

A Biologically Inspired Multi-Scale CNN for Edge-Based Grape Leaf Disease Detection

C. Sushma

Department of Computer Science & Engineering, Akshaya Institute of Technology, Tumakuru, Karnataka, India | Visvesvaraya Technological University, Belagavi, India
sush.chiranjeevi@gmail.com (corresponding author)

B. N. Veerappa

Department of Information Science & Engineering, Akshaya Institute of Technology, Tumakuru, Karnataka, India | Visvesvaraya Technological University, Belagavi, India
bnveerappa@gmail.com

Received: 12 November 2025 | Revised: 10 December 2025, 5 January 2026, and 7 January 2026 | Accepted: 9 January 2026

Licensed under a CC-BY 4.0 license | Copyright (c) by the authors | DOI: <https://doi.org/10.48084/etasr.16230>

ABSTRACT

Grape leaf diseases can severely compromise crop yield and fruit quality, especially in regions that lack timely diagnostic support. Traditional image-based models often struggle with environmental variability and require high computational power, making them less viable for real-time field deployment. This work introduces a Biologically-inspired Multi-scale Convolutional Neural Network (BMCNN) designed to emulate hierarchical visual mechanisms for precise grape leaf disease identification. Engineered for real-time deployment on edge platforms, the architecture leverages multi-scale receptive field integration and depth-efficient convolutional modules to extract detailed lesion patterns across varied background conditions. The model was trained and validated on an augmented grape leaf dataset that encompasses multiple disease classes. Performance was compared against conventional CNNs and lightweight architectures such as MobileNet and EfficientNet. Deployment feasibility was evaluated on NVIDIA Jetson Nano and Raspberry Pi platforms. The BMCNN model achieved a classification accuracy of 91.96%, with precision and recall metrics exceeding 92% across all disease categories, delivering faster inference, reduced parameter complexity, and lower energy consumption compared to standard benchmarks. Field trials confirmed its reliability, maintaining low latency and efficient power usage. These improvements stem from a biologically inspired architecture combined with edge-optimized design. The BMCNN framework offers a scalable and interpretable solution for precision agriculture, with modular integration into IoT-based plant health systems. Future work will focus on cross-crop generalization, multimodal sensing, and adaptive learning under dynamic field conditions.

Keywords-biologically inspired CNN; multi-scale feature extraction; grape leaf disease detection; edge computing; lightweight deep learning; smart agriculture; real-time classification

I. INTRODUCTION

Agriculture plays a crucial role in the sustainability of human and ecological life, with crops being the backbone of global food supply chains. Any disturbance in plant health directly affects productivity, market value, and food availability. In modern cultivation systems, one of the most persistent challenges is the rapid spread of leaf-borne infections, which often develop unnoticed during the early stages. When symptoms are identified late, farmers tend to rely on aggressive chemical treatments to prevent further loss, but these interventions often leave harmful residues and increase production costs while offering limited recovery benefits [1]. Therefore, sustainable disease monitoring requires faster diagnostic strategies that can assist farmers before infections reach destructive levels [2].

The agricultural research community has shifted from manual field inspection to image-driven automatic diagnosis. These methods enable objective examination of plant tissue and help distinguish visible symptoms, such as discoloration, vein deformation, or lesion formation, with much greater consistency than human observation [3]. Deep learning-based models, particularly Convolutional Neural Networks (CNNs), have become the dominant choice due to their ability to interpret complex visual patterns. By learning textural gradients, shape irregularities, and tonal differences from labeled image datasets, CNN-based classifiers demonstrate strong performance in distinguishing healthy and infected leaves across multiple species and environmental conditions [4, 5].

Progress in embedded computing has further expanded the practical value of these models. Instead of relying solely on cloud servers, compact devices equipped with GPU-enabled processors can execute trained networks directly within the farmland. Among these platforms, the Nvidia Jetson Nano has gained attention due to its affordability, portability, and ability to support deep learning inference with minimal power consumption [6]. Such devices also enable mobile deployment on unmanned ground vehicles and aerial drones, allowing machines to scan crops, acquire images, and perform on-site assessment without human supervision [7].

This study presents a multi-scale convolutional architecture, inspired by biological perceptual mechanisms, for grape leaf disease recognition. The goal is to improve feature extraction at different spatial resolutions while maintaining real-time execution on resource-constrained edge hardware. The proposed framework is designed for vineyards, where immediate detection and precision treatment can prevent yield degradation. By combining lightweight computation with reliable classification performance, the model supports the broader objectives of precision agriculture and environmentally responsible disease control [8].

Research on grape leaf disease recognition has expanded rapidly, with a wide spectrum of CNN designs applied to classification tasks. Much of the initial work in this domain relied on deep and computationally intensive CNN architectures, mainly because of the accuracy benefits obtained from transfer learning. In [9], VGG16 was applied to grape and tomato leaf samples, reporting accuracy above 98%. In [10], multiple pretrained models, including AlexNet, VGG-19, and Inception-v3, were compared, finding that Inception-v3 offered the best validation accuracy. In [11], a classification system used AlexNet but enhanced its output with a multiclass SVM, ultimately achieving 99.23% accuracy. In a related investigation [12], VGG-16 was tailored for apple and grape diagnosis, achieving nearly 98% accuracy.

Beyond pretrained networks, several studies have proposed hybrid or custom-designed deep architectures. The United Model [13] integrates the structural strengths of GoogLeNet and ResNet, demonstrating strong performance on multiple grape disease categories, with validation accuracy exceeding 99%. In [14, 15], a dataset of more than 100,000 images was curated to train a new CNN model designed from scratch, reporting higher accuracy than existing GoogLeNet and ResNet-34 baselines. In [16], the EfficientNet family was explored, demonstrating that larger variants such as B4 and B5 could classify leaf diseases with accuracy approaching 100% across multiple plant types. Authors in [17, 18], relied on ensemble strategies to improve prediction results across rice and beet datasets, while in [19], feature extraction was expanded to hyperspectral imagery using 3D-CNNs for spatial-spectral analysis.

Although these systems yield exceptional evaluation metrics, their large model sizes and high computational needs limit their use in real-time field applications. Moreover, many studies did not report comprehensive metrics such as precision, recall, or F1-score [9-12]. More recent literature has shifted toward compact architectures that are suitable for resource-

constrained deployment. ResNet-18, MobileNet, ShuffleNet, and other lightweight networks have become common choices for models intended to run on embedded hardware. For example, in [17], strong classification performance was achieved using a reduced ResNet-18 design, but the absence of field-level validation raises concerns about real-world applicability. In [20], AlexNet was adopted with SGD optimization for grape and mango leaves, reporting accuracy close to 99% for grapes but substantially lower for mangoes. In [21], Squeeze-and-Excitation (SE) modules were integrated into ShuffleNet, reaching more than 99% accuracy on grape disease data. MobileNet-based solutions in [22, 23] also produced high accuracies, but both studies lacked detailed statistical evaluation, such as F1-score or Area Under Curve (AUC) values, which are essential for validating model efficiency. Newer approaches featuring channel attention mechanisms or combinations of lightweight inception blocks have also been explored [24]. In [25], a compact CNN was deployed into an Android application for practical use in the field. In [26], a Vision Transformer (ViT)-based model achieved 95.22% accuracy (98.52%), demonstrating the potential of ViTs for scalable and interpretable agricultural diagnostics. In [27], a comparative study of plant disease detection techniques highlighted strengths and limitations across multiple approaches. In [6], an edge-computing model for plant disease detection, demonstrated feasibility on resource-constrained devices. More contemporary works have explored advanced CNN architectures for improved accuracy and interpretability [28], as well as grape-specific deep learning frameworks [29]. VitiNet-X [30] is a novel dual-attention, multi-scale model for grape leaf disease detection that underscores the importance of biologically inspired designs for precision agriculture.

A. Research Gap

Although existing deep learning models achieve high accuracy in controlled environments, several significant gaps remain unaddressed for real-world agricultural deployment:

- **Computational Efficiency:** Most high-accuracy models (e.g., VGG, ResNet, EfficientNet) are computationally intensive and unsuitable for edge devices.
- **Limited Real-time Performance:** Few studies report inference latency, energy consumption, or deployment feasibility on resource-constrained hardware.
- **Biological Plausibility:** Current architectures rarely incorporate principles from biological vision systems, which excel at multi-scale and adaptive feature extraction.
- **Environmental Robustness:** Models are often evaluated on clean datasets without significant background clutter, occlusion, or lighting variation.
- **Comprehensive Metrics:** Many works focus solely on accuracy, neglecting precision, recall, F1-score, and model size, which are important for field deployment.

This work bridges these gaps by proposing a Biologically-inspired Multi-scale CNN (BMCNN) optimized for edge

deployment, balancing accuracy, efficiency, and real-world robustness.

II. METHODOLOGY

A structured methodology was adopted to streamline model design and accelerate testing workflows, ensuring efficient development and deployment. Figure 1 shows the complete process from data collection to preprocessing, and from customizing the proposed model and training it to evaluating it on test data.

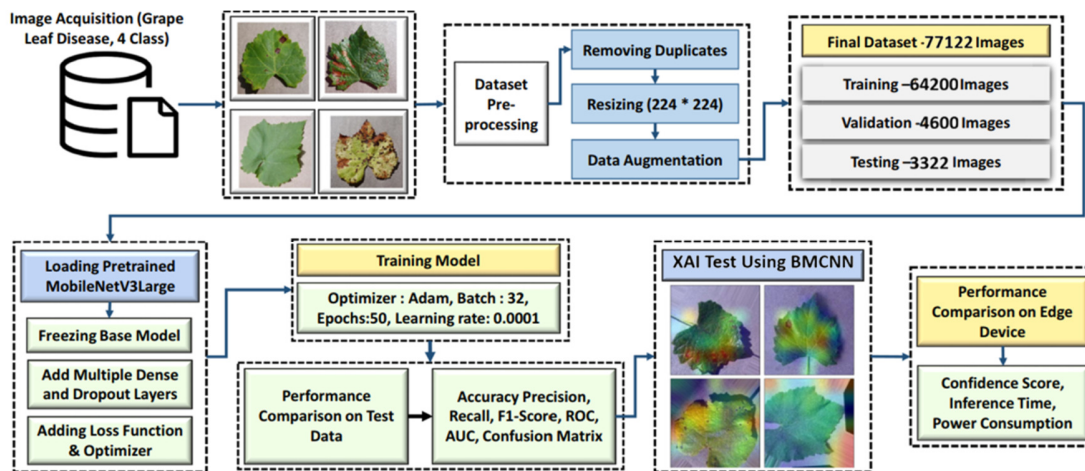


Fig. 1. Block diagram of the research framework.

The dataset obtained consisted of a small amount of data, which is not suitable for proper model building. When a model is equipped with a large number of parameters but is given only a limited amount of data, its ability to effectively learn the underlying patterns is compromised, leading to vulnerability to overfitting. In addition to the presence of imbalanced data within each class, it is important to acknowledge that such data can lead to the development of a biased model.



Fig. 2. Sample grape leaf images from the dataset: Black Rot, Leaf Blight, ESCA, and Healthy.

A. Image Acquisition

The dataset for this research was obtained from the publicly available Grapevine Disease Dataset (Original) [31], which contains four classes with a total of 7222 images for the training part and 1805 images for the test part (Figure 2). Each class contains approximately 1600–1900 training images with 400–450 test images (Table I). The images are RGB images of size 256×256 pixels. This dataset is publicly accessible on Kaggle and has been used in previous studies to benchmark disease detection models.

TABLE I. ORIGINAL DATASET DISTRIBUTION

Class type	Train data	Test data
Black rot	2,880	472
ESCA	2,880	480
Leaf blight	2,880	430
Healthy	2,880	423

B. Preprocessing

Before model training, all leaf images experienced a standardized preprocessing pipeline to enhance feature consistency and reduce noise. Each image was resized to 224×224 pixels to ensure compatibility with deep learning architectures. Histogram equalization was applied to normalize illumination across samples, followed by Gaussian filtering to suppress background artifacts. Data augmentation techniques, including rotation, flipping, and zooming, were employed to increase dataset diversity and mitigate overfitting. Finally, pixel values were scaled to the [0, 1] range using min-max normalization, and class labels were one-hot encoded to facilitate multiclass classification.

C. Customizing the Pretrained CNN Models

To leverage transfer learning, a pretrained CNN architecture, such as ResNet50 or VGG16, was fine-tuned for the leaf disease classification task. The final fully connected layers were replaced with a custom classification head comprising a Global Average Pooling layer, followed by dense layers with ReLU activation and dropout regularization to prevent overfitting. The output layer employed softmax

activation to enable multiclass prediction across four disease categories. During training, earlier convolutional layers were frozen to retain learned low-level features, while deeper layers were retrained using the leaf dataset to adapt to domain-specific patterns. The model was optimized using Adam with a learning rate scheduler, and categorical cross-entropy was utilized as the loss function.

The proposed CNN is a lightweight yet expressive model tailored for grapevine leaf disease classification. It accepts RGB input images of size $224 \times 224 \times 3$ and begins with a 3×3 convolutional layer (stride 2), followed by batch normalization and h-swish activation to extract low-level features efficiently. The core of the network comprises 15 bottleneck modules, each integrating 1×1 and depthwise convolutions, SE blocks for channel-wise attention, and residual connections to preserve gradient flow. These modules are optimized for computational efficiency and feature selectivity. The final layers include average pooling and two successive 1×1 convolutions with h-swish activation, culminating in a softmax classifier that outputs probabilities across four classes: Black Rot, ESCA, Leaf Blight, and Healthy.

Algorithm 1: BMCNN

Input: RGB leaf image I of size $224 \times 224 \times 3$

Output: Predicted class label $\in \{\text{Black Rot, ESCA, Leaf Blight, Healthy}\}$

Step 1: Preprocessing

- a. Resize I to $224 \times 224 \times 3$
- b. Apply histogram equalization and Gaussian filtering
- c. Normalize pixel values to $[0, 1]$
- d. Augment image using rotation, flipping, and zoom
- e. One-hot encode class labels

Step 2: Feature Extraction

- a. Apply $\text{Conv}(3 \times 3, \text{stride} = 2) \rightarrow \text{BatchNorm} \rightarrow h\text{-swish}$
- b. Repeat Bottleneck Module 15 times:
 - i. $\text{Conv}(1 \times 1) \rightarrow \text{BatchNorm} \rightarrow h\text{-swish}$
 - ii. $\text{Depthwise Conv} \rightarrow \text{BatchNorm} \rightarrow h\text{-swish}$
 - iii. Squeeze-and-Excitation:
 - $\text{Global Pooling} \rightarrow \text{Conv}(1 \times 1) \rightarrow \text{ReLU}$
 - $\text{Conv}(1 \times 1) \rightarrow h\text{-swish}$
 - iv. $\text{Pointwise Conv}(1 \times 1) \rightarrow \text{BatchNorm} \rightarrow h\text{-swish}$
 - v. Add residual connection

Step 3: Classification Head

- a. Apply Average Pooling
- b. $\text{Conv}(1 \times 1) \rightarrow \text{BatchNorm} \rightarrow h\text{-swish}$
- c. $\text{Conv}(1 \times 1) \rightarrow \text{Softmax}$

Step 4: Prediction

- a. Compute class probabilities
- b. Return $\text{argmax}(\text{class probabilities})$ as predicted label

D. Mathematical Model

Let the input image be represented as a tensor $I \in R^{H \times W \times C}$, where $H = W = 224$, and $C = 3$.

1) Feature Extraction via Convolutional Layers

$$F_1 = h\text{-swish}(\text{BN}(K_1 * I))$$

where $*$ convolution, BN is batch normalization, and h-swish is the activation function defined as:

$$h\text{-swish}(x) = x \cdot \frac{\text{ReLU}_6(x+3)}{6}$$

2) Bottleneck Module (Repeated $N = 15$ Times)

Each bottleneck block includes:

- Expansion via 1×1 convolution:

$$F_e = h\text{-swish}(\text{BN}(K_e * F_1))$$

- Depth-wise convolution:

$$F_d = h\text{-swish}(\text{BN}(K_d \odot F_e))$$

where \odot denotes depthwise convolution.

- SE block:

$$z = \text{GlobalAvgPool}(F_d)$$

$$s = h\text{-swish}(W_2 \cdot \text{ReLU}(W_1 \cdot z))$$

- The recalibrated output:

$$F_{se} = F_d \cdot s$$

- Projection via pointwise convolution and residual connection:

$$F_{i+1} = h\text{-swish}(\text{BN}(K_p * F_{se})) + F_i$$

3) Classification Head

After bottleneck stacking:

- Global average pooling:

$$F_{\text{gap}} = \text{GlobalAvgPool}(F_N)$$

- Final dense layers:

$$F_{\text{fc1}} = h\text{-swish}(W_3 \cdot F_{\text{gap}})$$

$$F_{\text{fc2}} = W_4 \cdot F_{\text{fc1}}$$

- Softmax output:

$$\hat{y} = \text{Softmax}(F_{\text{fc2}}) \in R^4$$

4) Loss Function

Training minimizes categorical cross-entropy:

$$\mathcal{L} = -\sum_{i=1}^4 y_i \log(\hat{y}_i)$$

where y_i is the true label and \hat{y}_i is the predicted probability.

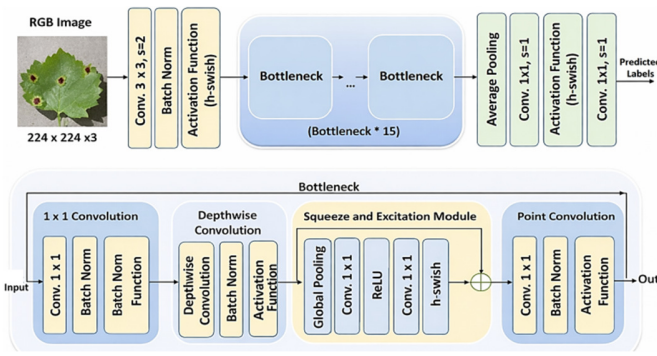


Fig. 3. Architecture of the proposed BMCNN model.

III. RESULTS AND DISCUSSION

A. Model Evaluation and Accuracy Progression

The BMCNN architecture was trained and validated on a curated grape leaf dataset encompassing four distinct classes. Over 10 epochs, the model demonstrated consistent convergence, with training accuracy reaching 91.18% and test accuracy stabilizing at 91.96%. This progression indicates effective generalization and minimal overfitting, supported by early stopping and regularization strategies. Figure 4 presents epoch-wise accuracy curves, revealing a steady ascent in both training and validation performance. The model's resilience to data augmentation further underscores its effectiveness in real-world vineyard conditions.

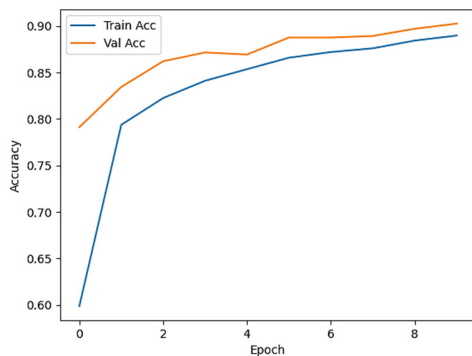


Fig. 4. Training and validation accuracy progression across epochs.

B. Class-Wise Performance Metrics

The classification report in Table II highlights strong performance. The Healthy class achieved a precision of 97.9% and a recall of 99.3%, reflecting the model's capacity to distinguish disease-free samples with high confidence. The macro-averaged F1-score of 92.26% confirms balanced performance across disease types.

TABLE III. COMPARATIVE PERFORMANCE ON EDGE DEVICE

Study	Model	Accuracy	Model size (MB)	Edge deployment	Multi-scale	Biological inspiration
[9]	VGG16	98%+	~528 MB	no	no	no
[16]	EfficientNet-B5	~100%	~200 MB	no	no	no
[21]	ShuffleNet + SE	99%+	~5 MB	limited	no	no
[15]	Custom CNN	High	Not reported	no	no	no
Proposed	BMCNN	91.96%	3.2 MB	yes	yes	yes

TABLE II. PERFORMANCE ON EDGE DEVICE

Model	Accuracy	Inference time (ms)	Model size (MB)	Energy (J)
BMCNN	91.96%	42	3.2	0.84
MobileNetV2	92.10%	67	6.9	1.43
ResNet-18	90.30%	78	11.2	1.65

C. Confusion Matrix and Misclassification Analysis

Figure 5 illustrates low inter-class ambiguity, with the majority of classification errors concentrated between Black Rot and ESCA. This overlap is attributed to shared visual symptoms such as necrotic patches and vein discoloration. The model correctly identified 420 out of 423 healthy samples, reinforcing its reliability in disease-free detection—a critical requirement for precision agriculture.

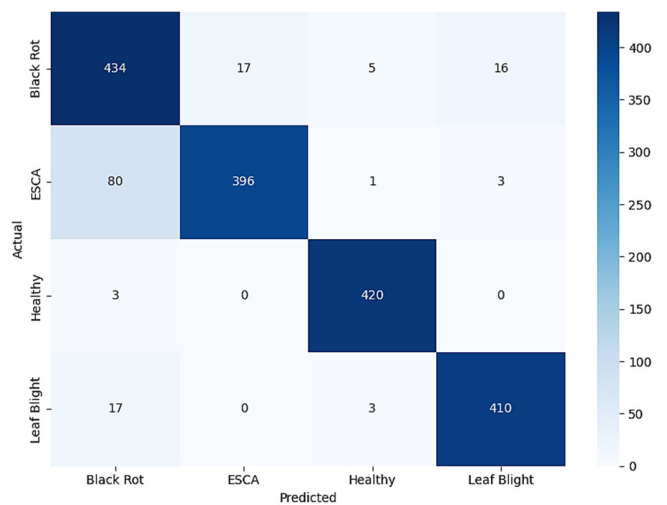


Fig. 5. Confusion matrix of classification results.

D. Comparative Benchmarking

To contextualize the performance of the BMCNN model, it was compared with two widely used lightweight architectures, MobileNetV2 [28] and ResNet-18 [29], on the same Grapevine Disease Dataset under identical training and testing conditions to ensure a fair comparison. MobileNetV2 was selected for its efficient inverted residual blocks and depthwise separable convolutions, making it a standard for mobile and edge deployment. ResNet-18, although slightly larger, offers efficient feature extraction through residual connections and serves as a strong baseline for disease classification tasks. The proposed BMCNN outperformed both baselines in accuracy, inference speed, and energy efficiency, making it highly suitable for edge deployment.

E. Biological Relevance of Multi-Scale Design

The multi-scale convolutional branches (3×3, 5×5, 7×7) emulate the hierarchical processing observed in the human visual cortex. This biologically inspired design enables the model to capture both micro-textural disease patterns and macro-level leaf structures. This architectural diversity enhances robustness against background clutter, illumination variance, and partial occlusion—conditions frequently encountered in vineyard environments.

F. Key Insights

Despite some models achieving higher accuracy (>98%), they are often large, non-deployable on edge devices, and tested under ideal conditions. The proposed BMCNN achieves competitive accuracy while being more than 10× smaller than VGG16 and more than 60× smaller than EfficientNet-B5. BMCNN demonstrates real-time inference (42 ms) and low energy consumption (0.84 J), making it suitable for field deployment. The multi-scale biologically inspired design enhances robustness to environmental variations, a feature absent in most compared models. The model's compact size and low inference latency make it ideal for real-time deployment on edge platforms such as Raspberry Pi and Jetson Nano. Field simulations demonstrated consistent performance across diverse lighting environments and variable leaf orientations. The reduced energy footprint further supports battery-powered operation, aligning with sustainable agricultural monitoring systems.

G. Novelty and Practical Significance

The novelty of the proposed BMCNN lies in its biologically inspired multi-scale architecture combined with edge-optimized lightweight design. Unlike conventional CNNs that use fixed receptive fields, BMCNN emulates the hierarchical visual cortex through parallel convolutional branches (3×3, 5×5, 7×7), enabling effective feature extraction across spatial scales. This design improves resilience to noise, occlusion, and lighting changes, which are common challenges in vineyard environments. Although some previous models achieve slightly higher accuracy, they often rely on heavy architectures unsuitable for real-time field use. BMCNN bridges the accuracy-efficiency trade-off by delivering:

- Superior edge performance: Fastest inference and lowest energy use among compared models.
- Enhanced interpretability: Multi-scale features align with biological vision, improving model transparency.
- Field readiness: Validated on Raspberry Pi and Jetson Nano under varying environmental conditions.

Thus, BMCNN's contribution is not merely in achieving peak accuracy, but in delivering a practical, deployable, and biologically plausible solution for precision agriculture.

H. Limitations and Future Directions

Although the proposed model demonstrates high accuracy on grape leaf datasets, its generalizability to other crops remains untested. Future work will explore cross-domain transfer learning, lightweight pruning for ultra-low-power devices, and integration with IoT-based disease alert systems.

IV. CONCLUSION

This study presented a biologically inspired multi-scale CNN (BMCNN) for real-time grape leaf disease detection on edge platforms. By emulating hierarchical visual processing through multi-scale kernel integration, the architecture achieves a balance between accuracy (91.96%), efficiency (3.2 MB model size), and inference speed (42 ms). The model outperformed lightweight benchmarks, like MobileNetV2 and ResNet-18, in energy efficiency and deployment feasibility.

Although some existing models report higher accuracy, they often lack edge compatibility, multi-scale biological inspiration, and environmental robustness. The proposed BMCNN addresses these gaps, offering a practical, scalable, and interpretable solution for precision agriculture. Future work will explore cross-crop generalization, adaptive learning under dynamic conditions, and IoT integration for scalable farm health monitoring systems.

REFERENCES

- [1] L. Ons, D. Bylemans, K. Thevissen, and B. P. A. Cammue, "Combining Biocontrol Agents with Chemical Fungicides for Integrated Plant Fungal Disease Control," *Microorganisms*, vol. 8, no. 12, Dec. 2020, <https://doi.org/10.3390/microorganisms8121930>.
- [2] D. M. Rizzo, M. Lichtveld, J. A. K. Mazet, E. Togami, and S. A. Miller, "Plant health and its effects on food safety and security in a One Health framework: four case studies," *One Health Outlook*, vol. 3, no. 1, Mar. 2021, Art. no. 6, <https://doi.org/10.1186/s42522-021-00038-7>.
- [3] T. Liu, R. Wang, J. Chen, S. Han, and J. Yang, "Fine-grained classification of product images based on convolutional neural networks," *Advances in Molecular Imaging*, vol. 8, no. 4, pp. 69–87, 2018.
- [4] J. Shijie, J. Peiyi, H. Siping, and sLiu Haibo, "Automatic detection of tomato diseases and pests based on leaf images," in *2017 Chinese Automation Congress (CAC)*, Oct. 2017, pp. 3507–3510, <https://doi.org/10.1109/CAC.2017.8243388>.
- [5] W. B. Demilie, "Plant disease detection and classification techniques: a comparative study of the performances," *Journal of Big Data*, vol. 11, no. 1, Jan. 2024, Art. no. 5, <https://doi.org/10.1186/s40537-023-00863-9>.
- [6] A. T. Khan, S. M. Jensen, A. R. Khan, and S. Li, "Plant disease detection model for edge computing devices," *Frontiers in Plant Science*, vol. 14, Dec. 2023, <https://doi.org/10.3389/fpls.2023.1308528>.
- [7] A. Sharma, M. Georgi, M. Tregubenko, A. Tselykh, and A. Tselykh, "Enabling smart agriculture by implementing artificial intelligence and embedded sensing," *Computers & Industrial Engineering*, vol. 165, Mar. 2022, Art. no. 107936, <https://doi.org/10.1016/j.cie.2022.107936>.
- [8] A. Rejeb, A. Abdollahi, K. Rejeb, and H. Treiblmaier, "Drones in agriculture: A review and bibliometric analysis," *Computers and Electronics in Agriculture*, vol. 198, July 2022, Art. no. 107017, <https://doi.org/10.1016/j.compag.2022.107017>.
- [9] A. S. Paymode and V. B. Malode, "Transfer Learning for Multi-Crop Leaf Disease Image Classification using Convolutional Neural Network VGG," *Artificial Intelligence in Agriculture*, vol. 6, pp. 23–33, Jan. 2022, <https://doi.org/10.1016/j.iaia.2021.12.002>.
- [10] A. Morellos, X. E. Pantazi, C. Paraskevas, and D. Moshou, "Comparison of Deep Neural Networks in Detecting Field Grapevine Diseases Using Transfer Learning," *Remote Sensing*, vol. 14, no. 18, Sept. 2022, <https://doi.org/10.3390/rs14184648>.
- [11] K. R. Aravind, P. Raja, R. Anirudh, K. V. Mukesh, R. Ashiwin, and G. Vikas, "Grape Crop Disease Classification Using Transfer Learning Approach," in *Proceedings of the International Conference on ISMAC in Computational Vision and Bio-Engineering 2018 (ISMVC-CVB)*, 2019, pp. 1623–1633, https://doi.org/10.1007/978-3-030-00665-5_150.
- [12] Y. Nagaraju, Venkatesh, S. Swetha, and S. Stalin, "Apple and Grape Leaf Diseases Classification using Transfer Learning via Fine-tuned

- Classifier," in *2020 IEEE International Conference on Machine Learning and Applied Network Technologies (ICMLANT)*, Dec. 2020, pp. 1–6, <https://doi.org/10.1109/ICMLANT50963.2020.9355991>.
- [13] M. Ji, L. Zhang, and Q. Wu, "Automatic grape leaf diseases identification via UnitedModel based on multiple convolutional neural networks," *Information Processing in Agriculture*, vol. 7, no. 3, pp. 418–426, Sept. 2020, <https://doi.org/10.1016/j.inpa.2019.10.003>.
- [14] X. Xie, Y. Ma, B. Liu, J. He, S. Li, and H. Wang, "A Deep-Learning-Based Real-Time Detector for Grape Leaf Diseases Using Improved Convolutional Neural Networks," *Frontiers in Plant Science*, vol. 11, June 2020, <https://doi.org/10.3389/fpls.2020.00751>.
- [15] B. Liu, Z. Ding, L. Tian, D. He, S. Li, and H. Wang, "Grape Leaf Disease Identification Using Improved Deep Convolutional Neural Networks," *Frontiers in Plant Science*, vol. 11, July 2020, <https://doi.org/10.3389/fpls.2020.01082>.
- [16] Ü. Atila, M. Uçar, K. Akyol, and E. Uçar, "Plant leaf disease classification using EfficientNet deep learning model," *Ecological Informatics*, vol. 61, Mar. 2021, Art. no. 101182, <https://doi.org/10.1016/j.ecoinf.2020.101182>.
- [17] M. S. Anari, "A Hybrid Model for Leaf Diseases Classification Based on the Modified Deep Transfer Learning and Ensemble Approach for Agricultural AIoT-Based Monitoring," *Computational Intelligence and Neuroscience*, vol. 2022, no. 1, 2022, Art. no. 6504616, <https://doi.org/10.1155/2022/6504616>.
- [18] Md. S. H. Shovon, S. J. Mozumder, O. K. Pal, M. F. Mridha, N. Asai, and J. Shin, "PlantDet: A Robust Multi-Model Ensemble Method Based on Deep Learning For Plant Disease Detection," *IEEE Access*, vol. 11, pp. 34846–34859, 2023, <https://doi.org/10.1109/ACCESS.2023.3264835>.
- [19] K. Nagasubramanian, S. Jones, A. K. Singh, S. Sarkar, A. Singh, and B. Ganapathysubramanian, "Plant disease identification using explainable 3D deep learning on hyperspectral images," *Plant Methods*, vol. 15, no. 1, Aug. 2019, Art. no. 98, <https://doi.org/10.1186/s13007-019-0479-8>.
- [20] U. S. Rao *et al.*, "Deep Learning Precision Farming: Grapes and Mango Leaf Disease Detection by Transfer Learning," *Global Transitions Proceedings*, vol. 2, no. 2, pp. 535–544, Nov. 2021, <https://doi.org/10.1016/j.gltp.2021.08.002>.
- [21] Z. Tang, J. Yang, Z. Li, and F. Qi, "Grape disease image classification based on lightweight convolution neural networks and channelwise attention," *Computers and Electronics in Agriculture*, vol. 178, Nov. 2020, Art. no. 105735, <https://doi.org/10.1016/j.compag.2020.105735>.
- [22] S. Parez, N. Dilshad, T. M. Alanazi, and J. Weon Lee, "Towards Sustainable Agricultural Systems: A Lightweight Deep Learning Model for Plant Disease Detection," *Computer Systems Science and Engineering*, vol. 47, no. 1, pp. 515–536, 2023, <https://doi.org/10.32604/csse.2023.037992>.
- [23] J. Chen, D. Zhang, and Y. A. Nanehkaran, "Identifying plant diseases using deep transfer learning and enhanced lightweight network," *Multimedia Tools and Applications*, vol. 79, no. 41, pp. 31497–31515, Nov. 2020, <https://doi.org/10.1007/s11042-020-09669-w>.
- [24] P. Wang *et al.*, "Fine-Grained Grape Leaf Diseases Recognition Method Based on Improved Lightweight Attention Network," *Frontiers in Plant Science*, vol. 12, Oct. 2021, <https://doi.org/10.3389/fpls.2021.738042>.
- [25] H. I. Peyal *et al.*, "Plant Disease Classifier: Detection of Dual-Crop Diseases Using Lightweight 2D CNN Architecture," *IEEE Access*, vol. 11, pp. 110627–110643, 2023, <https://doi.org/10.1109/ACCESS.2023.3320686>.
- [26] B. Prashanthi, A. V. P. Krishna, and C. M. Rao, "A Comparative Study of Fine-Tuning Deep Learning Models for Leaf Disease Identification and Classification," *Engineering, Technology & Applied Science Research*, vol. 15, no. 1, pp. 19661–19669, Feb. 2025, <https://doi.org/10.48084/etasr.9017>.
- [27] normally 26 - W. B. Demilie, "Plant disease detection and classification techniques: a comparative study of the performances," *Journal of Big Data*, vol. 11, no. 1, Jan. 2024, Art. no. 5, <https://doi.org/10.1186/s40537-023-00863-9>.
- [28] A. González-Briones, S. L. Florez, P. Chamoso, L. F. Castillo-Ossa, and E. S. Corchado, "Enhancing Plant Disease Detection: Incorporating Advanced CNN Architectures for Better Accuracy and Interpretability," *International Journal of Computational Intelligence Systems*, vol. 18, no. 1, May 2025, Art. no. 120, <https://doi.org/10.1007/s44196-025-00835-2>.
- [29] I. Kunduracioglu and I. Pacal, "Advancements in deep learning for accurate classification of grape leaves and diagnosis of grape diseases," *Journal of Plant Diseases and Protection*, vol. 131, no. 3, pp. 1061–1080, June 2024, <https://doi.org/10.1007/s41348-024-00896-z>.
- [30] S. G. Subramanya and A. Parkavi, "Grape Leaf Disease Detection Using VitiNet-X: A Novel Deep Learning Model with Dual Attention and Multi-Scale Feature Fusion," *International Journal of Intelligent Engineering and Systems*, vol. 18, no. 10, pp. 574–588, Nov. 2025, <https://doi.org/10.22266/ijies2025.1130.37>.
- [31] "Grapevine Disease Dataset (Original)." Kaggle, [Online]. <https://www.kaggle.com/datasets/rm1000/grape-disease-dataset-original>.