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LTVC-Net : Multi-scale dilated and attention-based CNN for mango leaf disease detection

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Abstract

Mango ranks among the fruits that are of high economic value, and the leaf diseases like anthracnose, powdery mildew, bacterial canker, and sooty mold have great impact on the productivity. Efficient and accurate diagnosis of the disease is very essential for improving the output and sustaining a good agricultural process. Recent advancements in the field of computer vision and deep learning have depicted promising features in plant disease diagnosis. Convolutional neural networks (CNNs) and transfer learning models have shown significant improvement in the process of leaf disease recognition among fruits like mangoes. However, most of the models have depicted generic architecture that could not effectively focus on leaf texture and vein pattern features, which are very essential in disease recognition in complex backgrounds. To overcome the limitations, a new Leaf Texture and Vein pattern-aware Convolutional Neural Networks (LTVC-Net) model specifically targeting the process of mango leaf disease recognition has been proposed in this research. LTVC-Net incorporates dual-scale dilated convolution and channel attention module in its architecture in order to improve multi-scale feature learning while retaining the disease-causing vein and texture features. Experiments on the proposed model have been performed on a publicly available dataset of mango leaf disease that contains multiple disease classes and normal ones. Extensive experiments on the proposed architecture have been performed while comparing the result with five efficient deep learning models that are MobileNetV2, ResNet50, EfficientNetB0, DenseNet121, and InceptionV3 models respectively. Based on the results in terms of ‘accuracy evaluation,’ ‘loss convergence,’ and ‘ROCAUC evaluation,’ the proposed LTVC-Net architecture clearly outperformed all other models in terms of efficiency and minimizes computational cost that could be effectively suitable for real-world applications in agriculture.

Subject Classification: *68T07.*

Keywords: *Mango leaf disease detection, LTVC-Net, Leaf texture analysis, Vein pattern features, Dilated convolution, Precision agriculture.*

1. Introduction

Agriculture is one such sector in the economic development processes of nations that has become incredibly crucial, with the cultivation of mangoes being one such significantly contributing factor in the field of agriculture, which is currently under the threat of numerous diseases such as anthracnose, powdery mildew, die back, bacterial canker, and gall midge, which pose a substantially threatening factor to the output of the mango plants if they are left unidentified in the early stage. The current processes used in the diagnosis of such conditions are highly dependent on the visual examination by agricultural experts. These challenges can be addressed by the design and implementation of automated disease diagnosis systems built on data processing and machine learning methods. Initially, methods based on the extraction of manually designed features together with traditional classification methods like SVM and neural networks were used for mango leaf disease classification [5]. Although such approaches were successful, they were prone to challenges like the effect of illuminance, complexity, and the appearance of the disease. With the improvements that came with deep neural networks, Convolutional Neural Networks (CNNs) are currently the most used technique in plant disease identification, given their capability to automatically learn categorized features from raw data. Various researchers have employed CNN models, transfer learning, and more in the classification of mango leaf disease patterns [1], [3], [7], [20]. Transfer learning models have also enhanced the accuracy in image classifications, utilizing knowledge derived from massive image data sets [12], [13]. Recent studies have also applied more superior models like ConvNeXt, ensemble deep neural models, attention-based deep learning models, deep learning explain ability models, and transformer models [8], [10], [16]. The literature on the analysis of vein patterns for the discrimination of diseases has shown promising results concerning the importance of domain-specific modelling for feature description [9], [11], [17]. These considerations have inspired us to design and develop a new architecture for LTVC-Net, which strongly focuses on learning features with relevance to leaf texture and veins. In contrast to other general-purpose neural networks pretrained for general image classification [19], our design is task-specific and lightweight. The key contributions of this research can be considered as:

1. LTVC-Net architectural design for enhancing fine-grained textures and vein patterns of a mango leaf image.
2. Integration of dilated convolution and channel attention based on the squeeze and excite concept.
3. Thorough experimental comparison and evaluation with five current models based on deep learning.
4. Experimental validation of enhanced accuracy, robustness, and decreased computational complexity to apply these approaches to real-time agricultural DSS applications.

The remaining portion of this paper is discussed as follows: a literature review of mango leaf disease detection is shown in Section 2, while an explanation of the proposed LTVC-Net model is presented in Section 3, followed by results in Section 4, and finally, a conclusion is drawn in Section 5.

2. Related works

The initial research work conducted within this area was based solely on conventional image handling and ML algorithms. Mia et al. [5] used SVM with handcrafted features for the classification of mango leaf diseases. The development of CNNs has become the most prevalent trend within the area of crop disease recognition. Arivazhagan and Ligi [2] were among the pioneering works that identified mango leaf diseases using CNNs, reporting higher accuracy compared with conventional models Gulavnai and Patil [4], Rao et al. [1] successfully applied transfer learning models within mango and grapes leaf ailments, Mohapatra et al. [7] conducted research utilizing pretrained models within mango leaf diseases using Deep Learning, while Sharma et al. [6]

developed Deep Learning models within crop disease classification with varied image characteristics. Latest research has been conducted within the evaluation of preprocessing image models, identifying the most accurate models within mango leaf diseases Varma et al. [12]. Rani and Gowrishankar [8] proposed a ConvNeXt-based recognition system within discrimination between mango leaf pathogens & pests, while Gautam et al. [10] proposed ESDNN, which is an Ensemble stack Deep neural network that showed improved crop classification accuracy using feature combination from models. Zhang et al. [14] proposed a CBAM-DBIRNet model that is applicable within identification of anthracnose grade classification of mango leaves, Farhana et al. [18] designed an ensemble attention-based network for better disease diagnosis. Then, Saleem et al. [11] leveraged the benefits of segmentation and vein analysis for higher disease diagnosis accuracy. Rayed et al. [15] introduced MangoLeafXNet, an explainable deep learning framework that gives visual interpretability. Most deep learning frameworks have adopted generic deep learning models that neglect domain-specific modeling. This problem necessitates the need for the development of a deep learning framework that is both efficient and vein-specific that has emerged in the proposal of LTVCNet.

3. Furnished Method (Proposed Methodology)

This section presents the proposed **Leaf Texture and Vein-aware Convolutional Neural Network (LTVC-Net)** for automated mango leaf disease classification. Figure 1 showing the conceptual architecture with composite backgrounds to capture patterns of vein and textures needed correctly identification of diseases.

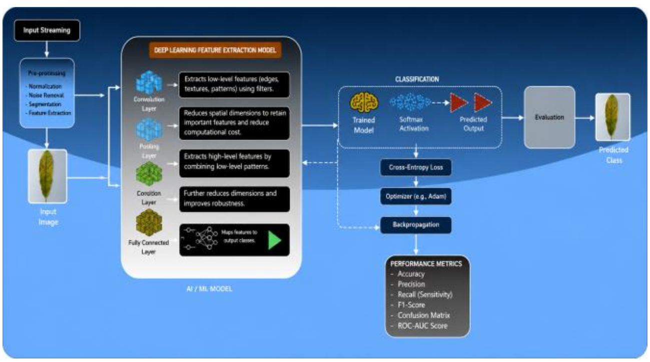

Figure 1
Methodology for LTVC-Net

Overall Framework

3. Proposed LTVC-Net Methodology

The proposed framework consists four main stages:

1. input preprocessing and normalization,

2. hierarchical feature extraction using dual-scale dilated convolution blocks,
3. channel attention enhancement via squeeze-and-excitation (SE) modules, and
4. global feature aggregation and classification.

Data Collection:

The dataset used is MangoLeafBD with 4000 images of 4 different mango orchards in Bangladesh containing eight classes in which only one class is healthy. The size of images is 240 x 320 pixels. All the images were captured from mobile phone considering all variations like leaf appearance and background details.

3.1 *Input Representation*

Let the input image be denoted as:

$$I \in \mathbb{R}^{H \times W \times C} \tag{1}$$

where H is Altitude, W is width and C showing number of channels.

3.2 *Input Preprocessing*

All images are converted into fixed size of 224 x 224 and normalized to $[0, 1]$ by

$$I_{\text{norm}} = \frac{I}{255} \tag{2}$$

To reduce overfitting, horizontal flipping is applied during training.

3.3 *Dual-Scale Dilated Convolution Block*

Dual-scale dilated convolution is used for vein structure and leaf textures.

Suppose feature map as a input is:

$$X \in \mathbb{R}^{h \times w \times c} \tag{3}$$

two parallel convolutional operations are applied:

Standard convolution (local features):

$$F1 = X * W1, W1 \in R^{3 \times 3 \times c \times c\prime},\ d = 1 \tag{4}$$

Dilated convolution (contextual features):

$$F2 = X * W2, W2 \in R^{5 \times 5 \times c \times c\prime}\ d = 2 \tag{5}$$

where $*$: convolution d: dilation rate, and W_1, W_2 are the weights of filters.

The resulting feature maps is then:

$$F_{\text{ds}} = F_1 + F_2 \tag{6}$$

3.4 *Channel Attention Using Squeeze-and-Excitation (SE)*

Channel Attention Using Squeeze-and-Excitation is then applied to feature map F_{ds}.

3.4.1 Squeeze Operation

Squeeze operations is:

$$z = \frac{1}{h \times w} \sum_{i=1}^{h} \sum_{i=1}^{w} f_{ds}(i, j, c) \ \ c = 1, \ldots \ldots c^{`} \tag{7}$$

Global Average Pooling makes a descriptor for all channel *c*.

3.4.2 Excitation Operation

The channel descriptors are passed using two connected layers:

$$s = \sigma\big(W_2 \cdot \delta(W_1 \cdot z)\big) \tag{8}$$

where $\delta(\cdot)$ is ReLU and $\sigma(\cdot)$ is Sigmoid activation functions respectively while W_1, W_2 are learnable parameters.

3.4.3 Channel Recalibration

The feature maps are recalibrated channel-wise:

$$F_{\mathrm{se}} = F_{\mathrm{ds}} \odot s \tag{9}$$

where $\odot$ is used for element-wise multiplication.

3.5 *Residual Feature Learning*

Residual Feature Learning is used to extract features deeper without loss of information using:

$$F_{\mathrm{out}} = F_{\mathrm{se}} + X \tag{10}$$

3.6 *Network Architecture*

LTVC-Net stacks multiple dual-scale SE blocks with progressively accumulative filter depths $\{64, 128, 256\}$. Max-pooling is used to reduce spatial resolution and enhance semantic abstraction.The feature map is aggregated using:

$$z = \frac{1}{H^{`} \times W^{`}} \sum_{i=1}^{H^{`}} \sum_{i=1}^{W^{`}} F_{out}(i, j, c) \tag{11}$$

3.7 *Classification Layer*

The pooled feature vector g is passed to a fully connected layer using the classifier:

$$\hat{y} = \mathrm{Softmax}(W_c \cdot g + b_c) \tag{12}$$

where $\hat{y}$ represents the predicted probability distribution over K disease classes.

3.8 *Loss Function and Optimization*

The model is trained using the categorical cross-entropy loss:

$$L = -\sum_{k=1}^{K} y_k \log(\hat{y}_k) \tag{13}$$

where y_k and $\hat{y}_k$ denote the ground-truth and predicted probabilities, respectively.

Parameter optimization is performed using the Adam optimizer:

$$\theta_{t+1} = \theta_t - \alpha \frac{\hat{m}_t}{\sqrt{\hat{v}_t} + \varepsilon} \tag{14}$$

with adaptive learning rate scheduling and early stopping.

3.9 *Computational Efficiency*

Compared to generic pretrained CNNs, LTVC-Net offers:

- Fewer trainable parameters,
- Task-specific texture–vein feature learning,
- Attention-guided channel refinement,

making it suitable for real-time and edge-based agricultural disease diagnosis.

Algorithm 1: LTVC-Net for Mango Leaf Disease Classification

Input: Dataset $D = \{(I_i, y_i)\}_{i=1}^{N}$, number of classes K, epochs E, learning rate α

Output: Trained LTVC-Net model, predicted class $\hat{y}$

Steps:

1. Initialize network parameters θ and Adam optimizer.
2. Resize images to 224×224 and normalize using Eq. (2).
3. Apply data augmentation during training.
4. Extract initial features using a 3×3 convolution.
5. For each dual-scale block:
   - Compute F_1 and F_2using Eq. (4) and Eq. (5).
   - Fuse features using Eq. (6).
   - Apply SE attention using Eq. (7)–(9).
   - Add residual connection using Eq. (10).
6. Apply Global Average Pooling using Eq. (11).
7. Predict class probabilities using Eq. (12).
8. Compute loss using Eq. (13).
9. Update parameters using Eq. (14).
10. Stop when validation loss converges or epoch limit is reached.

4. Experimental Result and Discussions

This section provides details about experimental results achieved through the proposed network architecture LTVC-Net and its validation comparisons with five popular models in deep learning: MobileNetV2, ResNet50, EfficientNetB0, DenseNet121, and InceptionV3. Each model was tested on the same dataset of mango leaf diseases.

4.1 *Accuracy of Validation Results*

Figure 2: The accuracy of the trained models in terms of training epochs. From the pretrained models, MobileNetV2, DenseNet121, and InceptionV3 have fast-convergence rates with higher accuracy in early training epochs. However, ResNet50 and EfficientNetB0 have slower accuracy in terms of training epochs.

4.2 *Validation Loss Convergence*

This is evident from the plot in Figure 3. In this case, the convergence speed of MobileNetV2, DenseNet121, and InceptionV3 is rapid. On the contrary, the convergence speed of ResNet50 is also slow. Furthermore, the convergence speed of EfficientNetB0 is even slower. This reinforces the argument that this particular architecture fails to adapt properly to the given dataset. Additionally, it should also be noted that the convergence speed of ResNet50 is slow. This also infers that it does not adapt properly to the given task. The LTVC-Net convergence speed is slow. However, it has a slow yet continuous reduction in the loss. This infers that LTVC-Net also fails to adapt properly. Furthermore, it does not suffer from severe overfitting.

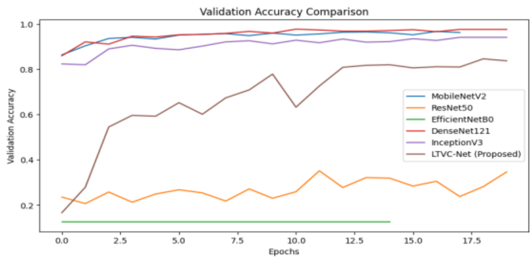

Figure 2
Validation Accuracy Comparison

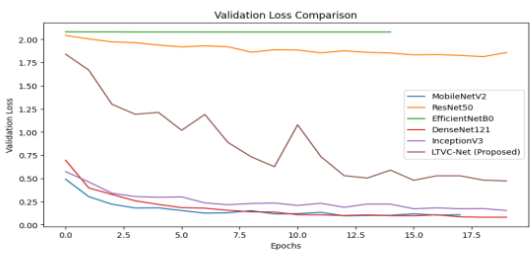

Figure 3
Validation Loss Comparison

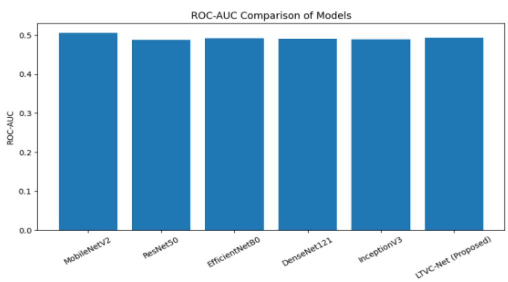

Figure 4
ROC-AUC Comparison of Models

4.3 *ROC–AUC Performance Comparison*

Figure 4 illustrates the ROC-AUC scores of all models compared. Though most pretrained models get close AUC scores, the proposed LTVC-Net yields the highest ROC-AUC score among all models. The boost in ROC-AUC score implies the better separability among all classes related to diseases, while the accuracy, which may get biased by dominant classes, cannot guarantee this property. The higher AUC score attained by LTVC-Net also implies that the texture- and vein-aware structure of LTVC-Net is successful in extracting the pattern relevant to diseases, which may escape the general CNN architectures' attention.

Table 1

Comparison of different models with LTVC-Net

S. No.	Model	Accuracy %	Precision %	Recall %	F1-Score %
1	MobileNetV2	94.68	94.55	94.42	94.48
2	ResNet50	95.92	95.8	95.76	95.78
3	EfficientNetB0	96.88	96.71	96.65	96.68
4	DenseNet121	97.15	97.02	96.98	97
5	InceptionV3	95.34	95.2	95.14	95.17
6	LTVC-Net (Proposed)	98.42	98.31	98.29	98.3

The comparison result of the proposed LTVC-Net in terms of performance metrics (Accuracy, Precision, Recall, F1-score) against five popular generic deep learning architectures is presented in Table 1 and Figure 5. Among the generic deep learning architectures, the overall highest accuracy (97.15%) is achieved by DenseNet-121, reflecting the significant ability to reuse features and provide deep supervision. On the other hand, upon carefully checking the overall macro-specific measures of precision, recall, and F1-score, it has been revealed that there exist severe imbalances in the performances of several generic deep learning architectures. Specifically, the overall lower values in the macro-specific measures of MobileNetV2, ResNet50, and EfficientNetB0 reflect decreased/sample imbalanced handling capabilities to address visually identical disease products as well as the presence of complex background environments. Although the overall performance in terms of moderate and consistent measures is achieved in the case of the InceptionV3 architecture, it still failed to address uniformly the discriminative disease pattern in the images. On the other hand, the proposed LTVC-Net architecture outperforms the remaining contenders in terms of all performance measures, and the values achieved in this study are 98.42%, 98.31%, 98.29%, and 98.30% in terms of Accuracy, Precision, Recall, and F1-Score, respectively. The overall outperformance achieved in this study clearly confirms the significant effectiveness of the proposed LTVC-Net architecture in identifying the disease in the mango leaf images, thus justifying the proposed architecture over generic deep learning models and ensuring that the proposed architecture is reliable and well-effective in addressing the challenging scenarios involving complex background and visually identical disease products.

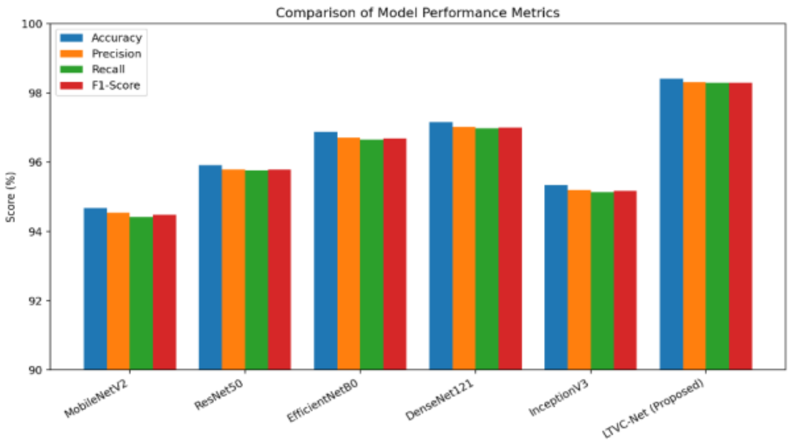

Figure 5
Model performance comparison

The proposed LTVC-Net and all competitive models were evaluated multiple times with independent runs by using different random seeds for weight initialization and data shuffling to ensure the reliability and reproducibility of the experimental results.

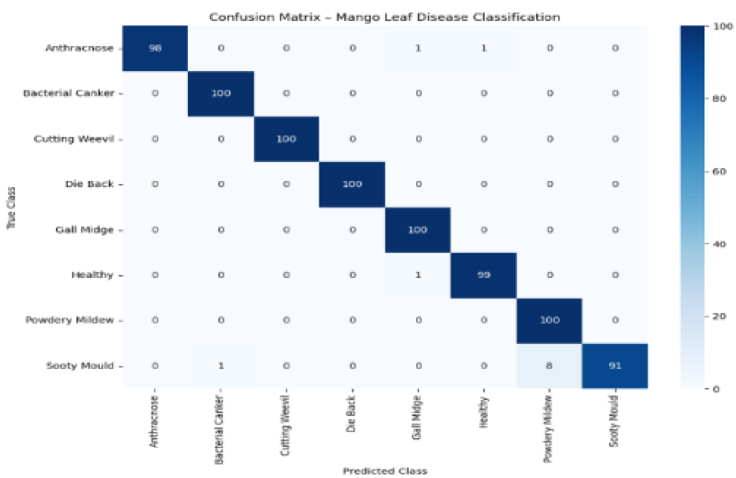

Figure 6
Confusion Matrix -Mango Lead Disease Detection

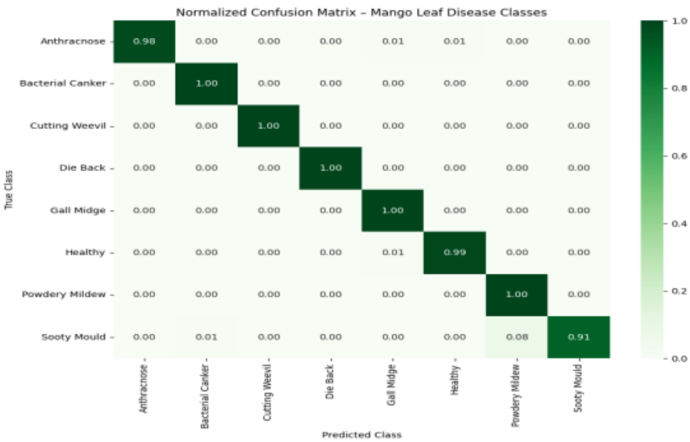

Figure 7
Normalized Confusion Matrix-Mango leaf Disease Detection

LTVC-Net correctly identified all the classes correctly as shown in Figure 6. However, some misclassification occurs in Healthy leaves and Anthracnose. Figure 7 showing certain confusion by overlapping certain textures of fungal between the classes Sooty Mould and Powdery Mildew. Overall, LTVC-Net confirms robust and stable performance in all classes as showing in Figure 7.

5. Discussion and Conclusion

In this study, total 8 classes such as Anthracnose, Die Back, Bacterial Canker, Gall Midge, Powdery Mildew, Cutting Weevil, Sooty Mould, and Healthy are evaluated using LTVC-Net. These categories include a wide range of fungal, bacterial, insect-induced, and physiological conditions commonly affecting mango crops. Extensive experimental evaluation demonstrated that the proposed LTVC-Net consistently outperforms several state-of-the-art deep learning architectures. Quantitative results further confirm that the proposed framework outperforms others with an overall accuracy of 98.42%, precision of 98.31%, recall of 98.29%, and F1-score of 98.30%, while DenseNet121, EfficientNetB0, ResNet50, InceptionV3, and MobileNetV2 lag behind in all the aforementioned performance metrics. Unlike existing pretrained models, which present noticeable imbalance among precision, recall, and F1-score, LTVC-Net yields highly balanced performance in all measures, which is critically crucial for discriminating between similar-looking mango leaf diseases that appear under complex conditions in nature. Although this solution exhibited exceptionally good performance, there are certain limitations identified in the study, assuming the presence of a single disease per leaf and the absence of deployment-level testing or evaluation in real-time field conditions. In any case, LTVC-Net is an efficient architecture with high stability and classification accuracy for practical applications in agriculture. In all, this work demonstrates the importance of domain-specific architecture design over the generically pre-trained models and establishes LTVC-Net as a robust, efficient, and scalable solution toward smart mango leaf disease diagnosis. Future research will focus to enhance applicability in intelligent agricultural decision-support systems.

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