DeepD381v1—A Deep-Learning Architecture for the Automatic Detection of tomato leaf disease

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要旨

We developed a new deep learning convolution neural network architecture DeepD381v1 with Swish and Batch-Instance Normalization layers. This approach has achieved breakthroughs in improving network performance, achieving over 99.0% classification accuracy through training, 97.5% through validation, and 98.0% through the test dataset. Network also demonstrates stable performance under any combination of the imbalance data and doesn't overfit on the validation dataset. Then, we visualize the network performance and show the diseased areas of leaves. We hope that this research will help in the early detection of leaf diseases and reduce the losses by preventing disease transmission.

キーワード

Convolution neural network，Plant disease，Classification，Deep learning，Visualization

はじめに

Pests and diseases have a devastating effect on food security as it caused 20 to 40% loss of global food production (Food and Agriculture organization of the United Nation, International plant protection convention, 2017). A timely and accurately diagnosis-based monitoring system could effectively reduce the loss by preventing disease from spreading (Barbedo, 2018).

Now a days, the convolution neural network based deep learning technique has made breakthrough in image classification and achieved extraordinary accuracy to predict plant diseases. Figure 1 shows a taxonomy of various deep network architectures and our proposed network.
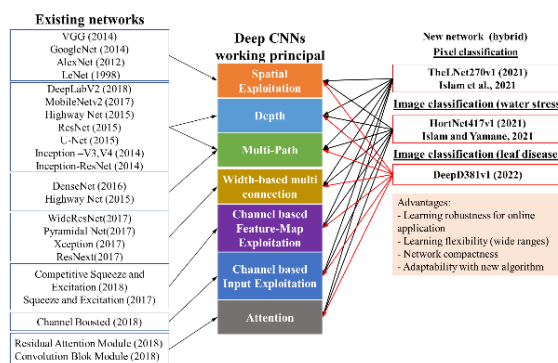

Fig.1. Deep networks (modified from Islam et al., 2021).

材料および方法

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 224x224x3 and stored in the corresponding disease class folders. We used both public datasets from PlantVillage (Bacterial Spot (BS), Late Blight (LB), Septoria Leaf Spot (SLS), Target Spot (TS) and Two Spotted Spider Mite (TSSM)) and our own datasets (Healthy, TYLCV) from the plant factory od the Ehime University. A total of 28,000 images are used for training and validation purposes. An independent test dataset (100 images per class) was used to evaluate the prediction accuracy of the deep learning network.

We propose smaller filter sizes for convolution layers to achieve stronger feature generalization and extraction of low-level features from input images. The last convolution layer feeds its output to the Swish activation layer via an Instance normalization layer, thus an average pooling layer. We include Grouped convolution layers for efficient training, split

convolutions into multiple paths and use multiple GPUs for training to reduce the computation time. To optimise the model learning efficiency, we randomly turn off 5% of dead neuron in the shallow layers and 50% of the dead neuron in the deep layers of the network.

We added average pooling before the fully connected layer. This layer averages the features from the feature map, downsamples the height and width dimensions, and reduces the total number of parameters and minimises overfitting without sacrificing performance. All abstract features are integrated into a vector through a fully connected layer. The seven outputs corresponding to seven 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.

結果および考察

The total learnable parameters, number of neurons, weights, and biases of our proposed network are 2.86×10^7, 7.07×10^7, 2.86×10^7, 1.47×10^4, respectively. The order of classification error rate from low to high for each class is shown in Fig. 2.
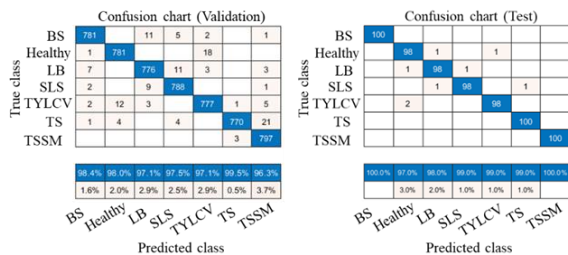

Fig.2. Confusion matrix chart

Fig. 3 shows that Network scored the highest for accuracy (0.9886), sensitivity (0.9886), specificity (0.9981), precision (0.9986), F1-Score (0.9886), MCC (0.987), and j (0.9867).
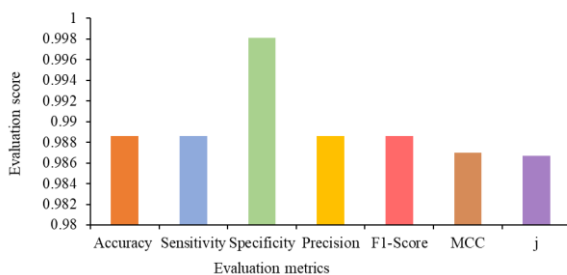

Fig.3. visualization of the network overall performance

Gradient-weighted Class Activation Mapping (Grad-CAM) techniques capturing the gradients of all successive feature maps flowing into the final convolutional layer and produce a coarse localization map in the form of intuitive representation of the important regions in the image for a predicted output class (shown in Fig. 4).
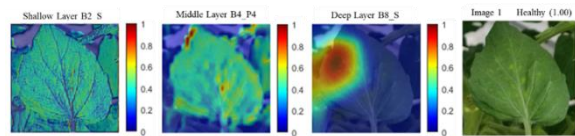

Fig. 4. Grad-CAM in different convolution layer

Fig. 5 visualizes the computed superpixel area for each image and shows which areas of the image are important to the classification.
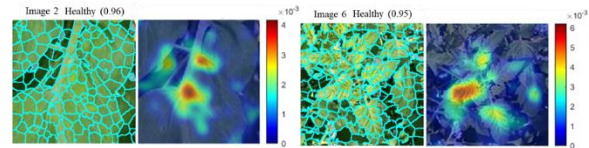

Fig. 5. Visualization based on weight similarity

結論

In this paper, we develop a network with 381 layers (DeepD381v1) and classified seven classes for real-time tomato leaf disease classification in the farmer's field. We observed that images downloaded from PlantVillage were identical due to consistent lighting, distance, viewing angle, size, color, and background conditions. Consequently, all networks achieved 100% test accuracy with datasets from PlantVillage. In the future, we will collect datasets of these classes (BS,LB,SLS,TS,TSSM) from plant factory.

引用文献

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