novel fungus dataset.

Table 4. Identification of categories using Alex-Net

Sl. No.	Species	Accuracy
1	Spore_CG	100%
2	Spore_CC	100%
3	Hyphae_CG	89.5%
4	Hyphae_CC	85.2%

Table 5. Identification of categories using Squeeze-Net

Sl. No.	Species	Accuracy
1	Spore_CG	95.5%
2	Spore_CC	71.4%
3	Hyphae_CG	89.5%
4	Hyphae_CC	90%

Table 6. Identification of categories using ResNet50

Sl. No.	Species	Accuracy
1	Spore_CG	100%
2	Spore_CC	100%
3	Hyphae_CG	94.5%
4	Hyphae_CC	91.2%

Table 7. Identification of categories using CNN- KNN

Sl. No.	**Species**	**Accuracy**
1	Spore_CG	82.2%
2	Spore_CC	80%
3	Hyphae_CG	89.5%
4	Hyphae_CC	81.5%

Table 8. Identification of categories using CNN- LDA

Sl. No.	**Species**	**Accuracy**
1	Spore_CG	97.8%
2	Spore_CC	93.3%
3	Hyphae_CG	84.2%
4	Hyphae_CC	92.6%

Table 9. Identification of categories using CNN- SVM

Sl. No.	**Species**	**Accuracy**
1	Spore_CG	97.8%
2	Spore_CC	93.3%
3	Hyphae_CG	94.7%
4	Hyphae_CC	77.8%

Table 10. Confusion Matrix obtained using AlexNet

	Spore_CG	Spore_CC	Hyphae_CG	Hyphae_CC
Spore_CG	**45**	0	0	0
Spore_CC	0	**30**	0	0
Hyphae_CG	0	1	**17**	1
Hyphae_CC	1	0	3	**23**
Accuracy in %				**95.3%**

Table 11. Confusion Matrix obtained using SqueezeNet

	Spore_CG	Spore_CC	Hyphae_CG	Hyphae_CC
Spore_CG	**64**	2	0	1
Spore_CC	1	**42**	0	1
Hyphae_CG	0	0	**20**	8
Hyphae_CC	2	0	2	**36**
Accuracy in %				**90%**

Table 12. Confusion Matrix obtained using ResNet50

	Spore_CG	Spore_CC	Hyphae_CG	Hyphae_CC
Spore_CG	**64**	0	0	0
Spore_CC	0	**42**	0	0
Hyphae_CG	0	1	**26**	1
Hyphae_CC	0	0	1	**38**
Accuracy in %				**97.5%**

Table 13. Confusion Matrix obtained using CNN- KNN

	Spore_CG	Spore_CC	Hyphae_CG	Hyphae_CC
Spore_CG	**37**	7	1	0
Spore_CC	6	**24**	0	0
Hyphae_CG	1	1	**17**	0
Hyphae_CC	1	0	4	**22**
Accuracy in %				**82.6%**

Table 14. Confusion Matrix obtained using CNN- LDA

	Spore_CG	Spore_CC	Hyphae_CG	Hyphae_CC
Spore_CG	**44**	1	0	0
Spore_CC	2	**28**	0	0
Hyphae_CG	1	1	**16**	1
Hyphae_CC	2	0	0	**25**
Accuracy in %				**93.4%**

Table 15. Confusion Matrix obtained using CNN- SVM

	Spore_CG	Spore_CC	Hyphae_CG	Hyphae_CC
Spore_CG	**44**	0	0	1
Spore_CC	2	**28**	0	0
Hyphae_CG	0	0	**18**	1
Hyphae_CC	1	2	3	**21**
Accuracy in %				**91.7%**

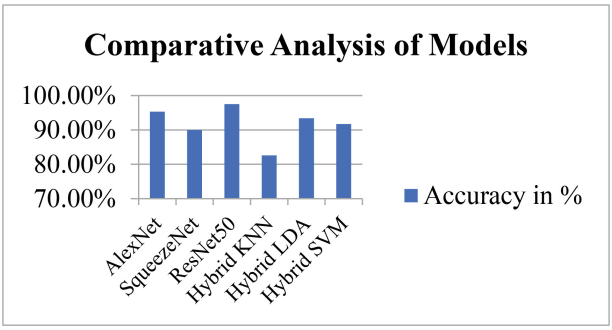

Fig. 12. Comparative Analysis of models

Table 16. Performance metrics utilizing transfer learning: precision, recall, and F1 score.

Using Transfer Learning				
	Precision	**Recall**	**F1score**	**Accuracy**
Alex-Net	0.9366	0.9386	0.9376	95.3%
Squeeze-Net	0.8757	0.8905	0.8832	90%
ResNet50	**0.9634**	**0.9278**	**0.9538**	**97.52%**
Using Feature Extraction				
CNN- KNN	0.8329	0.8362	0.8346	82.6%
CNN- LDA	0.9198	0.9482	0.9338	93.4%
CNN- SVM	0.9091	0.9229	0.9159	91.7%

7 Conclusions

In this study, we created a brand new dataset of fungi. To develop the fungus, we carefully nurture the PDA medium. Under a 40X high power objective lens microscope, the developing fungus are examined. As there is no standard available dataset for fungi which are obtained from leaf, this is one of first of its kind work. We have used different

algorithms and techniques to establish the comparison between different ML, DL and the hybrid approach of ML & DL techniques. The novel fungus dataset is evaluated using 5 fold cross validation. According to Table 18's performance metrics, the ResNet50 model did well, with an average classification result of 97.52%.

8 Future Scope

A lot of research on classification of microscopic fungi of plant diseases needs to be done. It includes the microscopic examination of steam, bark, fruit, flower of crops and plants. In this article we have focused only on the leaf part of the plant. Hence, there is a lot of scope to expand and generalize solution for the problem.

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