

Performance evaluation of DeepD381v2 for automatic classification of tomato leaf abnormalities

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Abstract

Robust and automated classify of plant leaf diseases based on deep learning has faced considerable challenges linked to environmental noise (humidity, cloudy-sunny, fog, rain), occlusion, low-contrast and variability in crops and pose over time. This paper presents an optimized deep learning architecture DeepD381v2 (Deep disease 379 layers version 2) that classify plant leaf disease in real-time. The network improves classification accuracy by 98.52% by training, 98.46% by validation, and 98.48% by test dataset by abstracting multi-scale context information at reduced memory cost.

Keyword

Convolution neural network, Plant disease, Classification, Deep learning

Introduction

Traditional leaf disease monitoring requires manual observation, which is time-consuming and labor-intensive. We propose an encoder architecture (down sampling) based on multi-branch convolutions to improve feature extraction performance by maintain spatial resolution during down sampling task (Kaur et al., 2022). The depth of the DeepD381v2 network allows the extraction of low-level, mid-level, and high-level features at different depths of the network, thereby improving the accuracy of classification with noisy images. The comparative learning parameters of the previously developed DeepD381v1 (Islam et al., 2022) and proposed DeepD381v2 network are shown in Table 1.

Table 1. Learning parameters

Network name	Total parameters	Number of layers	Input Image size, pixel
DeepD381v1	2.86×10^7	381	112x112, 224x224
DeepD381v2	2.35×10^7	379	112x112, 224x224, 240x240, 300x300

Materials and Methods

In this study, images of tomato leaves were obtained at the Plant factory of Ehime University in Matsuyama, Japan from October 2021 to the present. Tomato leaves with close-up view

showing the textural elements, full view of the leaf reveals the pattern and the distance view provide a spatial view. We photographed from several angles, time, period, lighting, background conditions, weather conditions, aspect ratio, pixel resolutions, mobile devices and cameras. Then, the captured images were resized to 112x112x3,224x224x3, 240x240,300x300 and stored in the corresponding disease class folders. We used both public datasets from PlantVillage (Bacterial Spot, Bacterial mold, Early blight, Gray spot, Late Blight, Leaf mold, Powdery mildew, Septoria leaf spot, Target Spot, Tomato mosaic virus, and Two Spotted Spider Mite and our own datasets (Healthy, Powdery mildew, Magnesium deficiency, TYLCV) from the plant factory of the Ehime University. To address the class imbalance problem, we proposed a data oversampling technique as shown Fig.1. A total of 310,534 augmented images are used for training, validation, and test purposes.

We propose smaller filter sizes for convolution and grouped convolution layers to achieve stronger feature generalization and extraction of low-level, mid-level and high-level features from input images. The last convolution layer feeds its output to the Softmax layer (Fig.2). The 14 outputs corresponding to 14 classes are input to the softmax layer. The Softmax layer uses the cross-entropy function to calculate the predicted probability (ranging from 0 to 1, higher is better) that the predicted image belongs to its relevant class and passed to the classification output layer.

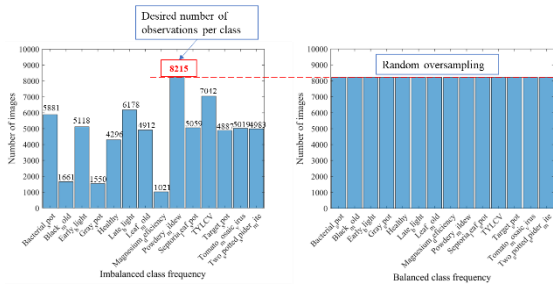


Fig.1. Random oversampling technique to address the class imbalance problem.

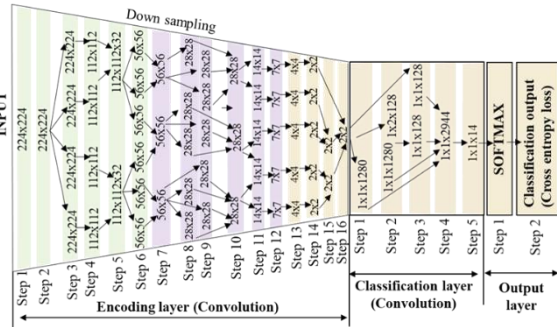


Fig.2. Network architecture of the DeepD381v2.

Results and discussion

DeepD381v2 achieves higher accuracy in training, validation, and testing performance, as shown in Table 2, with a mini-batch size of 42, a maximum number of epochs of 15, and a learning rate drop factor of 0.0001.

Table 2. Network training, validation and test performance

Input size	Time (min:sec)	Tr. Acc., %	Val. Acc., %	Test Acc., %
300x300	3041.22	99.51	98.46	98.59
240x240	1228.56	98.36	98.45	98.24
224x224	1123.53	98.52	98.46	98.48
112x112	508.5	97.78	98.02	97.87

We conducted a test performance using Healthy leaf data which mimics the various disease conditions such as TYLCV, Powdery mildew, Late Blight, Leaf mold, and Bacterial Spot. In all cases shown in Figure 3 and Table 3, DeepD381v2 correctly predicted the high-scoring healthy category.

Furthermore, we conducted an occlusion sensitivity analysis using a TYLCV effected tomato leaf as shown in Fig. 4. The red and blue in the occlusion map are shown in Fig.4, represent that the DeepD381v2 highlighted the leaf part effected by TYLCV disease.

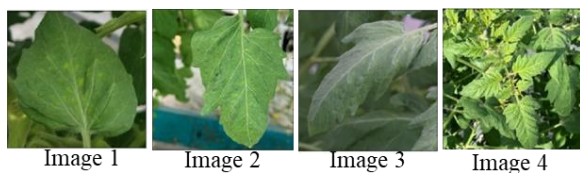


Fig. 3. Health classes that mimic various disease conditions

for testing purposes.

Table 3. Comparison of the classification score

Network Name	Image No. 1	Image No. 2	Image No. 3	Image No. 4
DeepD381v1	1.00	1.00	0.92	0.95
DeepD381v2	1.00	0.99	0.90	1.00

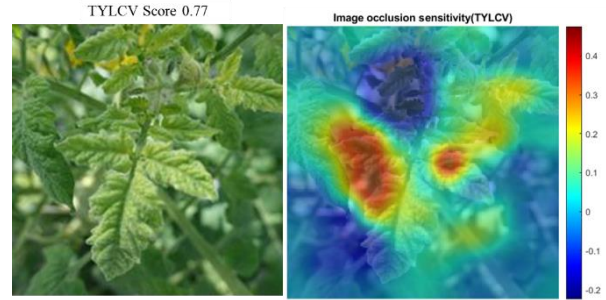


Fig. 4. Occlusion sensitivity analysis.

Conclusions

This paper presents a modified version of the previously reported network DeepD381V1, which classifies 14 classes (diseases and nutrient deficiencies of tomato leaves) with improved accuracy. We propose to oversample the input data to reduce the class imbalance problem. We also observed that removing the fully connected layers and the average pooling in the output layer of the network did not reduce the accuracy of the network's learning and prediction. Furthermore, we train the modified network DeepD381 V2 with various input image sizes of 112x112x3, 224x224x3, 240x240x3, and 300x300x3, and the training accuracy of the network exceeds 98% in all cases.

References

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