



Robust Optimization of MobileNet for Plant Disease Classification with Fine Tuned Parameters

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Abstract—Vegetables are enriched with vitamins, essential for mental as well as physical health, are used in our routine life. Vegetable farming is one of the wide-scale businesses across the world. Many times, Vegetable plants are attacked by different diseases which consequences a heavy deficit for farmers. Early prognosis of these plant diseases can help to overcome this loss. Due to the variation of these diseases, it is difficult to identify the attacking disease. Deep learning models can be used for early detection of these diseased plants and appropriate measurements can be taken to minimize deficit. In this paper, we proposed a deep learning-based model for the early prognosis and classification of plant diseases. We have tuned a deep learning-based pretrained model in 2 folds over a publicly available dataset that contains images of different plants suffering from different diseases as well as healthy plants. We are envisioned to classify each instance as healthy or the name of the disease, the plant is being suffered. This transfer learning method has achieved remarkable results on this data-set of tomato plants and achieved 98.89% accuracy. To the best of our knowledge, this model is lightweight than other states of the art model with such significant results. This deep learning-based system can be used in real life for the detection of diseases of plants.

Keywords—Plant Disease Classification, Transfer Learning, MobileNet, Image Classification

I. INTRODUCTION (HEADING 1)

In the modern age of the huge population, the world needs food on a large scale to feed people. But plant diseases are ruining the plants that are leading to a heavy deficit for farmers and everyone. These plant diseases are responsible for the loss of 30% rice, 21.5 % wheat, 17.2% potato, 21.4% soybean, and 22.5% maize per season at the global level [1]. The plant diseases classification based on images is a hard problem with an extensive range of associated problems, containing the occurrence of symptoms with a wide variety of visual characteristics, the probability of several concurrent disorders in a particular plant, and numerous disorders with similar symptoms, amongst others [2]. External variables such as image background interference and lighting variations associated with capture conditions add even more difficulty to the problem. The conventional image classification technique requires the prominent representation of features that are provided to the training classifier. Such features may be the color, shape of color images, or texture,

but it is difficult to isolate the traits in the case of plant disease and categorize an image based on these traits [3].

Due to these limitations of traditional machine learning, the researcher's attention has drawn to deep learning based convolution neural networks (CNN) to automatically learn the features. Recent research has shown that CNNs can automatically extract low-level (edges and shapes) and high-level features (semantics and texture) due to the abstraction power of their layers [4]. Researchers have used various classifications, image recognition, computer vision, machine learning, and deep learning-based methods to work on segmentation, identification, data generation, and classification of images of different domains [5] [6]. For the plant classification diseases, M.S.Mustafa et al. [7] developed an automatic hybrid intelligent system for herb plant classification and early detection of herb plant disease. The method of manual identification was an extensive process that involves prior awareness of the plant itself, like texture, shape, and odor. Their study purpose was to explain the computerized system of identifying organisms and detecting early herbal diseases by referring to these functions. Their research has developed a method for identifying the species and using electronic nose and computer vision to identify the initial herb disease, which focuses on color, odor, shape, and extracting texture of herb leaves, along with hybrid intelligent method involving the Naïve Bayes, fuzzy inference system, support vector machine classifier and probabilistic neural network [8].

Barbedo et al. [9] presented the dataset size Impact and variation on the effectiveness of deep learning and transfer learning for the classification of plant diseases. The topic of automated plant disease detection was focused on traditional machine learning methodologies like Decision Trees, Multilayer Perceptron Neural Networks, and Support Vector Machines(SVM). The dominant approach, however, was moved to incorporating deep learning techniques, based on (CNNs)Convolution Neural Networks. These kinds of approaches involved massive datasets containing a broad number of situations for operating properly. These were major restraints, considering the many problems involved in

the creation of an adequate database of images. Their research explores how the scale and complexity of the datasets influence the effectiveness of deep-learning approaches implemented to plant pathology. Their study was focused on an image database of 12 species of plants, each with somewhat different features in terms of the no of samples, amount of diseases, and range of circumstances. Experimental findings suggest that while the technological limitations associated with the classification of automatic plant disease were mostly overcome, they used small image datasets for training had various negative implications that also avoid this form of technology from being efficiently disseminated.

De Chant et al. [10] presented automatic detection of northern leaf blight diseased maize plants from field imagery by applying deep learning. Their presented system detected the absence and existence of a disease in an image, most commonly information was used to estimate the incidence of the disease. Their methodology used a CNN(convolution neural network) computational framework to overcome the complexities of minimal data and the various irregularities that occur in field-grown plant images. The time is taken to manually identify images used for CNN training was the major limitation of their system. They achieved 96.7% accuracy was obtained by the system on the set of test images though not in training.

These CNN's performed well and automatically extract the features, but the constraint of CNN's is that they are data-hungry and need enormous training data. Transfer learning is used to solve this problem [11]. Many studies used the pre-trained models to classify the diseased plants. Alvaro Fuentes et al. [12] presented a detector based on deep learning for real-time diseases recognition in tomato plants and pets They address three primary families of detectors: SSD(Single-Shot Multibox Detector), Faster R-CNN(Faster Region-based Convolution Neural Network), and R-FCN(Region-Based Fully Convolution Network), which were referred as "Deep learning meta-architectures" in their work. They combined these meta deep learning architectures with 'deep features extractors' like ResNet (Residual Network) and VGG net. Kamal KC et al. [13] presented depth-wise separable convolution architectures for plant disease classification. They presented two versions of two types of building blocks containing a depth-wise separable convolution. They performed training and testing of used models on a publicly accessible PlantVillage dataset that contains 82,161 images and 55 different classes of diseased and healthy plants. Less precision and a high increase in convergence speed are obtained by these depth-wise separable convolutions. Many other models were trained and tested, from which Reduced MobileNet attained a 98.34% classification accuracy.

D.oppenheim et al. [14] used VGG16 [15], which utilizes these different appearances and recent developments in computer vision greatly enhanced via deep learning. There were distinct visual signs of certain plant diseases that can be used to accurately recognize and classify them. The algorithm utilizes a deep (CNN)convolution neural network to group the tubers into 5 categories, four classes of diseases and a balanced class of potatoes. Similarly, Yang LU et al. [16] presented rice disease identification using Alexnet [17]. The proposed method was qualified to classify 10 different rice diseases, they used the dataset of natural 500 images of healthy and diseased rice leaves and stems taken from experimental fields of rice. Their suggested CNN-based model achieved 95.48% accuracy under the 10 cross-fold validation approach. Effects of the simulation to classify rice diseases determine the effectiveness and feasibility of the suggested approach. The comparison of these studies is shown in table 1.

Table 1 Comporsion of different state of the art studies

Studies	Dataset	Methods	Classes	Accuracy %
Barbedo et al. [9] (2018)	12 plants	GoogLeNet	56	84%
De Chant et al. [10] (2017)	Corn Images	Pipeline	2	97 %
Fuentes et al. [12] (2017)	Tomato images	Multiple networks	10	83%
KC et al. [13] (2019)	Plant Village	MobileNet	55	98%
Oppenheim et al. [14] (2017)	Potato Images	VGG	5	96%
LU et al. [16] (2018)	Rice Images	AlexNet	10	95%
Sinha et al. [18] (2020)	Plant Village	Pipeline	55	74%
Chen et al. [19] (2021)	Crop Disease (own)	CNN	4	93.75%

In this paper, we proposed a multi-class plant disease classification model to classify the different plant diseases. We find-tuned the MobileNet CNN(convolutional neural network) [20] pre-trained on 1.3 million images and train on the publicly available plant disease classification dataset that is available on Kaggle [21]. This dataset contains 87,900 images of 38 different classes and using the MobileNet on this dataset we achieved 98.89% accuracy. The methodology of our proposed work is discussed below in the methodology section, the detailed description of the dataset and results is given in section 3.

II. METHODOLOGY

To design the multiclass plant disease classification model, we adopted the following methodology.

A. Data Preprocessing

The dataset contains 87,900 images of 38 different classes including the healthy as well as diseased plants images. For the experimentation, data was split into 3 categories training, validation, and testing. At first, for the training 70295, for

validation 17572, and for testing 33 images were separated. We take the original number of images for the training but for the testing of our model, we make the batches of size 32 and took 440 batches for validation and 110 for the testing model at the end of the training. Furthermore, to improve the robustness of our model we performed the augmentation of horizontal random flip and random rotation of 0.2. This led to a better classification of data even using the different positions of images. The augmentation results are shown in figure 1.

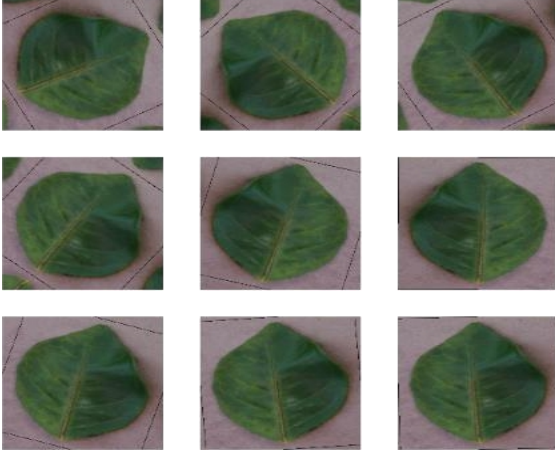


Figure 1 Augmentation of the dataset using horizontal RandomFlip and random rotation of 0.2

B. Models Finetuning and Training

To train the plain disease classifier using this dataset we have used the pre-trained model MobileNet in two folds. In the first fold, we imported the Mobilenet with pre-trained ImageNet weights and freeze all the trainable layers. We used the default processing input layers of MobileNet v2 and then we add a 2D global average pooling layer and passed the features batch of the training dataset to it. Finally, we pass the inputs to the augmentation layer and this augmentation layer was the input of the processing input layer and the base model. We added the global average layer next to it and drop out of 0.2 and trained the model. In the second fold, we finetuned the model and enable the trainable layers of the imported model. The base model contains the 155 layers but we start to finetune the layer from 100 to 155 and make the first 100 layers untrainable. The architecture of both models is shown in figure 2 and hyperparameters of both folds are displayed in table 2.

Table 2: Hyperparameters of our proposed methodology

Models	Optimizer	Learning rate	Metric	Loss	Epochs
MobileNet	Adam	0.0001	Accuracy	Sparse Categorical Crossentropy	50
Tuned MobileNet	RMSprop	0.0001/10	Accuracy	Sparse Categorical Crossentropy	50

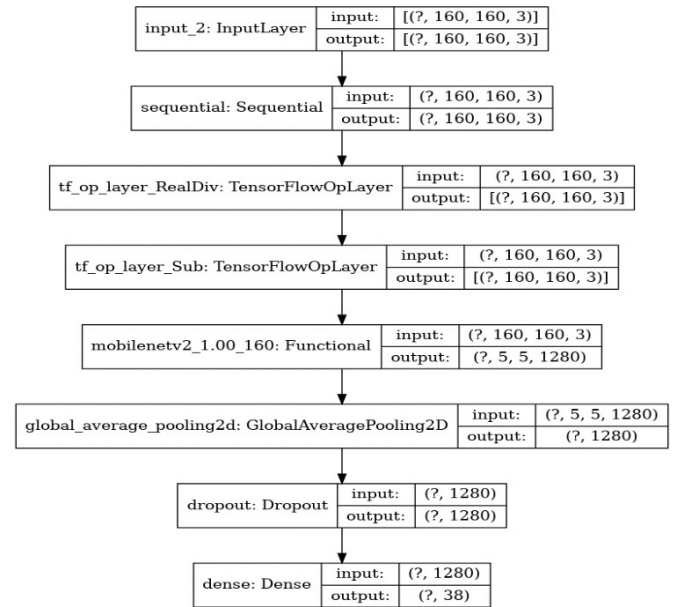


Figure 2: Our Proposed model architecture

We have used accuracy as an evaluation measure. The accuracy can be represented by equation 1.

$$= \frac{TP}{TP + FP + FN}$$

Where:

TP signifies the recall or truly predicted image, TN indicates the True negative, FP indicates the false positive and FN indicates the false negative.

III. RESULTS AND DISCUSSION:

The experiments were performed using the 20 GB of RAM, Core i7-7800, and GTX 1080-Ti. The performance of models was measure by using the accuracy and loss curves, and comparison with the state-of-the-art studies.

A. Dataset description:

The used dataset in this study has the 38 classes of Apple, blueberry, corn, cherry, Grape, Peach, Orange, Potato, Raspberry, Strawberry, Squash, Soybean, and Tomato. This dataset includes the healthy as well as diseased images of these plants. Some images of these plants are shown in figure 3 to show that how difficult it is to identify the plant disease at the initial stage.

A detailed description of the name of classes and the no of images in the classes present in the dataset for the training and validation of data is shown in table 3.

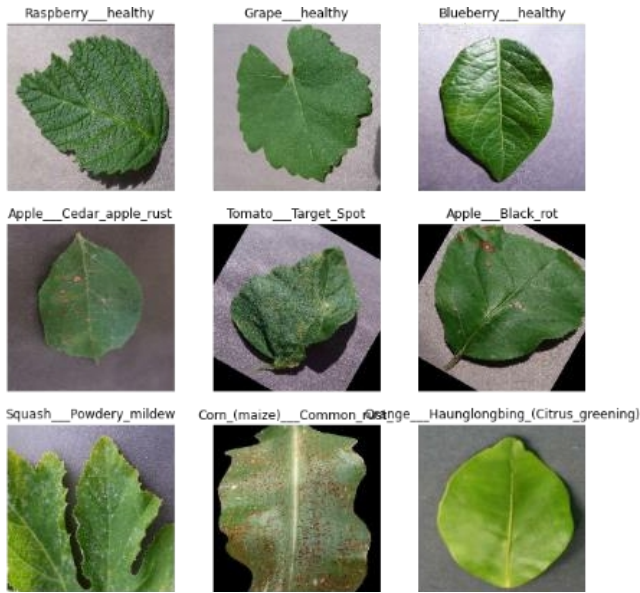


Figure 3: Images of healthy and diseased Plants

Table 3: Distribution of classes in the dataset

Classes	Train Images	Validation Images	Total Images
Apple-Cedar_apple_rust	1741	435	2176
Apple-Black rot	1888	472	2360
Apple-Apple scab	1920	480	2400
Apple-healthy	1781	445	2226
Blueberry-healthy	1824	456	2280
Corn [maize]_Northern Leaf Blight	1859	465	2324
Cherry-[including sour]_healthy	1908	477	2385
Corn [maize]_Cercospora-leaf spot Gray leaf spot	1827	457	2284
Cherry-[including sour]_Powder-mildew	1760	440	2200
Corn [maize]_healthy	1745	436	2181
Corn [maize]_Common rust	1826	456	2282
Grape-healthy	2022	505	2527
Grape Black rot	1774	444	2218
Grape-Leaf blight [Isariopsis Leaf Spot]	1790	448	2238
Grape Esca [Black Measles]	2008	502	2510
Orange-Haunglongbing [Citrus greening]	1722	430	2152
Peach-healthy	1728	432	2160
Peach-Bacterial spot	1907	477	2384
Pepper,-bell Bacterial spot	1961	490	2451
Potato-Early-blight	1851	463	2314
Potato-Late blight	1838	459	2297
Pepper,-bell-healthy	1913	478	2391
Potato-healthy	1736	434	2170
Raspberry-healthy	1939	485	2424
Soybean-healthy	1939	485	2424
Strawberry-healthy	1824	456	2280
Squash-Powdery mildew	1926	481	2407
Strawberry-Leaf scorch	1987	497	2484
Tomato-Early blight	2016	504	2520
Tomato-Bacterial spot	1920	480	2400
Tomato-Septoria leaf spot	1816	454	2270
Tomato-Late blight	1988	497	2485
Tomato-Leaf Mold	1882	470	2352
Tomato-Target Spot	2010	503	2513
Tomato-Tomato Yellow leaf curl Virus	1642	410	2052

Tomato-Spider mites Two-spotted spider mite	1702	425	2127
Tomato-Tomato mosaic virus	1692	423	2115
Tomato-healthy	1683	421	2104
Total	70925	17572	88497

B. Results and Comparison with other studies:

To evaluate the performance of our methodology, we used the accuracy and loss of the model. In the first fold, we achieved validation accuracy of 93.37% and a loss of 0.1973. Our model has a total of 2.3 million parameters that are very low as compared to other studies. For the first model, 48,678 parameters are trainable out of 2.3 million while Oppenheim et al. [14] have 14.7 million parameters, LU et al. [16] (2018) have 3.3 million parameters and KC et al. [13] has 3.2 million parameters. In the finetuning, we have 1.9 million trainable parameters that are less than all comparative studies and show how lightweight our proposed model is. The accuracy and loss curves of our designed model without fine-tuning are displayed in Figure 4 and with fine-tuning in Figure 5.

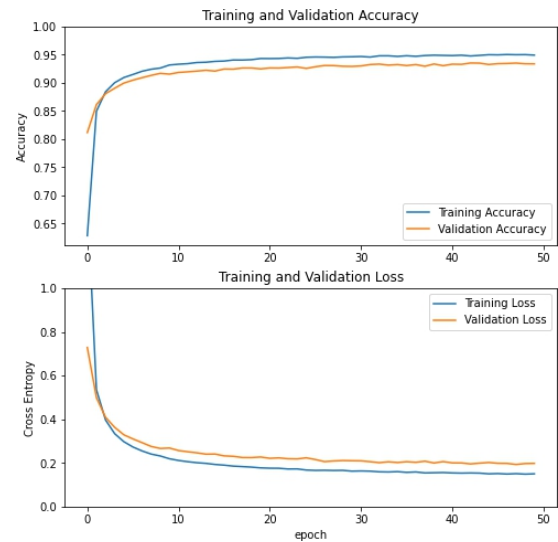
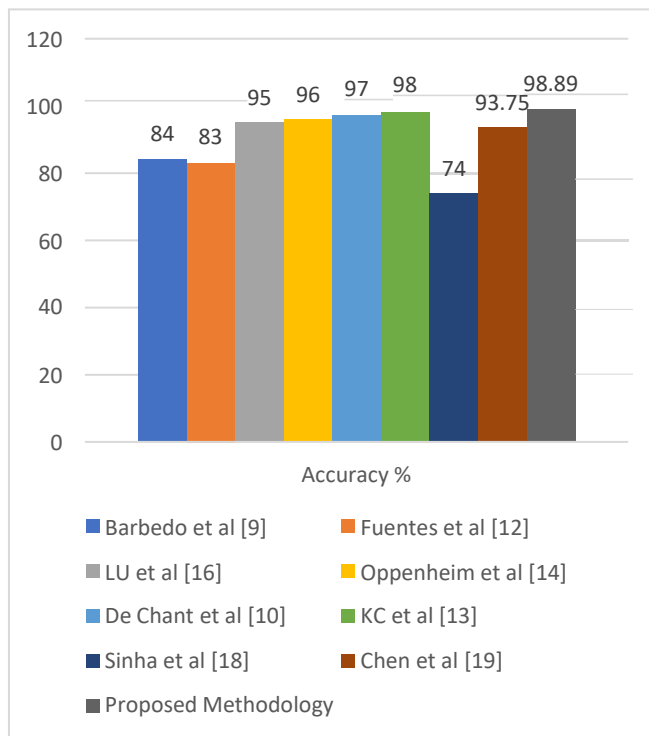


Figure 4: Accuracy and loss curves of our model without fine-tuning



Figure 5: Accuracy and loss curves of our model with fine-tuning

We achieved a validation accuracy of 98.93 and a validation loss of 0.0483. then, we computed the final test accuracy and loss on the test batches and achieved 98.89% and 0.0507 respectively. Furthermore, we compared our model's performance with other state-of-the-art studies including Barbedo et al. [9], De Chant et al. [10], Fuentes et al. [12], KC et al. [13] Oppenheim et al. [14], LU et al. [16], Sinha et al. [18] and Chen et al. [19]. Our proposed methodology overcomes the results of all previous studies. The comparison of our methodology with recent studies is shown in figure 5. Furthermore, our model has a small number of parameters than all previous studies and it can be easily used in mobile and other low specification devices.



IV. CONCLUSION

Early plant disease detection is very significant for the survival of plants and the economy. It is very difficult for farmers to identify the attacking disease on plants with the naked eye that lead to the destruction of plants. There is a system needed that can help farmers and In this paper, we suggested a very lightweight multi-class plant disease classification model using a pre-trained MobileNet CNN(convolutional neural network) with significant accuracy. We trained the model on the publically available dataset that contains 38 classes of 14 plants. These images are of plants that are both healthy and diseased. We achieved the 98.89% of accuracy on the 38 classes using our methodology which is more than state-of-the-art models. Furthermore, our model is also very light and it can be easily used in mobile phone applications and it categorizes the plants within 2-3 seconds.

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