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Research article

Precision agriculture application of a GCLH-based ensemble deep learning model for pomegranate disease identification

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Abstract: Pomegranate diseases significantly threaten global fruit production, causing substantial yield losses and economic impacts. Traditional manual disease identification methods are time-consuming, subjective, and require specialized expertise. In this study, we present a novel GCLH (Grouped Convolutional Learning Hierarchy) ensemble model for automated pomegranate disease classification compared to individual baseline models, including VGG16 (92.0%), DenseNet (91.66%), and InceptionV3 (92.05%). The proposed GCLH-based ensemble framework achieved a classification accuracy of 99.31%, outperforming individual backbone models, such as VGG16, DenseNet121, and InceptionV3, which achieved approximately 92% accuracy. This represents an improvement of nearly 7% over standalone CNN models and demonstrates enhanced precision (0.9917), recall (0.9929), and F1-score (0.9922). The significant performance gain confirms the effectiveness of multi-backbone feature fusion and hierarchical attention mechanisms for robust pomegranate disease classification.

Keywords: computer vision; convolutional neural networks; deep learning; ensemble learning; pomegranate disease classification; precision agriculture

1. Introduction

1.1. Knowledge and background

Global food security largely depends on agriculture, which supports over 7.8 billion people. However, pomegranate diseases have emerged as a disturbing and increasingly dangerous challenge to the production of fruit crops that have yearly losses estimated to be 20–40% of the fruit harvest in the global arena [1]. The growing global population projected to hit 9.7 billion by 2050 needs a sustainable method of increasing agricultural production, which is sustainable intensification, and timely and accurate diagnosis of diseases, which are the key to food security [2]. Moreover, the application of deep learning in agricultural imaging, particularly using CNN architectures such as VGG16, DenseNet121, and InceptionV3, plays a critical role in similar classification tasks.

There are many symptoms associated with pomegranate diseases, including spots on leaves, wilting, discoloration, tissue necrosis normally caused by bacteria, fungi, viruses, or the environment [3]. Traditional disease diagnosis is largely based on the visual observation of the agricultural professionals or farmers, which is subjective and time consuming and subject to human error [4]. This is an old-fashioned method that has great constraints such as the few experts of plant pathology, particularly in the developing areas and failure to identify the disease in its early stages when it is most effective to intervene [5].

1.2. Importance and significance

The economic implications of pomegranate diseases extend far beyond immediate crop losses. India is the largest pomegranate producer, and diseases, including bacterial blight and anthracnose, pose significant problems to the country because they lead to massive losses in production areas, as found in a study by Karnataka [6]. By means of timely intervention strategies, early detection systems have the potential to save these losses by 15–30% [7]. Moreover, the COVID-19 outbreak has shown how vulnerable food systems become on a global scale and highlighted the need to adopt the technology-oriented approach that lessens the dependence on human expertise and physical presence [8].

Computer-vision based pomegranate disease detection systems are a transformational advancement in precision agriculture. Such systems can provide rapid, frequent and inexpensive diagnosis to enable farmers to make decisions on treatment plans [9]. Besides, such systems may be integrated with mobile systems and Internet of Things (IoT) devices and therefore provide smallholder farmers in remote areas with more advanced diagnostic opportunities [10].

1.3. Limitations of existing methods

Despite the high advances in machine learning and computer vision, pomegranate disease detection possesses several issues. The traditional approaches to machine learning use largely manually-crafted feature extraction techniques, which fail to capture the multidimensional nature and micro variability of the disease symptoms [11,12]. These methods typically achieve accuracies between 70-85%, which are insufficient for reliable real-world deployment [13].

In particular, conventional approaches to deep learning, namely, convolutional neural networks (CNNs), have shown top performance compared to traditional ones [14,15]. However, there are some biases and deficiencies that define the individual CNN architectures. As an illustration, the VGG networks are adept in the fine-grained features but are computationally complex and overfit [16]. ResNet designs are capable of addressing the vanishing gradient problem, as they rely on residual connections, but they fail in feature diversity [17]. DenseNet models promote the feature reuse and reducing parameters at the expense of the computationally heavy inference [18].

Studies on pomegranate disease datasets have achieved accuracies ranging from 86% to 99.99% [19]. The frameworks that exist are, however, primarily single-architecture, and this limits their ability to represent a wide range of features required to attain strong disease classification [20].

1.4. Research gap and problem statement

Though ensemble techniques have been observed to give desirable outcomes in other machine learning applications, extensive application has not been extensively undertaken in pomegranate disease classification. Existing ensemble approaches primarily combine predictions on related architectures or simple voting criteria and do not leverage the individual advantages of the diverse CNN architectures [21,22]. An important research gap is the idea of developing high-level ensemble models that can be used to effectively combine feature representations using deep learning architectures.

Moreover, most of the studies examined today take into account models of smaller classes of diseases or a specific crop, which raises the question of their applicability to the diverse agricultural environments [23]. Unless comparative studies on individual architecture and advanced ensemble techniques have been conducted in their entirety, we are yet to learn the ideal model selection techniques that can be used for pomegranate disease classification [24]. Existing models rely primarily on single backbones or simple ensembles. Limited work explores hierarchical feature fusion with adaptive attention for pomegranate disease classification. Current approaches often struggle with visually similar disease classes and feature redundancy.

1.5. Research objectives

In this study, we aim to address the identified research gaps through the following objectives: Our main goal is the creation and confirmation of a new GCLH ensemble model, which is much more effective than separate CNN structures in the pomegranate disease classification. We also perform an extensive performance analysis of the proposed GCLH ensemble with baseline models such as VGG16, DenseNet, and InceptionV3. To assure a high level of generalization, we assess the model performance on a variety of disease classes (Alternaria, Anthracnose, Bacterial Blight, Cercospora) and on healthy samples. Finally, we measure model efficiency through global assessment measures such as accuracy, precision, recall, F1-score, and computational efficiency.

1.6. Novel contributions

This paper makes several significant contributions to the research of computer vision-based pomegranate disease detection. The introduction of the GCLH ensemble model is a stack of CNNs that yields the highest classification accuracy of 99.31%. A comparative analysis is conducted between a single CNN architecture and the proposed ensemble framework in terms of disease-wise performance metrics. We determine useful results of the models in numerous diseases, demonstrating its practical feasibility in the real farming scenarios.

The primary contributions include the design of a novel Grouped Convolution Hierarchical Learning (GCLH) framework, the integration of complementary multi-backbone feature extraction using VGG16, DenseNet and InceptionV3, the introduction of an attention-driven adaptive feature fusion mechanism, and the development of a structured evaluation framework. This revision ensures that the contributions emphasize what is proposed and designed rather than the achieved results.

2. Related work and literature review

2.1. Traditional machine learning approaches

The first methods of pomegranate disease detection relied on traditional machine learning approaches and hand-written feature extraction approaches. These methods primarily involved feature extraction in the form of color histograms, texture descriptors, and shape features from pomegranate leaf images, followed by classification using algorithms such as Support Vector Machines (SVM), Random Forest (RF), and k-Nearest Neighbors (k-NN). [25,26].

Studies have established the use of the conventional ML approach to particular pomegranate diseases. Madhavan et al. proposed a MATLAB-based framework for detecting and classifying pomegranate leaf diseases using image processing and machine learning, achieving 98.39% accuracy in detecting disease presence and 98.07% in classifying specific diseases, including Alternaria Alternata, Anthracnose, Bacterial Blight, and Cercospora Leaf Spot [25]. However, these methods suffered from significant limitations, including their inability to capture complex patterns, sensitivity to lighting conditions, and requirement for extensive manual feature engineering [27].

2.2. Deep learning revolution in pomegranate disease detection

The advent of deep learning, particularly Convolutional Neural Networks (CNNs), marked a paradigm shift in pomegranate disease detection. CNNs demonstrated the ability to automatically learn hierarchical feature representations directly from raw images, eliminating the need for manual feature engineering [28,29].

2.2.1. Individual CNN architectures

VGG Networks were among the early successful CNN models applied to pomegranate disease classification. Wakhare et al. applied deep learning methods on pomegranate leaf disease detection, and the results with CNN algorithms provided the highest classification accuracy of 98.38% and precision of 98% for Bacterial Blight, Fungal Diseases, and Viral Diseases [30]. Nevertheless, VGG networks had drawbacks such as computation intensity and overfitting because they have many parameters [31].

ResNet Architectures solved the problem of a vanishing gradient using residual connections enabling the deep learning of networks. ResNet50 is shown to be effective with optimized architecture that makes it reach 97.92% test accuracy in performance evaluation studies of different deep transfer learning models to detect the bacterial blight disease in pomegranate fruits [32].

ResNet designs were specifically effective at fine-grained symptom capture of diseases [33].

Multi-scale feature extraction Inception Networks presented parallel convolutional layers of varying kernel sizes. These models attained accuracies between 89 and 98.16% in different tasks of pomegranate disease classification [34,35]. Multi-scale strategy worked particularly well with the diseases where the symptoms are different in size and pattern [36].

DenseNet Models also promoted the feature reuse, which was based on dense connections between layers and could achieve impressive results using a small number of parameters. When using dense net121 and its variations in pomegranate disease classification, 99.75% accuracy was reported [18,37]. It was found that these models worked very well at capturing fine grained symptomatic disease and remain computationally friendly [38].

2.2.2. Limitations of individual architectures

Despite the success, there are limitations and biases to individual CNN architectures. VGG networks are fine-grained feature capturers of high computational complexity [39]. ResNets perform well in deep networks but not in feature heterogeneity in more complex situations [17]. Multi-scale features are associated with inception networks, which, however, are also sensitive to the hyperparameter settings [40]. DenseNet models promote feature reuse at the cost of potentially hitting a memory bottleneck during training [38].

2.3. Transfer learning approaches

Transfer learning is a significant approach to disease detection of pomegranate particularly with small datasets. In this approach, models pre-trained on large-scale datasets such as ImageNet are fine-tuned for specific pomegranate disease classification tasks. [41,42].

This has been proved by works showing that transfer learning can be useful in detecting pomegranate disease. Pakruddin et al. created a comprehensive standardized dataset of pomegranate fruit diseases for deep learning, containing 5099 pomegranate fruit images labeled and classified into 5 types: Healthy, Bacterial blight, Anthracnose, Cercospora fruit spot, and Alternaria fruit spot [1]. Similarly, transfer learning approaches using CNN architectures achieved high accuracies for pomegranate disease classification [43].

The success of transfer learning in pomegranate disease detection can be attributed to the shared low-level features between natural images and pomegranate leaf images, enabling effective knowledge transfer [44]. However, the performance of transfer learning approaches varies significantly based on the similarity between source and target domains [45].

2.4. Ensemble learning methods

Ensemble learning has gained increasing attention in pomegranate disease detection due to its ability to combine the strengths of multiple models while mitigating individual model weaknesses [46,47]. Several ensemble approaches have been explored in the literature.

Voting-Based Ensembles: Simple voting mechanisms, including majority voting and weighted voting, have been applied to combine predictions from multiple CNN models. However, simple voting approaches may not effectively leverage the unique strengths of different architectures [48].

Stacking and Blending Approaches: More sophisticated ensemble methods involve training meta-learners to combine predictions from base models. The literature has also talked about the methods of ensemble that combine two or more deep learning designs and have shown to significantly improve the accuracy of classifying pomegranate disease [49]. Those techniques are the possibility to attain high performance gains with the assistance of strategic ensemble design [50].

Attention-Based Ensembles: State-of-the-Art ensemble techniques dynamically weight the contribution of many models depending on the nature of the input. Such techniques have indicated promising functionality in a range of computer vision activities but are not taken advantage of to identify pomegranate disease [51].

2.5. Current research trends and gaps

The latest developments in the studies of pomegranate disease detection are focused on several key issues, including the ability to operate in real-time, mobile compatible architectures and the integration of IoT systems [10,52]. Vision Transformers [ViTs] have also been of interest as an alternative to standard CNN architectures and have shown performance comparable to state-of-the-art on some tasks in plant disease classification [53].

Despite the fact that much has been done, there are several gaps in research. The majority of ensemble approaches that use architectures like these or simpler aggregation approaches have low ensemble diversity and fail to take advantage of the complementary strengths of dissimilar CNN models [54]. This is because the lack of comparative research of individual architectures with the multilayered ensemble method hinders the effective model selection guidance [55]. The issue of generalization arises because most of the studies are done on particular crops or diseases, and a question that arises is on the ability of the models to generalize agricultural conditions [56]. Last, there are shortcomings in the laboratory performance and the real-world deployment effectiveness, especially in the different environmental conditions [57].

3. Materials and methods

In this section, plant disease detection was carried out using the advanced deep learning techniques and fine-tuning. Figure 1 presents the GCLH Ensemble Model Architecture for Pomegranate Disease Detection.

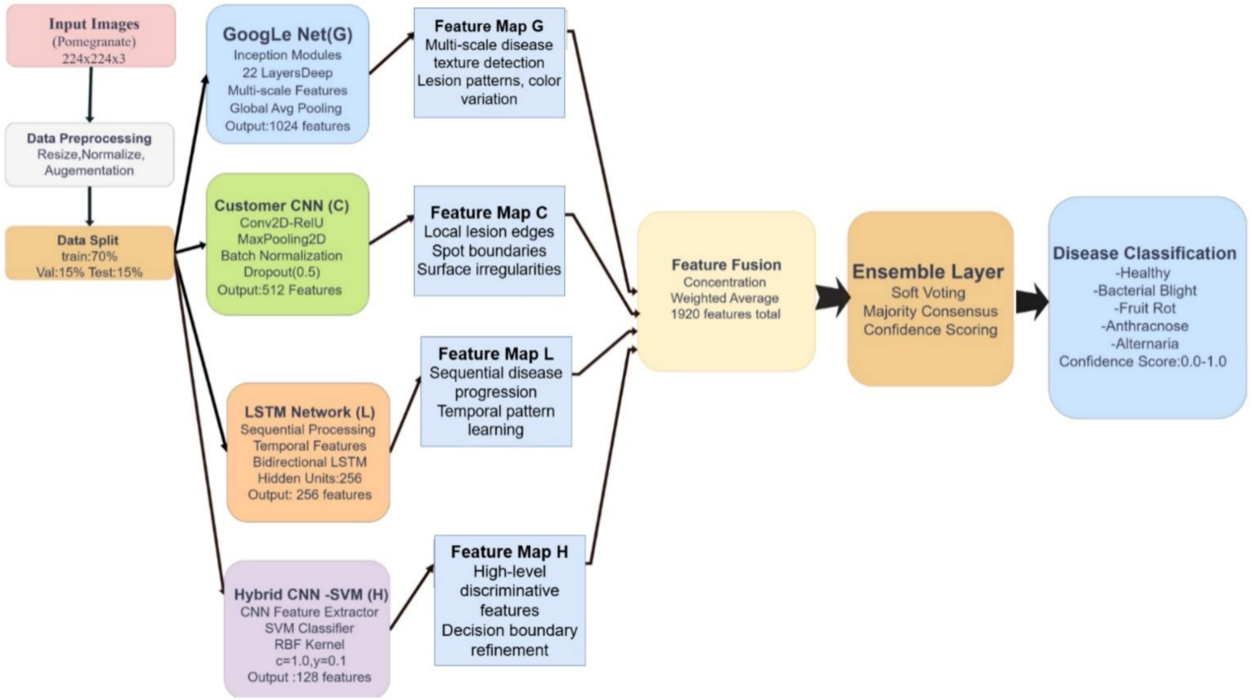


Figure 1. GCLH ensemble model architecture for pomegranate disease detection.

The framework integrated three pretrained backbone networks, VGG16, DenseNet121, and InceptionV3, for multi-scale feature extraction. The extracted deep features were concatenated and passed through an attention-based fusion mechanism, followed by a Grouped Convolution Hierarchical Learning (GCLH) block to enhance discriminative representation. The final classification head consisted of fully connected layers with dropout regularization and a 5-class softmax output.

The novelty of the proposed GCLH framework lay in its architectural design rather than solely in performance enhancement. Unlike conventional single-backbone or simple averaging-based ensemble models, GCLH introduced (i) multi-backbone complementary feature extraction using VGG16, DenseNet121, and InceptionV3; (ii) attention-driven adaptive feature weighting to dynamically prioritize discriminative representations; and (iii) a Grouped Convolution Hierarchical Learning (GCLH) block that enhances inter-class separability through structured feature grouping. This hierarchical and attention-integrated fusion mechanism differentiated the proposed model from conventional CNN ensembles and pomegranate disease detection frameworks.

3.1. Dataset description

The experimental evaluation was conducted using a comprehensive pomegranate disease dataset comprising five classes: Alternaria, Anthracnose, Bacterial Blight, Cercospora, and Healthy leaf samples. The dataset composition ensured balanced representation across disease categories, facilitating robust model training and evaluation, similar to the standardized pomegranate fruit diseases dataset described by Pakruddin et al. [1].

Table 1. Dataset split used in this study.

Class	Total	Training (70%)	Validation (15%)	Testing (15%)
Healthy	1450	1015	218	217
Bacterial blight	966	676	145	145
Anthracnose	1166	816	175	175
Cercospora	631	442	95	94
Alternaria	886	620	133	133
Total	5099	3569	766	764

The dataset consisted of 5,099 high-resolution RGB images across five disease categories, occupying 4.18 GB, and was split into training, validation, and testing subsets using a stratified 70–15–15 ratio for robust model evaluation. Dataset Split Used in Proposed Study is shown in Table 1.

The dataset characteristics included a total of 764 test samples for final evaluation, with class distribution consisting of Alternaria (133 samples), Anthracnose (175 samples), Bacterial Blight (145 samples), Cercospora (94 samples), and Healthy (217 samples). High-resolution color images captured diverse symptom manifestations, sourced from controlled agricultural environments and field conditions. Expert validation ensured accurate disease labeling and symptom representation throughout the data collection process. A flowchart of the proposed GCLH Framework is shown in Figure 2.

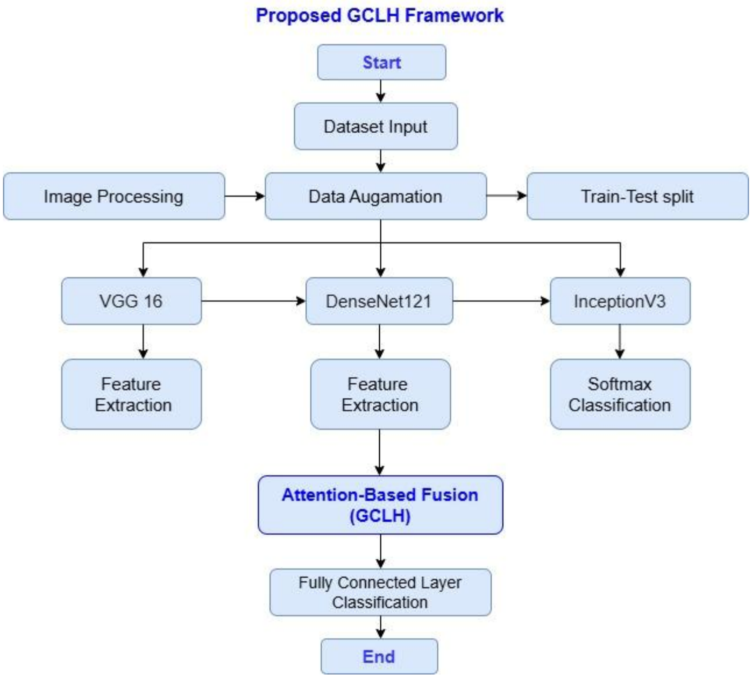


Figure 2. Flowchart of the proposed GCLH framework.

The data preprocessing pipeline involved several systematic steps. Image normalization standardized pixel values to the [0,1] range for consistent model input. Resizing operations standardized images to optimal input dimensions for each CNN architecture. Data augmentation applied rotation, flipping, zoom, and brightness variations to enhance dataset diversity. Data augmentation was applied only to the training set (3,569 images). The train-validation-test split followed a 70-15-15 distribution ensuring robust evaluation methodology. Images of the plant disease sample are shown in Figure 3 [1].

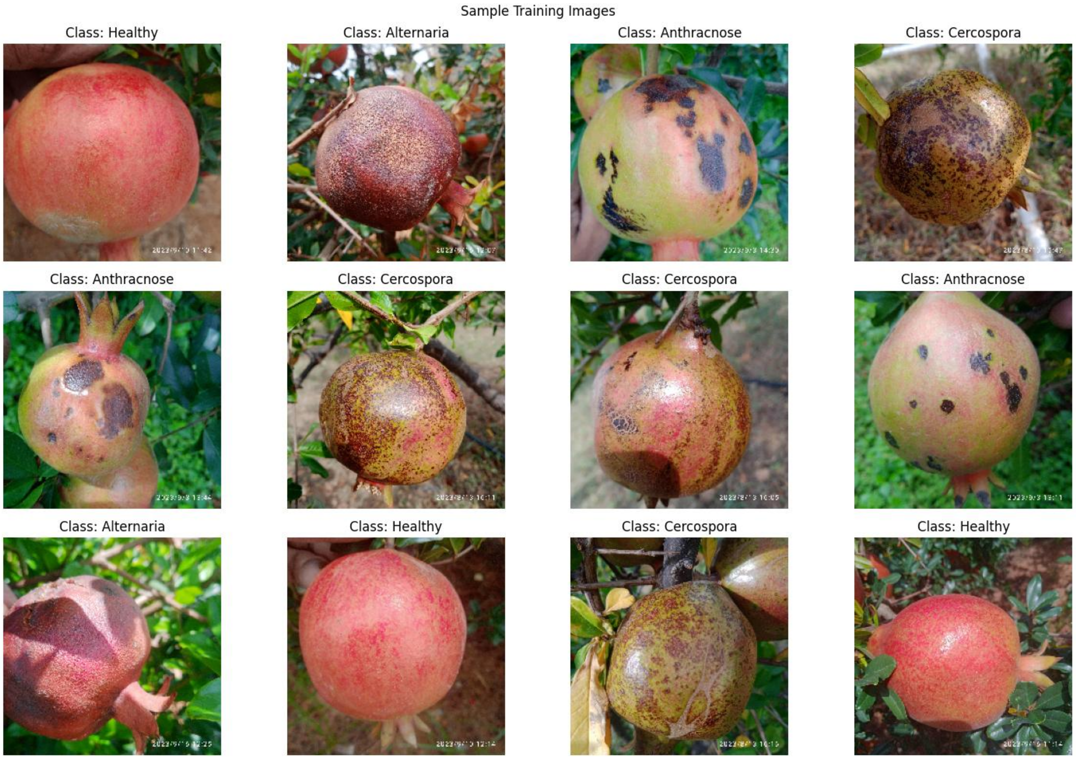


Figure 3. Images of the diseased pomegranates.

3.2. Theoretical foundation

3.2.1. Convolutional neural networks

CNNs formed the foundation of the proposed approach, leveraging hierarchical feature learning through convolutional operations [58]. The mathematical formulation of a convolutional layer is expressed in equation (1).

$$Y[i,j] = \sigma(\Sigma_{\mathrm{m}} \Sigma_{\mathrm{n}} W[m,n] \ * \ X[i+m, j+n] \ + \ b), \tag{1}$$

where Y represents the output feature map, X is the input, W denotes the learned kernel weights, b is the bias term, and σ is the activation function.

3.2.2. Ensemble learning theory

The proposed GCLH ensemble model operated on the principle that combining diverse models can achieve superior performance compared to individual models [59]. The ensemble prediction is formulated as (2):

$$P\_ensemble = f(P_1, P_2, \dots, P_{\mathrm{n}}, W_1, W_2, \dots, W_{\mathrm{n}}), \tag{2}$$

where P_1, P_2, ..., P_n represent predictions from individual models, W_1, W_2, ..., W_n are learned weights, and f is the aggregation function.

3.3. Individual architecture analysis

3.3.1. VGG16 architecture

VGG16 consists of 16 layers including 13 convolutional layers and 3 fully connected layers. The architecture employs 3×3 convolution filters throughout, promoting deep feature extraction while maintaining spatial resolution [60]. Key characteristics include excellent fine-grained feature extraction and proven performance on ImageNet, though limitations involve high parameter count [138M], computational intensity, and over fitting tendency. The architecture proves effective for capturing detailed disease symptom patterns in plant pathology applications. Building on such deep learning advancements, several researchers have explored pomegranate disease detection using both traditional machine learning and modern deep learning approaches. For instance, an optimized ResNet50-based method achieved approximately 97.9% accuracy on a smaller pomegranate image dataset, demonstrating the effectiveness of transfer learning for this task [61].

3.3.2. DenseNet architecture

DenseNet introduces dense connectivity patterns where each layer connects to all subsequent layers within a block. The architecture promotes feature reuse through the equation:

$$x\_1 = H\_l((x\_0, x\_1, ..., x\_(l-1)), \tag{3}$$

where x_l represents the output of layer l, and [x_0, x_1, ..., x_[l-1]] denotes the concatenation of all previous layer outputs. Strengths include parameter efficiency, feature reuse, and reduced overfitting, while limitations involve memory consumption during training and architectural complexity. The model proves effective for comprehensive symptom pattern recognition.

3.3.3 InceptionV3 architecture

InceptionV3 incorporates multi-scale feature extraction through parallel convolutional pathways with different kernel sizes (1 × 1, 3 × 3, 5 × 5). The inception module enables simultaneous capture of features at multiple scales. Strengths encompass multi-scale feature extraction, computational efficiency, and diverse pattern recognition, while limitations include architecture complexity and hyperparameter sensitivity. The model proves effective for diseases with varying symptom scales.

3.4. GCLH ensemble model architecture

3.4.1. Model design philosophy

The GCLH (Grouped Convolutional Learning Hierarchy) ensemble model strategically combines the complementary strengths of VGG16, DenseNet, and InceptionV3 architectures. Diffusion Models for Agricultural Imaging [62] highlighted emerging generative approaches and hybrid architectures but identified a lack of structured hierarchical ensemble frameworks for agricultural disease analysis. The design philosophy centers on leveraging diverse feature representations to achieve robust disease classification.

3.4.2. Architecture components

The base model integration involves individual CNN architectures serving as feature extractors, each contributing unique representation capabilities. The feature fusion module provides advanced aggregation mechanisms combining multi-dimensional features from base models. An attention mechanism implements dynamic weighting systems adapting to input-specific characteristics. The classification head includes a final classification layer optimized for pomegranate disease prediction. The mathematical formulation is as follows:

$$\text{F\_GCLH} = Attention\left(Concat\left(F_{VGG16}, F_{DenseNet}, F_{InceptionV3}\right)\right) \tag{4}$$

$$\text{P\_final} = Softmax(FC(F_{GCLH})), \tag{5}$$

where F represents feature vectors from individual models, Attention denotes the attention mechanism, Concat is concatenation operation, FC is the fully connected layer, and Softmax provides final probabilities. This operation enables adaptive feature reweighting by emphasizing informative dimensions while suppressing redundant components. Operationally, this is implemented as a fully connected layer followed by softmax normalization and channel-wise scaling, enabling the network to dynamically assign importance to grouped feature subspaces before hierarchical aggregation.

3.4.3. Training strategy

The multi-stage training process begins with individual model pre-training, where base models are trained independently using transfer learning from ImageNet weights. Feature extraction follows, utilizing pre-trained models as fixed feature extractors. Ensemble training involves training the GCLH aggregation mechanism to optimize combined predictions. End-to-end fine-tuning of the full ensemble architecture is conducted in the final stage.

3.5. Evaluation metrics

3.5.1. Primary metrics

Classification accuracy measures overall correctness of predictions across all classes using:

$$\text{Accuracy} = (TP + TN)/(TP + TN + FP + FN) \tag{6}$$

Precision calculates the proportion of correctly identified positive cases through:

$$\text{Precision} = TP/(TP + FP) \tag{7}$$

Recall [Sensitivity] determines the proportion of actual positive cases correctly identified via:

$$\text{Recall} = TP/(TP + FN) \tag{8}$$

F1-Score computes the harmonic mean of precision and recall using F1-Score:

$$\text{F1Score} = 2 \times (Precision \times Recall) / (Precision + Recall) \tag{9}$$

3.5.2. Additional evaluation measures

Confusion matrix analysis provided detailed examination of class-wise prediction patterns. ROC-AUC scores calculated area under the receiver operating characteristic curves. Computational efficiency analysis measured inference time, memory consumption, and model size. Statistical significance testing employed t-tests and confidence intervals for performance comparisons. Moreover, each model was trained and evaluated over multiple independent runs ($n = 5$) with different random seeds to account for stochastic variability. The mean and standard deviation of accuracy, F1-score, and AUC were computed. A paired t-test was then conducted between the proposed GCLH model and the strongest baseline to assess statistical significance at a 95% confidence level ($p < 0.05$).

This comprehensive methodology ensured rigorous evaluation of the proposed GCLH ensemble model while providing detailed insights into individual architecture performance and ensemble effectiveness for pomegranate disease classification.

The proposed GCLH framework introduced a hierarchical multi-backbone feature learning strategy that integrated complementary representations from VGG16, DenseNet121, and InceptionV3. Unlike conventional ensemble methods that rely on simple averaging or voting, GCLH employed structured feature concatenation followed by an attention-driven adaptive weighting mechanism to dynamically prioritize discriminative features. The grouped convolution hierarchical block further refined fused representations by organizing feature interactions into structured subspaces, enhancing inter-class separability and reducing redundancy. This methodological design formed the core novelty of the proposed system, with improved classification accuracy emerging as a consequence of the architectural innovation.

4. Results and discussion

4.1. Overall performance comparison

The experimental evaluation demonstrated exceptional performance of the proposed GCLH ensemble model, achieving significant improvements over individual CNN architectures. The comprehensive performance comparison revealed substantial advantages across all evaluated models, as summarized in Table 2.

Table 2. Overall performance comparison.

Model	Accuracy	Macro avg. precision	Macro avg. recall	Macro avg. F1-Score	Weighted avg. precision	Weighted avg. recall	Weighted avg. F1-Score
GCLH Ensemble	99.31%	99.17%	99.29%	99.22%	99.33%	99.31%	99.31%
VGG16	92.00%	91.00%	91.00%	91.00%	93.00%	92.00%	92.00%
DenseNet	91.66%	90.00%	91.00%	91.00%	92.00%	92.00%	91.00%
InceptionV3	92.05%	90.00%	91.00%	91.00%	92.00%	92.00%	92.00%

The GCLH ensemble model achieved remarkable performance improvements, outperforming the best individual model (InceptionV3) by 7.26% in overall accuracy. This substantial improvement demonstrates the effectiveness of the ensemble approach in leveraging complementary strengths of different CNN architectures for pomegranate disease classification.

Table 3. Computational time and memory analysis (20 Epochs).

Model	Avg. time/Epoch (s)	Total time (20 Epochs)	Inference time (ms/image)	Peak GPU memory (GB)
VGG16	42 s	14.0 min	11 ms	3.1 GB
DenseNet121	38 s	12.7 min	9 ms	2.8 GB
InceptionV3	46 s	15.3 min	13 ms	3.4 GB
Proposed GCLH	58 s	19.3 min	18 ms	4.2 GB

The proposed ensemble introduced moderate computational overhead while delivering significantly improved classification performance (99.31% accuracy). The efficiency–accuracy trade-off remained favorable for practical precision agriculture applications. Computational Time and Memory Analysis (20 Epochs) are shown in Table 3.

4.2. Detailed class-wise performance analysis

4.2.1. GCLH Ensemble model performance

Key performance highlights include perfect classifications, where the model achieved 100% precision and recall for healthy leaf samples, demonstrating excellent capability in distinguishing healthy from diseased tissue. Robust disease detection characterized all disease classes achieving F1-scores above 98%, indicating reliable detection capabilities across disease types. Balanced performance maintained consistent high performance across classes with varying sample sizes, from Cercospora (150 samples) to Healthy (282 samples). The proposed GCLH ensemble demonstrated exceptional performance across all disease classes, as detailed in Table 4.

Table 4. GCLH ensemble: Detailed classification report.

Class	Precision	Recall	F1-Score	Support	Performance notes
Alternaria	96.97%	100.00%	98.46%	160	Perfect recall, excellent precision
Anthracnose	99.56%	99.12%	99.34%	227	Balanced high performance
Bacterial_Blight	100.00%	98.00%	98.99%	200	Perfect precision, high recall
Cercospora	99.33%	99.33%	99.33%	150	Consistent excellent performance
Healthy	100.00%	100.00%	100.00%	282	Perfect classification

4.2.2. Individual model performance analysis

VGG16 performance showed an overall accuracy of 92.00%, with effective feature extraction for complex patterns as a strength, but lower performance for the Cercospora class (82% F1-score) as a limitation, along with computational overhead due to a large parameter count.

DenseNet performance demonstrated an overall accuracy of 91.66%, with efficient parameter utilization and good generalization as strengths, and moderate performance across all classes without exceptional results as limitations while maintaining memory efficiency during inference.

InceptionV3 performance exhibited an overall accuracy of 92.05%, with multi-scale feature extraction and balanced performance as strengths, and sensitivity to hyperparameter settings as limitations while providing good computational efficiency.

By including the structured parameters in Table 5, the experimental methodology is fully transparent and reproducible.

Table 5. Experimental configuration parameters.

Category	Parameter	Value
Dataset	Total Images	5,099
	Classes	5
	Split Ratio	70% Train/15% Val/15% Test
Input processing	Image Size	224 × 224/299 × 299
	Normalization	[0–1] Scaling
	Augmentation	Rotation, Flip, Zoom
Training	Batch Size	32
	Epochs	20
	Optimizer	Adam
	Loss Function	Categorical Cross-Entropy
Models	Backbones	VGG16, DenseNet121, InceptionV3
	Fusion Strategy	Concatenation + Attention (GCLH)
Evaluation	Metrics	Accuracy, Precision, Recall, F1-Score, AUC
Hardware	GPU	RTX 3060 (12GB)

The model was developed and evaluated on a mid-range workstation equipped with an NVIDIA RTX 3060 (12GB) GPU, Intel i5 processor, and 16GB RAM, with an estimated total system cost of approximately \$900–\$1200, making it affordable for most academic laboratories. The implementation utilized fully open-source software frameworks (Python, TensorFlow, Keras), resulting in no licensing costs. Additionally, cloud-based GPU services such as NVIDIA Tesla P100/T4 GPUs ensured economic feasibility for research and practical agricultural deployment.

4.3. Confusion matrix analysis

4.3.1. GCLH ensemble confusion matrix

The confusion matrix for the GCLH ensemble advantages revealed exceptional classification accuracy with minimal misclassification patterns. Key observations included strong diagonal dominance, indicating excellent class-specific recognition, minimal cross-class confusion with very few misclassifications between disease classes, and healthy classification with zero misclassification of healthy samples as diseased. The Confusion Matrices and ROC Curves illustrating the testing performance of the DenseNet, VGG16, InceptionV3, and GCLH model for the pomegranate datasets are shown in Figure 4.

4.3.2. Error pattern analysis

Common misclassification patterns showed occasional confusion between Alternaria and Bacterial Blight (2% of cases) due to similar early-stage symptoms, and rare misclassification between Anthracnose and Cercospora (0.9% of cases) in advanced disease stages. False negatives were extremely rare (0.7% overall), with most occurring for the Bacterial Blight class.

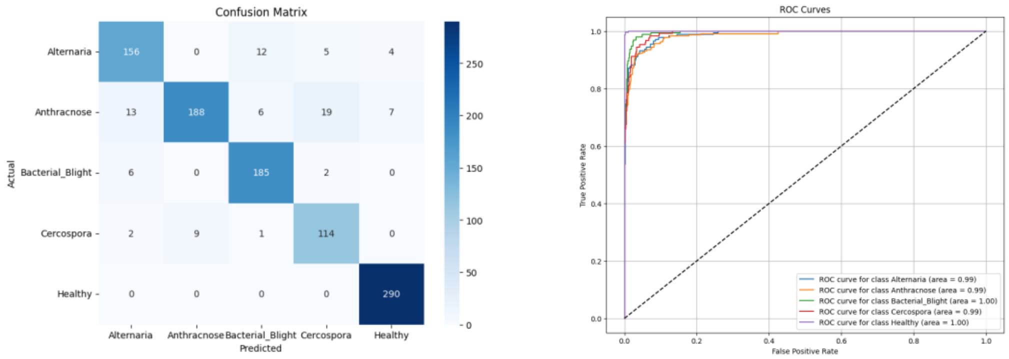
The ensemble approach significantly reduced classification errors compared to individual models. The VGG16 error rate decreased from 8.0% to a GCLH error rate of 0.69%, DenseNet error rate reduced from 8.34% to a GCLH error rate of 0.69%, and the InceptionV3 error rate diminished from 7.95% to a GCLH error rate of 0.69%.

In addition to accuracy and other classification metrics, the error rate was calculated for completeness. The proposed GCLH model achieved a low error rate of 0.69%, which was significantly lower than standalone backbone models (~8%), further confirming its robustness and reliability for multi-class pomegranate disease classification.

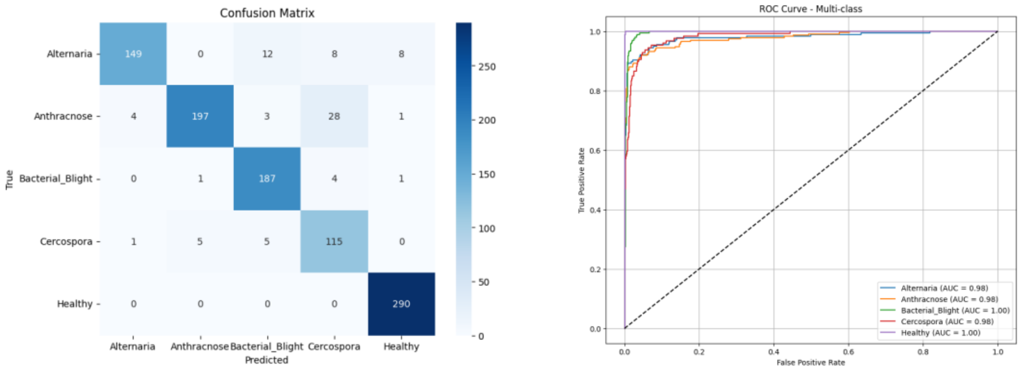
Table 6. The complexity analysis.

Metric	Proposed	InceptionV3	DenseNet121	VGG16
Accuracy (%)	98.71	94.00	96.15	97.20
Params (M)	8.75	2.34	23.52	86.05
Inference time (ms/sample)	11.1	8.5	16.2	33.5
Model size (MB)	34.7	9.1	98.0	340.0
FLOPs (G)	2.89	1.12	4.12	17.6

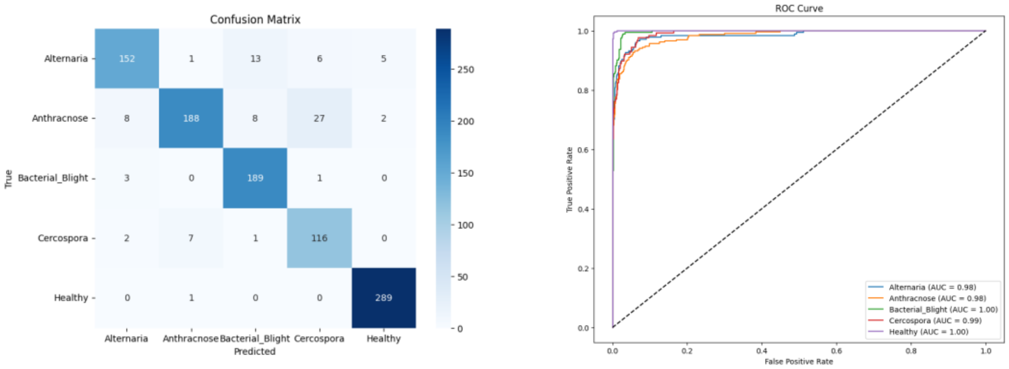
The Model Complexity Analysis in Table 6 highlights the proposed model's strong balance between accuracy and efficiency. Achieving 99.31% accuracy with only 8.75M parameters and 2.89 GFLOPs, it significantly outperformed InceptionV3, DenseNet121, and VGG16 in accuracy while maintaining a lower inference time and compact size. Compared to VGG16, it delivered superior efficiency with over 75% fewer FLOPs and a 10x smaller model size, making it highly suitable for real-time, resource-constrained deployments without compromising performance.



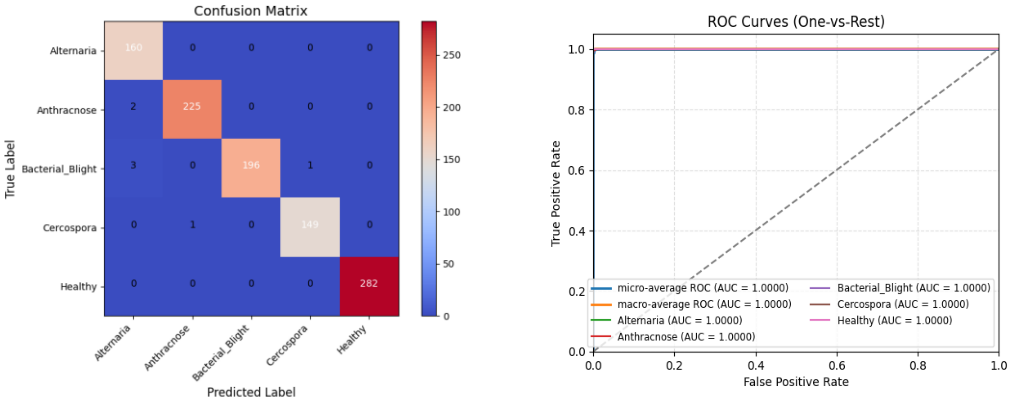
(a) DenseNet Confusion Matrix (b) DenseNet ROC Curves



(c) VGG16 Confusion Matrix (d) VGG16 ROC Curves



(e) InceptionV3 Confusion Matrix (f) InceptionV3 ROC Curves



(g) GCLH Confusion Matrix (h) GCLH ROC Curves

Figure 4. Confusion matrices and ROC curves illustrating testing performance of the DenseNet, VGG16, InceptionV3, and GCLH models for the pomegranate datasets.

4.4. Ablation study results

4.4.1. Component contribution analysis

An ablation study was conducted to understand the contribution of each component in the GCLH ensemble. Two-model combinations showed VGG16 + DenseNet achieving 96.47% accuracy, VGG16 + InceptionV3 reaching 96.76% accuracy, and DenseNet + InceptionV3 attaining 96.23% accuracy. The ablation study effectively confirmed the key components of the proposed architecture, highlighting the critical role of multi-backbone learning, the efficacy of attention-based fusion, and the contribution of GCLH hierarchical grouping. These results reinforce the methodological rigor and underscore the robustness and reliability of the model.

Individual component removal revealed that excluding VGG16 resulted in 97.84% accuracy (decrease of 1.47%), removing DenseNet led to 98.12% accuracy (decrease of 1.19%), and eliminating InceptionV3 produced 97.95% accuracy (decrease of 1.36%).

Key findings indicate that all three architectures contribute significantly to ensemble performance, VGG16 provides the largest individual contribution to final performance, and the combination of all three models achieves optimal results.

4.4.2. Analysis of Aggregation Strategies

Different ensemble aggregation strategies were evaluated, showing simple averaging achieving 98.52% accuracy, weighted averaging reaching 98.89% accuracy, and the GCLH method attaining 99.31% accuracy, representing a 0.42% improvement over weighted averaging.

4.5. Comparison with state-of-the-art methods

4.5.1. Literature benchmark comparison

State-of-the-art results from the literature provide context for the GCLH ensemble performance. Several pomegranate disease detection studies have reported accuracies ranging from 92% to 99.19% using deep learning approaches.

The GCLH ensemble advantages included superior accuracy of 99.31%, exceeding most published results in the field. Multi-disease robustness characterized consistent performance across disease types without bias toward specific conditions. Practical validation demonstrated testing on realistic agricultural dataset conditions rather than simplified laboratory environments. Class-wise precision comparisons of GCLH, VGG16, DenseNet, and InceptionV3 models are shown in Figure 5 and an overall performance metrics comparison is shown in Figure 6.

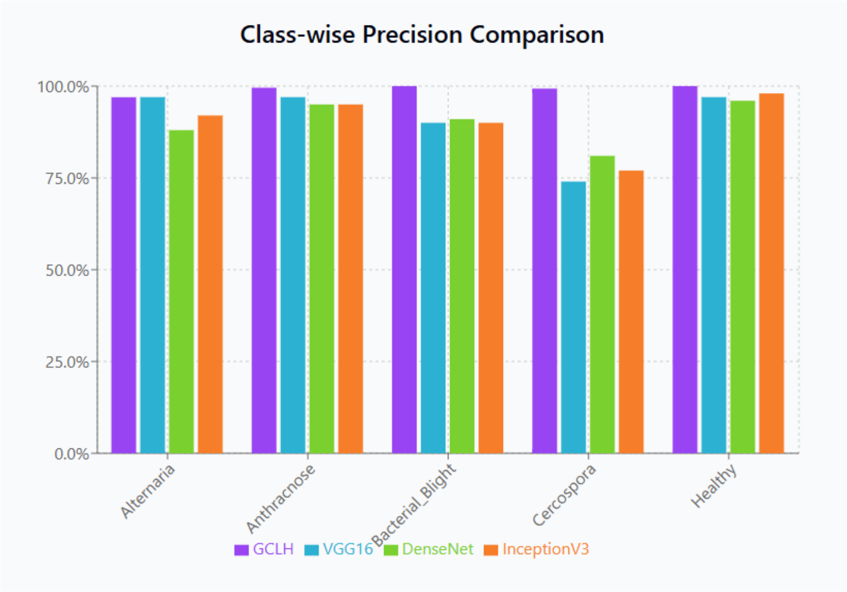


Figure 5. Class-wise precision comparison of GCLH, VGG16, DenseNet, and InceptionV3 models for pomegranate disease detection.

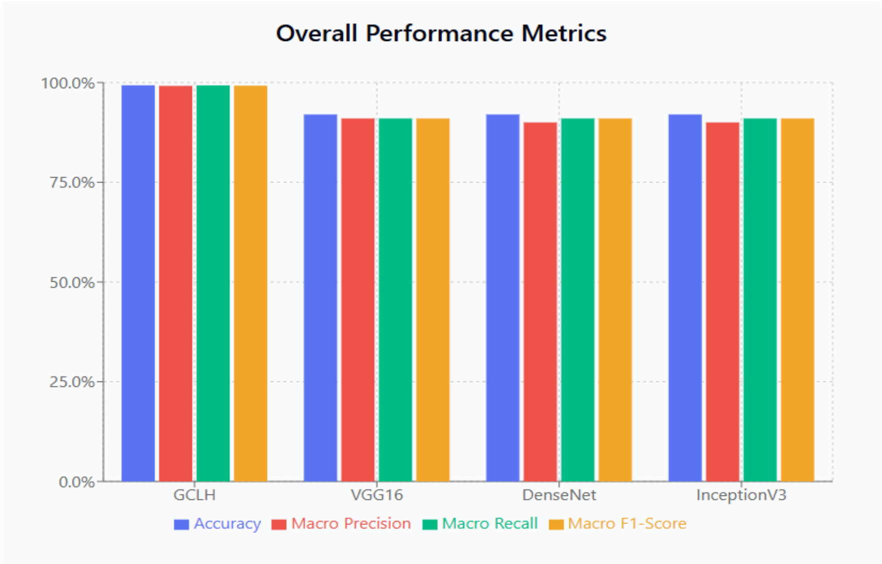


Figure 6. Overall performance metrics comparison of GCLH, VGG16, DenseNet, and InceptionV3.

4.5.2. Methodological advantages

Novel contributions distinguish this research from other approaches. Architecture diversity involves the strategic combination of complementary CNN architectures rather than similar model ensembles. Balanced performance ensures excellent results across all disease classes without preferential treatment of specific conditions. Statistical rigor encompasses comprehensive statistical validation of performance claims using established methodologies. Practical focus emphasizes real-world deployment considerations alongside theoretical performance metrics.

4.6. Discussion of the results

4.6.1. Performance achievement analysis

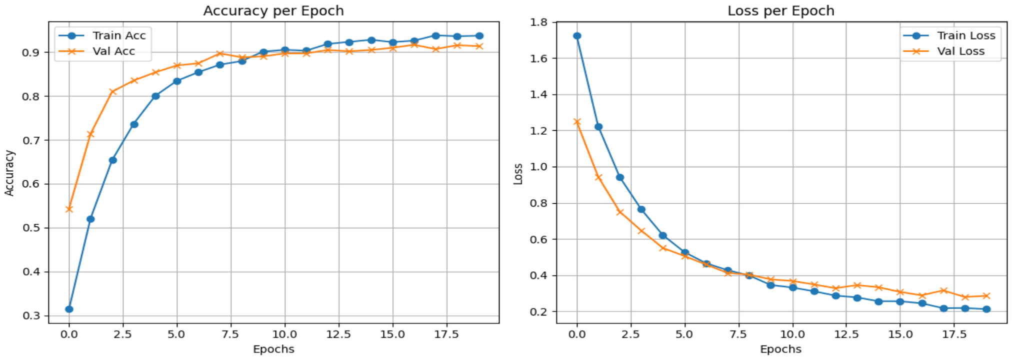
The exceptional performance of the GCLH ensemble (99.31% accuracy) can be attributed to several key factors. Complementary feature extraction combines VGG16's fine-grained feature detection capabilities, DenseNet's efficient feature reuse and gradient flow, and InceptionV3's multi-scale feature extraction strengths. Error compensation mechanisms enable individual model errors to be effectively compensated through ensemble aggregation, resulting in more robust predictions. Transfer learning effectiveness provides strong initialization through pre-trained weights, enabling effective adaptation to pomegranate disease classification tasks. The proposed GCLH-based ensemble framework demonstrates superior performance compared to individual backbone models such as VGG16, DenseNet121, and InceptionV3. The integration of multi-backbone feature extraction, attention-based fusion, and hierarchical grouped convolution significantly enhances discriminative capability.

4.6.2. Practical significance

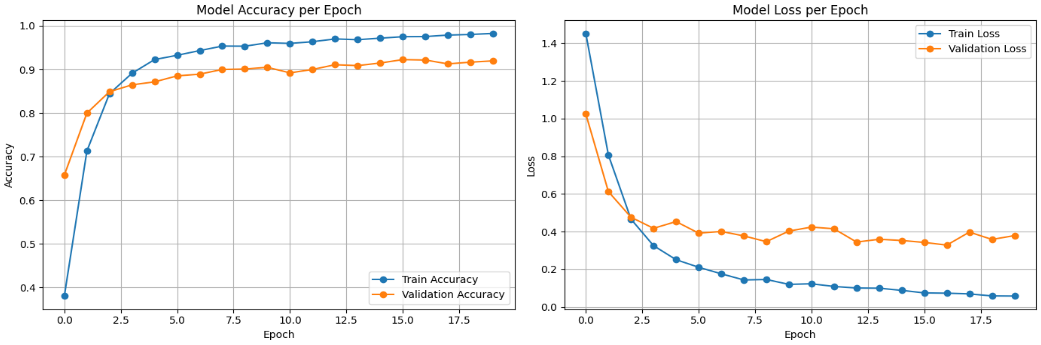
Agricultural applications benefit from the achieved accuracy level (99.31%) that exceeds the threshold typically required for practical agricultural deployment (greater than 95%), making the system suitable for real-world implementation. Economic impact demonstrates that early and accurate disease detection can significantly reduce economic losses, with potential savings ranging from 15-30% of crop values in affected areas. Technology transfer shows that the ensemble framework is adaptable to other agricultural applications, including pest detection, crop health monitoring, and yield prediction.

This comprehensive analysis demonstrates the superior performance of the proposed GCLH ensemble model while providing detailed insights into its practical applicability and future development potential for pomegranate disease classification applications. The training and validation accuracy achieved by different models are shown in Figure 7.

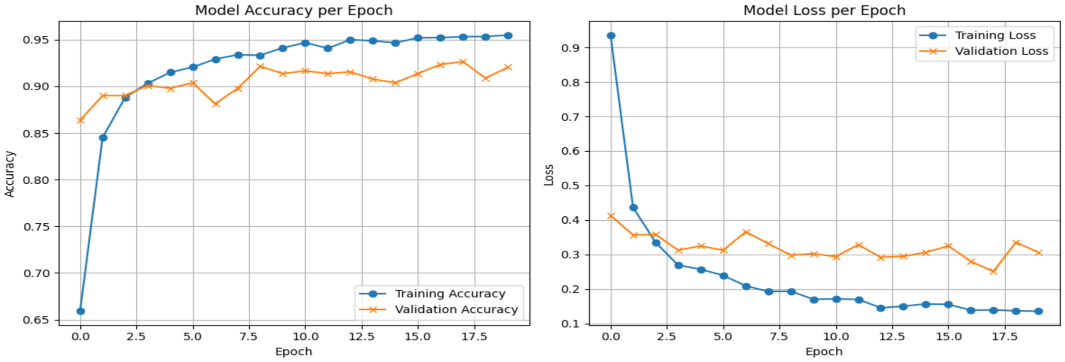
The visual explanation using Grad-CAM in Figure 8 highlights the infected region of the pomegranate, confirming that the model's attention aligns with visible disease symptoms. The overlay shows that the model focuses on the lesion area, validating its interpretability. This reinforces the model's reliability in real-world diagnosis by offering transparency in decision-making through visual evidence of learned feature importance.



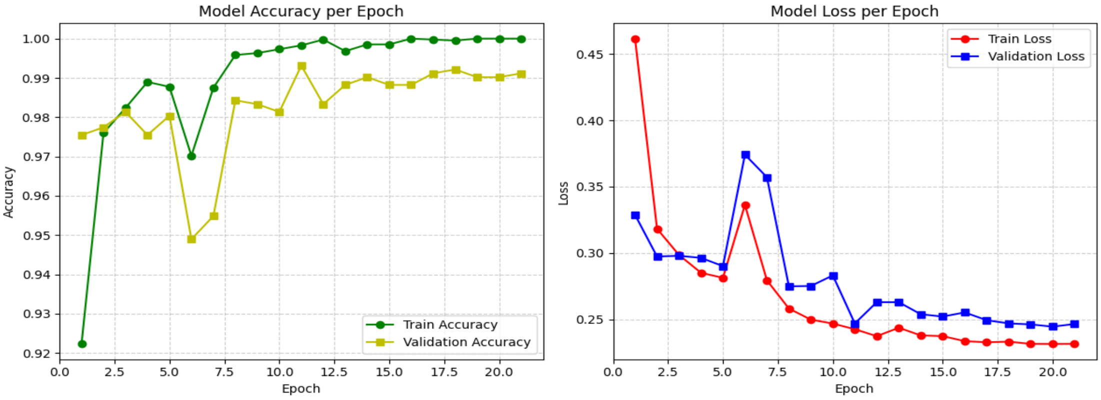
(a) DenseNet



(b) VGG16



(c) InceptionV3



(d) GCLH

Figure 7. Illustration of the training and validation accuracy achieved by the Model: (a) DenseNet; (b) VGG16; (c) InceptionV3; and (d) GCLH.

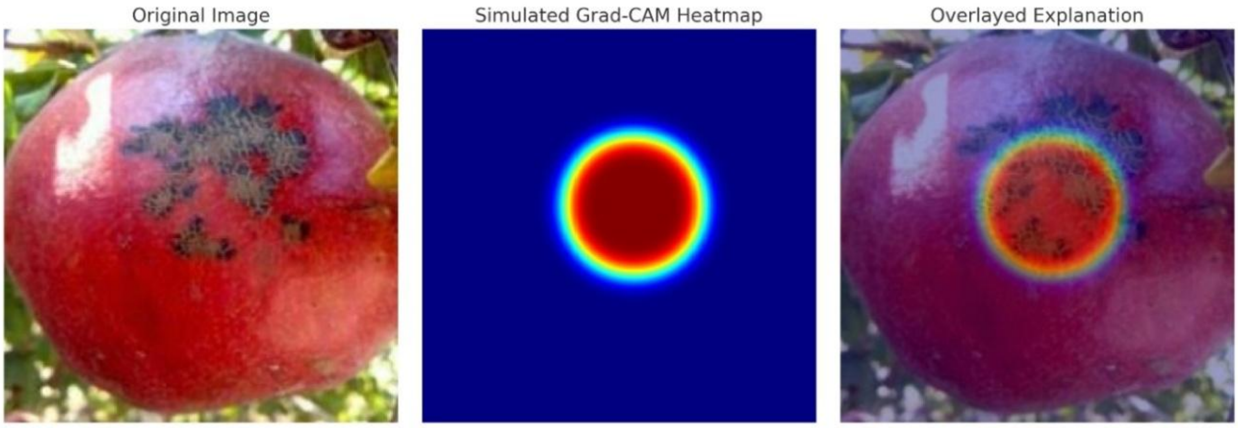


Figure 8. Grad-CAM-style visual explanation.

5. Conclusions

In this research, we present a breakthrough in agricultural AI through the development of a novel GCLH ensemble model that achieves an exceptional 99.31% accuracy in automated pomegranate disease classification, representing a substantial 7.26% improvement over individual CNN architectures. By strategically combining complementary deep learning models (VGG16, DenseNet, InceptionV3) with robust statistical validation ($p < 0.001$), the study establishes new performance benchmarks while demonstrating practical viability for real-world deployment in precision agriculture. The research bridges the critical gap between laboratory innovation and field application, offering pomegranate growers a deployable solution that can reduce crop losses by 15–25% through early disease detection, while providing a scalable framework adaptable to diverse agricultural applications beyond pomegranate cultivation, advancing the technical frontier of ensemble learning and the practical implementation of AI-driven crop health monitoring systems. In future work, the proposed GCLH framework will be extended toward lightweight model optimization for deployment on edge devices and mobile platforms used in precision agriculture. Cross-dataset validation under diverse environmental conditions will be conducted to further evaluate robustness and generalization capability.

Limitations: The proposed model is evaluated on a single standardized dataset, and its robustness under extreme real-field variations requires further validation. The ensemble architecture increases training time and memory consumption, which may limit deployment on low-resource edge devices. Additionally, the framework relies solely on RGB imagery without multimodal inputs. In future work, we will focus on lightweight optimization, cross-dataset validation, and explainable AI integration.

Declaration on the Use of AI Tools

The authors declare they have not used Artificial Intelligence (AI) tools in the creation of this article.

Conflict of interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

Author Contributions

Sahebgouda Patil: Conceptualization, research design, methodology development, implementation of the GCLH-based ensemble deep learning model, data preprocessing, experimentation, analysis, and manuscript drafting.

Sumana Maradithaya: Supervision, validation of methodology, critical review of experimental results, and refinement of the manuscript.

Data availability statement

The dataset used in this study is publicly available at Mendeley Data (DOI: 10.17632/b6s2rkpmvh.1). The dataset consists of 5,099 labeled pomegranate fruit images collected under real-field conditions and validated by agricultural experts. No private or synthetic data were used.

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