A LIGHTWEIGHT ATTENTION BASED CNN ARCHITECTURE FOR MANGO DISEASE DETECTION USING EXPLAINABLE AI

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Bachelor of Science

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Thesis submitted in fulfillment of the requirements
for the award of the degree of
Bachelor of Science

Department of Software Engineering (Major in Data Science)

DAFFODIL INTERNATIONAL UNIVERSITY

December 2025

ACKNOWLEDGEMENTS

The author appreciates the Department of Software Engineering at the Daffodil International University that provided the necessary academic support and resources that were of great importance in the conduction of this work. The truth is that the supervisor has been encouraging, given constructive feedbacks, and professional advice in the course of the research. The author also has identified the family members to have been motivated and their tolerance and support played a pivotal role in the success of this study.

Md Imdadul Islam
December 2025

DEDICATION

This paper is dedicated to my family, mentors, and friends who have so dedicated themselves to my cause through their support, encouragement, and inspiration that led to the completion of this thesis. This has been made possible by their management and trust in me.

ABSTRACT

The most significant limitations to commercial mango production are mango leaf diseases and pest infestation which usually lead to a significant loss in yield and poor quality of the fruits. The visual similarity between the symptoms of disease, changes in the environment, and the low generalization capacity of the standard pre-training deep learning (DL) models are the obstacles to timely and accurate identification. In order to overcome these issues, this paper presents MangoXPPNet, a special and lightweight CNN framework that provides highly discriminative feature extraction without instability in various imaging conditions. The model is tested on three benchmark datasets-MangoLeafBD, Mango Pest Classification and MLDID without changing its fundamental structure and shows good flexibility in the disease and pest categories. It has been experimentally shown that MangoXPPNet classifies MangoLeafBD with near-perfect accuracy (99.5%), as well as has a strong cross-dataset generalization on MangoPest (95.14%) and MLDID (98.33%). ROC-AUC experiments indicate that the separability is high in all classes, and the submission of analysis values to AUC values are close to 1.00 even in cross-domain conditions. Confusion matrices also demonstrate that there are consistent class-level precision of the models, especially those hard to see, like Gall Midge, Sooty Mould, and Powdery Mildew. Grad-CAM and saliency maps were combined to improve interpretation, and it was found that MangoXPPNet partially concentrates on biologically significant areas and thus guarantees clear and reliable forecasts. The findings have made MangoXPPNet a strong, interpretable and generalizable solution to automated mango disease and pest classification. Due to its stability, cross-dataset consistency, and XAI-based transparency, MangoXPPNet has great potential to be implemented in a real-world precision agriculture system that can be used to detect early diagnoses, minimize losses on crops, and sustain mango production.

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List of Abbreviations

Abbreviation	Full Form
AI	Artificial Intelligence
AUC	Area Under Curve
AUROC	Area Under Receiver Operating Characteristic
CNN	Convolutional Neural Network
DL	Deep Learning
Grad-CAM	Gradient-weighted Class Activation Mapping
MLDID	Mango Leaf Disease Identification Dataset
MangoLeafBD	Mango Leaf Bangladesh Dataset
MangoPest	Mango Pest Classification Dataset
MangoXPPNet	Mango Explainable Precision Prediction Network
ROC	Receiver Operating Characteristic
XAI	Explainable AI

Chapter 1

Introduction

1.1 Background and Motivation

Mango (*Mangifera indica* L.) has a great agricultural and economic value especially in tropical and subtropical areas because it is highly demanded and contributes a lot to the global markets of fruits. [1]. Nevertheless, the production of mangoes is under attack because of the many foliar diseases, which may have dire effects on the sustainability and profitability of the production process, including highly affecting the yield, quality, and global supply chain. Anthracnose, a disease that is caused by *Colletotrichum gloeosporioides*, is among the significant diseases and is the most devastating, causing 30-60 percent economic losses in the annual production by impacting both pre and postharvest phases [2]. The combination of digitalized tools and precision agriculture methods can help to increase the monitoring and control of the disease and transmit real-time information to facilitate decision-making and enhance crop protection measures [3]. In addition, new deep learning models have shown great accuracy in disease diagnosis of various mango leaf diseases, which in turn underpins the reduction of dependence on chemical fungicides which is environmentally and health hazardous [4]. Beyond preservation of yields, early disease detection is crucial in reducing the use of chemical fungicides, which are hazardous to the environment and human health [5].

1.2 Current Diagnosis Methods

The most common ways of diagnosing mango leaf diseases are manual inspection and field survey that are user-intensive, time-consuming and prone to human error and subjectivity. Such methods require professional expertise and are not scalable as they will not be efficient at covering vast agricultural lands or processing large amounts of data needed to manage various diseases in time [6, 7]. The introduction of the computer vision and machine learning has greatly improved the detection of mango leaf plant diseases and other plant diseases due to its speed, accuracy, and automation. Such technologies use imaging as a way to pick up inconspicuous visual signs of disease, thus decreasing labor expenses and decreasing the possibility of misdiagnosis [8]. Machine learning specifically deep learning is more accurate in diagnosing plant diseases by using the pre-trained models fine-tuned with datasets of specific plants, which increases the accuracy of the diagnosis, and spending less time during training [9]. Convolutional Neural Networks (CNNs) have gained the focus of plant disease classification owing to its ability to extract and learn hierarchical features of the images automatically, which is crucial in separating various diseases [10].

1.3 Advances in CNNs for Plant Disease Detection

Architectural inventions have also been applied to CNNs, including inception module and squeeze and excitation networks to enhance feature extraction and reduction of model complexity, thus achieving better performance and reduced convergence [11]. These CNNs developments together with hybrid models that combine CNNs with other CNN models like Vision Transformers have shown remarkable levels of accuracy and robustness in mango leaf disease classification; e.g. CNNs models have already been shown to achieve classification accuracy of greater than 99 per cent on test datasets [12]. In general, computer vision and machine learning systems, especially CNNs, have transformed the field of plant disease detection and provided a precision agriculture tool with scalable and objective diagnostic methods that are highly accurate [10, 13].

1.4 Challenges in CNN-based Mango Disease Classification

The CNN-based models to classify the mango leaf disease have a number of challenges especially when it comes to efficiency, scalability and robustness. Among the most notable ones is the prohibitive computational cost and the large number of parameters of traditional CNN models like ResNet, DenseNet, or EfficientNet that are not necessarily resource-efficient in agricultural environments that are resource-limited. The models are usually very computationally expensive, which is why they cannot be deployed to edge devices or real-time applications where fast and effective operation is essential [14] [15]. Additionally, due to the complexity of these models, it might also be hard to be particularly accurate in a complex field setting, where light changes, occlusions, and complicated backgrounds can disrupt disease identification [16] [17].

To deal with these issues, multiple studies have suggested lightweight and hybrid architectures that combine CNNs with other architecture methods such as transformers to improve feature extraction and decrease the computation cost. Such as, DSTANet and ConvTransNet-S are CNNs that use transformers to enhance local and global feature-modelling, and are relatively high in accuracy with fewer parameters and reduced computing cost [14] [16]. Equally, PMVT and HPDC-Net use lightweight architectures and novel modules such as depth-wise separable convolutions and attention mechanisms to achieve high accuracy with smaller model size and lower computational demands, which are more appropriate to be deployed to mobile and edge devices [18] [19]. Although these have been made, the real-time application of deep CNNs to detect agricultural disease has some considerable limitations. Complex models may be required due to the complexity of the conditions of the fields, where they are to operate in, and the absence of predictability that requires high accuracy and robustness [15]. Moreover, larger, labeled datasets that are commonly required to run these models may not always be available with each plant species or disease type [20]. Thus, although lightweight and hybrid models can be a good solution, continuous research is required to develop them further in terms of efficiency, scalability and durability to be applied in agriculture.

1.5 Proposed Solution: MangoXPPNet

When discussing the current issues that the diagnosis of mango leaf disease is facing, our research proposes MangoXPPNet, a compact but powerful hybrid CNN model that combines Ghost modules, Squeeze-and-Excitation (SE) blocks, and Efficient Channel Attention (ECA) mechanisms, enhancing the effectiveness of features and the ability to discriminate that will ensure the accurate classification. To strictly analyze the proposed model, we performed experiments with three benchmark datasets, i.e., MangoLeafBD, MangoPest and Mango Leaf Disease Identification Dataset (MLDID). The datasets include a great range of types of mango leaf diseases and differences in the environment, which is an all-encompassing assessment framework to evaluate the generalization. The proposed MangoXPPNet was benchmarked against four popular deep learning models VGG16, VGG19, ResNet50, and AlexNet which were used as the baseline models in line with the evaluation of accuracy, precision, recall, F1-score, and computational efficiency. These findings reveal that MangoXPPNet has always been superior to the traditional architectures and can attain better classification accuracy using less parameters and inference latency thus illustrating its applicability in disease monitoring real-time applications. Moreover, its hybrid mode of attention enhances the optimization of feature channel-wise and acquisition of global context that allows MangoXPPNet to identify disease-specific patterns which would otherwise be difficult to detect by standard CNNs. The combination of lightweight attention allows not only to increase the sensitivity of the model to inter-channel dependencies but also guarantees the minimum burden on the computer, which is important in terms of its implementation on compact and low-power devices in the agricultural environment.

1.6 Main Findings

In general, the main findings of this paper can be summarized as follows:

- It depicts MangoXPPNet, a convolutional neural network architecture that is both computationally efficient and has Ghost modules, squeeze-and-excitation (SE) and effective channel attention (ECA) schemes. These enable the precise classification of the mango leaf diseases with only a little computing energy.
- The MangoXPPNet was compared with other canonical models, including VGG16, VGG19, ResNet50, and AlexNet, on MangoLeafBD, MangoPest, and MLDID datasets, which allowed to determine its higher performance and the ability to be obtained across different datasets.
- The model was also found to be more efficient considering that similar or even better classification accuracy was attained with significantly lower parameter counts and less memory usage proving that the model is applicable to real-time implementation and embedded agricultural uses.

1.7 Structure of the Thesis

This paper has the following structure:

Chapter 2 provides the literature review and reveals the main gaps in the research on the approach to the mango leaf disease classification and efficient CNN design. Chapter 3 outlines the suggested MangoXPPNet methodology, model structure, data preparation and training setup. Chapter 4 contains the experimental findings, and the results of MangoXPPNets are compared to the performance of the baseline models and previous research. Chapter 5 addresses the general performance of the model, the existing shortcomings, and possible ways to improve it. Lastly, Chapter 6 is a conclusion of the research and outlines the future study directions.

Chapter 2

Literature Review

2.1 Convolutional Neural Networks in Plant Disease Classification

Convolutional Neural Networks (CNNs) have been applied to the performance of plant disease classification since 2016, and the works of Sladojevic et al. and Mohanty et al. provided the methodological basis of the field. Initial studies had shown that convolutional neural networks can perform better than traditional machine-learning models when it comes to automating feature extraction, and also by doing better classification with the use of deep learning. Sladojevic et al., one of the first to use CNNs to detect plant diseases, emphasized the capacity of the models to learn complex structures on the leaf imagery, and these abilities could not be regularly learned with traditional methods that utilized manual-selected features [7, 21]. The work by Mohanty et al. contributed to the development by training convolutional neural networks on the large publicly available dataset of the PlantVillage, thus improving the accuracy of the disease classification in the controlled laboratory setting and showing the strength and scalability of the trained models [22].

These successes have been extended to current studies exploring the different CNN architectures to improve the learning of features and the net performance of the classification. An example is DFNet that uses a dual-CNN approach, which exploits variety of the feature, and it obtains better results in leaf disease classification of both corn and coffee [23]. On the same note, DeepPlantNet and TrioConvTomatoNet present new architectural designs with multiple convolutional layers with optimization strategies, with a remarkable accuracy rate of 98.49 percent and 99.39 percent, respectively, in a range of plant diseases [24, 25]. All these developments highlight the effectiveness of CNNs in identifying plant diseases, which is significantly better than the older machine-learn models with increased accuracy, faster processing, and a more sophisticated ability to process complicated image data. Their incorporation of sophisticated mechanisms, including squeeze-excitation block and tensor subspace learning, also increases the computation adaptability of CNNs to non-homogeneous data and real circumstances in agriculture, e.g., HOWSVD-TEDA and a depth-wise CNN with residual links [26, 27]. In general, the history of CNN-based models has not only optimized the accuracy of plant disease diagnostics but it has also enabled the creation of useful precision-agriculture tools, thus overcoming the main issues concerning food security and sustainable agriculture practices [7, 10].

2.2 CNNs for Mango Leaf Disease Detection

A number of works have built CNN-based models, with the specific aim of detecting and classifying mango leaf disease, and they have shown high accuracy levels and did not require much computation power. After implementing ConvNeXt and Vision Transformer with a feature attention module, the MangoLeafCMDF-FAMNet model has demonstrated exceptional results, reaching classification rates of 99.78, 99.88 and 99.43 on various datasets, demonstrating its superiority and generalizability in the diagnosis of mango leaf disease [12]. Alternatively, there is a hybrid CNN architecture using Inception architecture and depthwise separable convolution, reducing the number of parameters by a huge margin and still reaching high accuracy, with a best accuracy of 99.27 per cent on a varied dataset [28]. Even though this is not specifically applied to mango leaves, a research that applied a modified depthwise CNN with squeeze-and-excitation blocks and residual skip connections demonstrated an accuracy of 98, highlighting how the model is computationally efficient and flexible to plant disease treatment [26]. Also, a survey of CNN uses in plant disease detection highlights the usefulness of the models in the agricultural sphere, and they may be utilized in a precision agricultural system [20]. Although no particular models were specified, including LeafNet, the models discussed show the possibility of CNNs to reach high accuracy and computational efficiency in mango leaf disease detection, with certain models optimised to operate on resource-constrained hardware, hence supporting the practical use of the technology in agriculture [29, 30]. Such innovations in CNN based systems to identify mango leaf disease play a major role in the area of precision agriculture, providing systems that result in the protection of crops and the maximisation of yield.

2.3 Pre-trained Deep Learning Models and Transfer Learning

Pre-trained deep learning models like VGG16, ResNet50, InceptionV3 and DenseNet169 have become common in the field of plant disease classification, and even when applied to particular crops, e.g. mango leaves. Transfer learning is used to adapt these models that are initially trained on large datasets like ImageNet to improve the accuracy and generalisation of the models in detecting plant diseases. Indicatively, DenseNet169 has been shown to have a better ability to generalise to later achieve higher accuracy rates of 81.60% when trained on RGBA images of the CD and S corn disease dataset, hence the importance of augmenting the dataset and excluding the background to enhance the overall performance of the model in fields [31]. In the same way, EfficientNetB3 as a multi-class plant disease classifier in combination with adaptive augmented deep learning has reached an impressive accuracy of 98.71% in this case, thus demonstrating how transfer learning can be used to increase model accuracy and real-time diagnostic possibilities [32].

However, in spite of these developments, there still exist a number of limitations. Ready-trained convolutional neural network models are difficult to use, both in terms of being expensive to run and difficult to set up, particularly where resources are limited. These models require a high level of computation, a large amount of memory and processing requirements, which may hinder their application in real-time agriculture [33]. Furthermore, the applicability of the models, trained with images obtained in the laboratory, to the field is still a major issue, and environmental variability may negatively influence the model accuracy [31]. To overcome them, researchers have investigated methods like fine-tuning and feature extraction, which does not only enhance the accuracy but also decrease the training time and trainable parameters, hence making the models more practical in usage [34]. In short, although there is a lot of potential in the use of pre-trained models in the detection of plant diseases, more studies are needed to address the shortcomings and to increase their relevance to various agricultural settings.

2.4 Lightweight CNNs for Resource-Constrained and Real-Time Applications

Studies of lightweight convolutional networks that could be used to identify plant diseases under resource-constrained or real-time working conditions have produced a number of encouraging architectures that achieve significant predictive performance with a significantly lower calculation cost. The most practical example of these is the MobRes architecture, a combination of residual learning and MobileNetV2 feature extractor, which is able to achieve 97.73 percent on the Plant Disease Expert and 99.47 percent on the PlantVillage, using just 3.51 million parameters, and which makes it well-suited to the mobile deployment [35]. Similarly, the ultra-lightweight efficient network (ULEN) uses residual depth-wise convolution and spatial pyramid pooling, which obtain high classification accuracy using only 100,000 parameters hence being suitable in devices with lower power consumption [15]. Based on the MobileViT architecture, the PMvt model adds a convolutional block attention module to refine the feature focus and achieves 93.6 per cent accuracy on a wheat dataset using only 0.98 million parameters and outperforming other light models including MobileNetV3 [18]. Grow-Light smart monitoring system uses down-scaled inception blocks and dense residual links, with very little parameterisation versus high performance, and dynamics is 96.75% on the PlantVillage dataset [36]. MS-Net proposes skip connections optimized with a whale optimization algorithm, and the model does not require many parameters, but the accuracy on the PlantVillage dataset is 99.8 per cent [37]. LSGNet, which is tomato disease detection oriented, employs effective channel attention and position-aware cells and is higher in accuracy compared to classical models with 0.75 million parameters only [38]. LiSA-MobileNetV2 enhances MobileNetV2 with Swish activation and attention to achieve 95.68 per cent on rice disease classification with drastically reduced parameters and floating-point operations [39]. Taken together, these results indicate that it is possible to achieve a good balance between the performance and efficiency of lightweight CNN architectures, making them useful in the real-time detection of plant diseases in resource-constrained settings.

2.5 Limitations and the Need for Hybrid Lightweight Models

The current deep learning systems of detecting mango leaf disease have few shortcomings, most of which concern efficiency and scalability as well as real-time applications in farm settings. The traditional CNNs and pre-trained models though they have high accuracy, they can take millions of parameters, which does not suit the resource-limited devices like mobile and embedded systems. This is the drawback that is reflected in the requirement of lightweight models, which are able to keep high performance and also minimize the computational cost and the number of parameters, which is observed in the proposed hybrid CNN models that combine depthwise separable convolutions and Inception models to realize a large reduction of parameters without more noticeable accuracy loss [28]. The difficulty of applying such models in real-life agricultural environments is also aggravated by the fact that these models must be able to operate in more complex field conditions, including different lighting and occlusions, which are difficult to handle using traditional CNNs because of their large computational cost and non-adaptability [15] [16]. Lightweight hybrid CNN architectures are required to address these problems and offer the ability to achieve a tradeoff between accuracy and computational cost. Combining Ghost modules with attention mechanisms like Squeeze-and-excitation (SE) and Efficient Channel Attention (ECA) has been shown to result in the high classification accuracy and, at the same time, be able to improve the overall effectiveness of the models. Ghost modules make use of the fact that they produce more feature maps with fewer parameters, whereas attention mechanisms enhance the feature differentiation by concentrating on disease-relevant information and reducing irrelevant background noise [40]. Such innovations enable creating models that are accurate and efficient enough to be deployed in the real-time in the agricultural setting, thus closing the significant gaps that exist in current models and advancing the sphere of precision agriculture [12, 41].

2.6 Comparative Analysis

The comparative analysis presented in Table 2.1 highlights the evolution and diversity of deep learning approaches for plant disease classification. As the research advancement went up, more advanced architectures such as DenseNet, InceptionV3 and hybrid models were presented, with each one trying to enhance accuracy, generalization and computational efficiency. The lightweight models like LeafNet and Mob-Res were also developed to support the requirement of the application of real-time and resource-constrained applications, and plant disease detection is even more available to the field deployment. It can also be seen in the table that though most of the models are quite accurate on benchmark conditions, there are still difficulties in generalizing to real-world conditions, dealing with class imbalances, and also being robust to different environmental conditions. Although some of them are performing well in controlled environments, some of them are not scalable or have high computational power, reducing their practical use.

In general, the comparative analysis highlights the critical role of accuracy, efficiency, and generalizability in creating plant disease classification systems. It also underscores the necessity of continuing to develop models capable of functioning reliably in various types of data sets as well as under various conditions that will enable future studies in strong, explainable, and field-ready deep learning solutions to agriculture.

Ref.	**Model**	**Dataset**	**Contribution**	**Challenges**
Sladojevic et al. (2016)	Deep CNN	Leaf images	Pioneered CNN use for plant disease detection; outperformed traditional ML.	Small dataset; not reliable under field noise or lighting variation.
Mohanty et al. (2016)	AlexNet, GoogLeNet (TL)	PlantVillage	Showed high DL accuracy and established PlantVillage as benchmark.	Overfits lab images; weak real-field generalization.
Prabu et al. (2019)	CNN + MobileNetV2 + SVM	Mango leaf dataset	Proposed optimized CNN for mango disease classification.	Limited geographic diversity; not field-tested.
Rizvee et al. (2021)	LeafNet (Lightweight CNN)	MangoLeafBD	Presented lightweight CNN excelling at mango leaf classification.	Generalization weak outside MangoLeafBD; no cross-site tests.
Hari et al. (2020)	CNN + Fine-Tuning	Mixed tropical leaves	Used augmentation and tuning for mango, banana, guava detection.	Suffers under variable lighting and occlusions.
Too et al. (2019)	DenseNet, ResNet (TL)	PlantVillage	Comprehensive TL comparison; DenseNet best-performing classifier.	Models heavy; unsuitable for real-time mobile use.
Varma et al. (2019)	InceptionV3 (TL)	PlantVillage	Showed strong feature extraction performance for plant disease tasks.	Dependent on clean, centered images.
Ferentinos (2018)	VGG, AlexNet, ResNet	87k images	Developed DL models for multi-crop disease detection.	Lower accuracy on unseen field images.
Naik et al. (2017)	VGG16/19, ResNet50 (TL)	Custom crop dataset	Applied TL for mango leaf and fruit classification.	Model complexity high for embedded applications.
Ashurov et al. (2025)	Depthwise CNN + SE + Residual	Plant diseases	Lightweight model with improved attention-enhanced feature learning.	Needs careful tuning; small models may overfit.
Tuncer (2021)	Inception + Depthwise CNN	Plant leaves	Hybrid CNN reduces parameters significantly.	Not mango-specific; performance varies across datasets.
Adnan et al. (2023)	EfficientNetB3 (TL)	Multiclass plant diseases	Achieved high accuracy using EfficientNet scaling.	Still compute-heavy for edge devices.
Ahmad et al. (2023)	DenseNet169 (TL)	Corn disease (RGBA)	Showed dataset preprocessing (BG removal) improves TL.	Still lower accuracy than newer approaches.
Pal et al. (2025)	Mob-Res (MobileNetV2 + Residual)	PlantVillage	Very lightweight (3.5M params) with strong performance.	Accuracy drops in real-field test scenarios.
Wang et al. (2023)	ULEN (Ultra-Light CNN)	Plant diseases	Extremely compact depthwise CNN with high accuracy.	Needs validation on mango-specific datasets.
Zhou et al. (2024)	Ghost + SE/ECA Hybrid CNN	Plant diseases	Ghost modules + attention give strong accuracy with minimal parameters.	Hyperparameter-sensitive; tuning required.
Ergün (2025)	MangoLeafCMDF-FAMNet	MangoLeafBD, MangoPest	Achieved 99.78–99.88% using ConvNeXt + attention fusion.	Model too heavy for real-time or mobile deployment.
Jian et al. (2025)	Lightweight Hybrid CNN	Crop diseases	Designed efficient lightweight CNN for real-time use.	Needs more diverse environmental evaluation.
Pham et al. (2020)	LeafNet variant	Plant disease datasets	Showed CNN feasibility on resource-constrained hardware.	Lower accuracy than recent hybrid CNNs.
Darwish et al. (2019)	CNN frameworks	General plant pathology	Reviewed CNN adoption in smart agriculture.	High-level review; no dedicated mango dataset.

Table 2.1: Twenty key CNN-based, transfer learning, and lightweight deep learning studies foundational to mango leaf disease classification.

Chapter 3

Methodology

3.1 Overview of the Proposed Framework

This part will outline the methodology used in the current study including data acquisition guidelines, predata processing and MangoLeafXNet architecture integration. Figure 1 shows in detail the stepwise description of the proposed methodology.

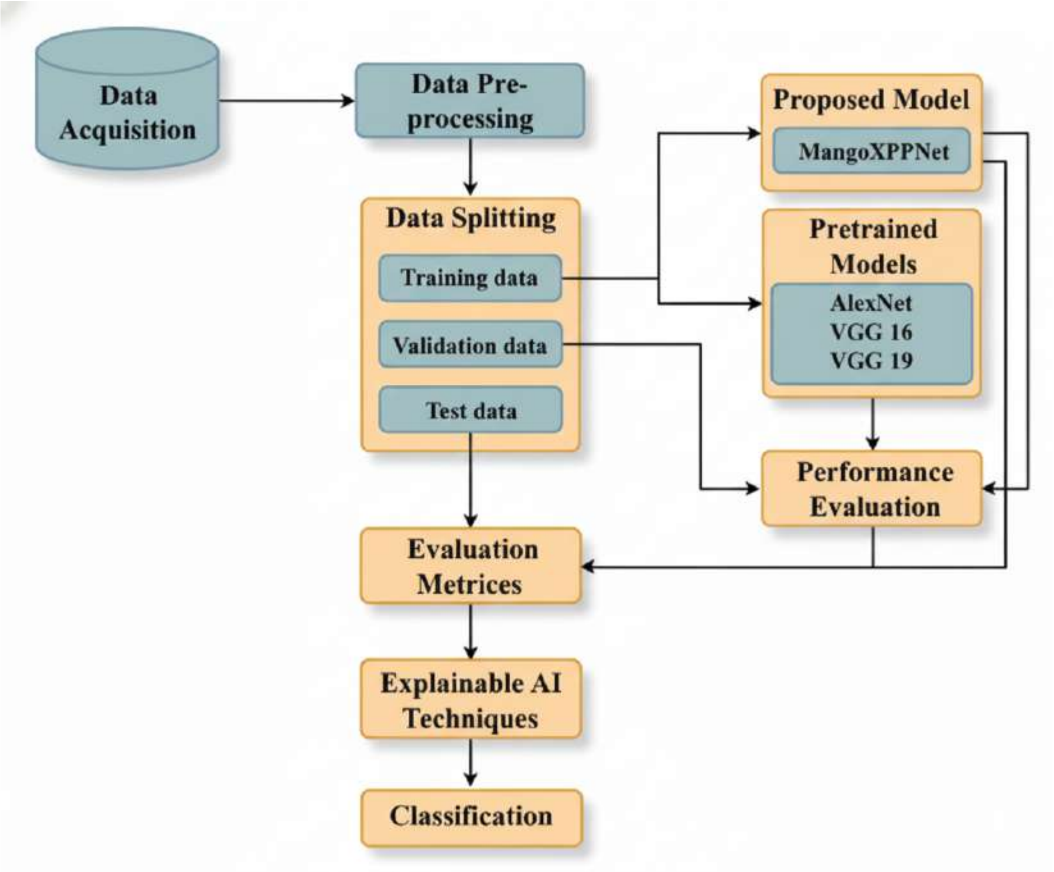


Figure 3.1: Workflow of the mango leaf disease classification process, including data acquisition, preprocessing, data splitting, and model evaluation using pretrained models and MangoLeafXNet.

3.2 Data Acquisition and Subsequent Pre-Processing

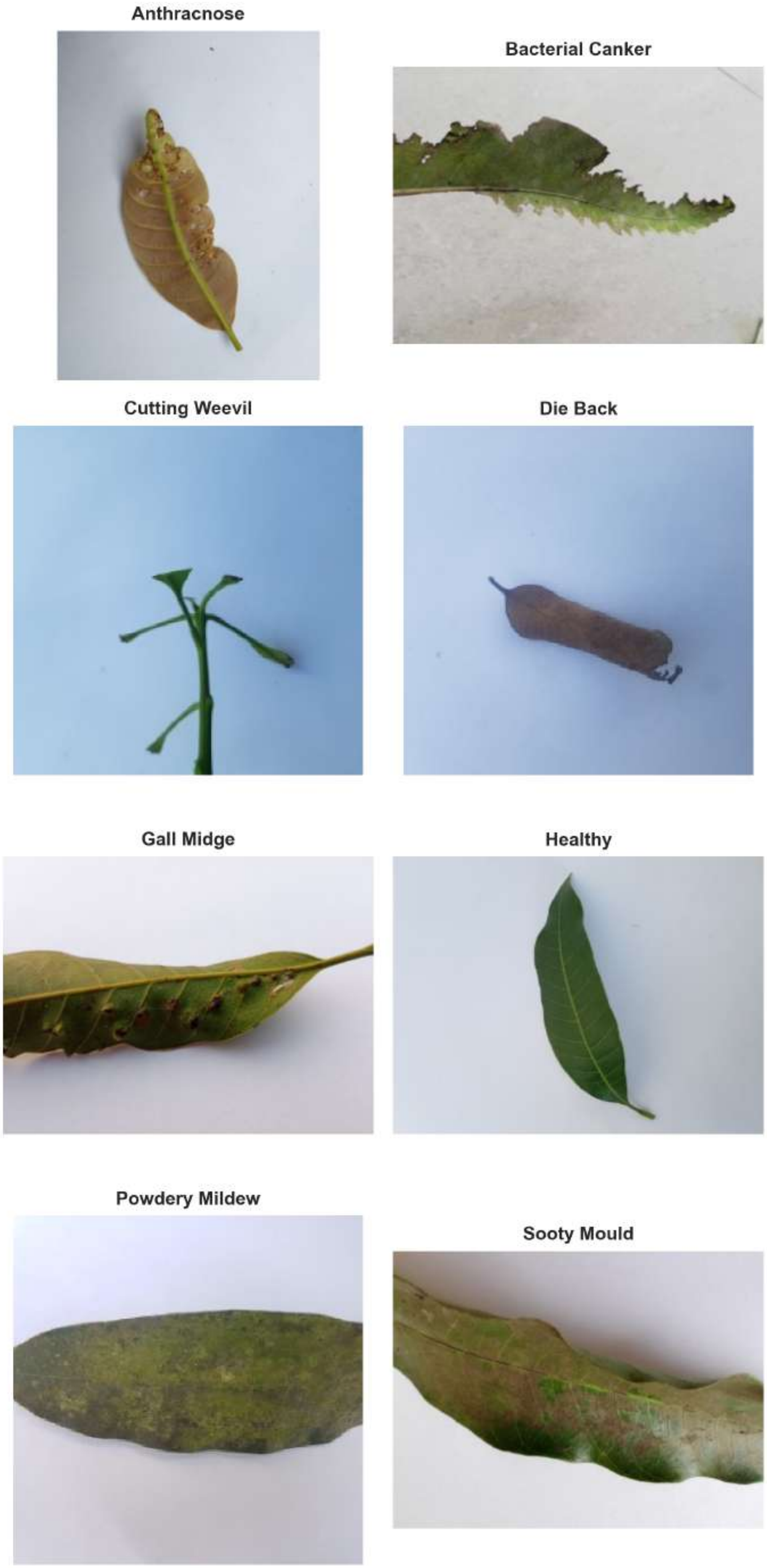
3.2.1 MangoLeafBD Dataset

The MangoLeafBD dataset [21] is primarily used in this research and it is the first comprehensive collection of mango leaf pathology images built in Bangladesh. Four mango orchards (Sher-e-Bangla Agricultural University (Dhaka), Jahangir Nagar University (Savar), Udaypur village (Rajbari), and Itakhola village (Nilphamari)) that are geographically separated to ensure regional coverage were used to assemble data. All in all, the corpus contains 4,000 chromatic images which have been taken using the mobile devices in ambient light and which are stored as JPEG files at a natural resolution of 240×320 pixels. MangoLeafBD consists of eight balanced groups where one includes healthy leaves, and the rest constitute major foliar diseases: Sooty Mould, Gall Midge, Die Back, Cutting Weevil, Anthracnose, Powdery Mildew as well as Bacterial Canker. All of the samples comprise 500 examples, hence, no sample will be disproportionately represented, and bias will be minimal. Figure 3.2 shows an overview of the distribution of classes and the examples.

The paper applies a number of important preprocessing operations to clean up the image data to facilitate training and validation. First, the dataset will be divided into training, testing and validation set in ratio of 80-10-10. All images are resized to 227 x 227 pixels in order to have the same size in terms of input size. Normalization is utilized to make the pixel values in the entire dataset standard. Also, data-augmentation like horizontal flipping, random rotation, width and height shifting, zooming and brightness are used. These tricks are used to increase the diversity of the data set, and the model is able to generalise to different object orientations and situations. Although the dataset is balanced, there may be certain biases related to the fact that the dataset is only gathered in four orchards in certain areas of Bangladesh, which might not be a complete representation of mango diseases variation depending on specific environmental factors or areas. We used Gaussian Blur and CLAHE (Contrast -Limited Adaptive Histogram Equalisation) to eliminate any possible image noise and improve the quality of the dataset. Gaussian Blur is used to remove small artefacts or noises in the images whereas CLAHE enhances the contrast and makes diseases features more visible and hence enhances the model to extract meaningful features and generalise more effectively.

3.2.2 MANGO PEST Dataset

To examine the robustness of the proposed method, we included the Mango Pest Classification dataset in Indonesia [42]. This dataset is an imagery that was recorded in mango orchards infested with fifteen different pest species, as well as an experimental category that contains healthy foliage. The damage that is caused by the pests are



Anthracnose

Bacterial Canker

Cutting Weevil

Die Back

Gall Midge

Healthy

Powdery Mildew

Sooty Mould

Figure 3.2: Overview of the distribution of classes and examples in the MangoLeafBD dataset.

visibly apparent through distinctive structural deformities and discolorations. The process of image acquisition was done using low cost imaging sensors, commonly used by local agrarian producers to collect data in an in-situ manner thus reflecting realistic agricultural settings. The most common resolution of the pictures is 500x 375 pixels. However, the data set shows that there is a severe class imbalance, since the sample sizes of the different categories of pests are uneven. The distribution of the classes in a visual representation is shown in Figure 3.3.

Figure 3.3: Visual representation of class distribution in the Mango Pest dataset.

In order to correct the imbalance, oversampling methodology was adopted. Classes with small sample sizes were replicated until the occurrence of the most populous classes were the same, such as in the case of the Mictis longicornis, which is composed of 86 images. Consequently, no classes were made disproportionate. Figure 3.4 illustrates the distribution of the dataset before and after performing the oversampling, and all the annotations of the sample are shown in Table 3.1.

After the balancing process, the images were all reduced to 227 x 227 pixels to ensure that they were similar across spatial dimensions hence aligning with the traditional input requirements of convolutional neural network designs. The intensity values of pixels were normalised in order to standardise the distribution and this improves the convergence stability, during the training stage.

Also, data augmentation techniques, including horizontal flipping, random rotation,

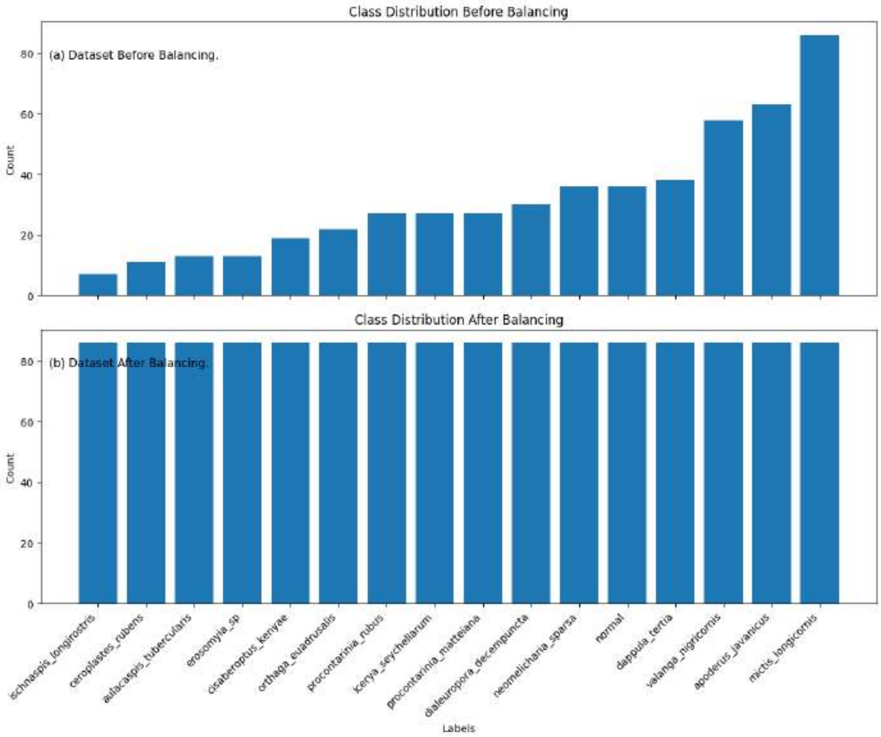


Figure 3.4: Distribution of the dataset before and after oversampling.

horizontal and vertical translations, zooming were used to artificially increase the variability of the dataset. These augmentations enable the ability of the model to generalize to previously unseen changes in image orientation, scale, and illumination, and eliminate the possibility of overfitting at the same time. The dataset was then divided into training `(80%)`, testing `(10%)`, and validation `(10%)` to provide a balanced framework of model training and, consequently, evaluation.

3.2.3 Mango Leaf Disease Identification Dataset (MLDID)

In order to assess the performance and generalizability of the suggested model even more, we used Mango Leaf Disease Identification Dataset (MLDID) [43]. The dataset comprises 3,000 high-resolution photos of mango leaves, that were collected in different areas in Bangladesh, and that were taken in different environmental conditions.

It has five different classes such as Gall Midge, Healthy Leaves, Die Back, Bacterial Canker and Anthracnose, whereby 600 samples represent each of the different classes to provide the balance. All images are scanned at 512x512 pixels and this provides enough detail to identify fine-grained disease presentations and morphology changes that are needed to have reliable classification. The general overview of the data and its class distribution is presented in Figure 3.5.

The preprocessing pipeline that was utilized in the MLDID data is consistent with the one that was applied to the other datasets in this study. All the images were rescaled

Class Name	Data Before Oversampling	Data After Oversampling
ischnaspis_longirostris	07	86
ceroplastes_rubens	11	86
aulacaspis_tubercularis	13	86
erosomyia_sp	13	86
cisaberoptus_kenyae	19	86
orthaga_euadrusalis	22	86
procontarinia_rubus	26	86
icerya_seychellarum	27	86
procontarinia_matteiana	27	86
dialeuropora_decempuncta	30	86
neomelicharia_sparsa	36	86
normal	36	86
dappula_tertia	38	86
valanga_nigricornis	58	86
apoderus_javanicus	63	86
mictis_longicornis	86	86

Table 3.1: Annotations of the sample before and after oversampling.

to the same size (227 x 227 pixels) thus meeting the dimensionality size criteria of the models used, and then normalised to standardise distributions of pixel intensities.

In order to increase the generalizability of the models, as well as decrease the overfitting risks, a complex combination of data augmentation methods was applied, including random rotations, zoom operations, and horizontal flips in both width and height, and translational shifts. These augmentations bring about an array of spatial orientations and scale changes thus making it easier to learn robust, invariant representations of disease manifestations in a variety of viewpoints and under varying illumination conditions.

The dataset was further split into training `(80%)`, validation `(10%)`, and test `(10%)` subsets after preprocessing thus creating a balanced dataset that was the basis of effective model optimization and strict performance assessment.

3.3 Proposed MangoXPPNet Architecture

The proposed MangoXPPNet is a lightweight but powerful convolutional neural network (CNN) specifically designed for the classification of mango leaf disease and pest. It balances computational efficiency with strong representational ability, making it suitable for resource-constrained agricultural environments.

The architecture is organized into two main modules:

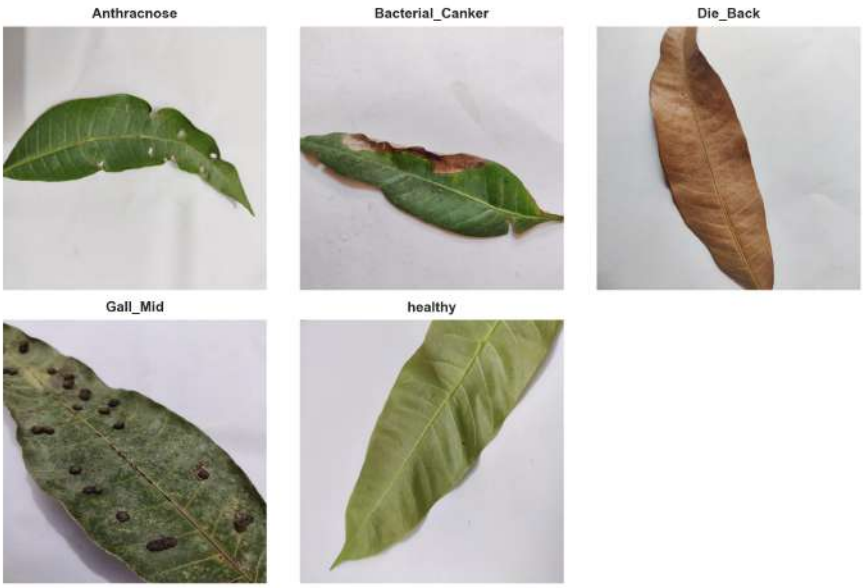


Figure 3.5: Overview of data and class distribution in the MLDID dataset.

- Feature extraction backbone – captures hierarchical visual information
- Classification head – makes the final categorical prediction

Table 3.2 depicts layer-specific details.

3.3.1 Convolutional and Feature Extraction Layers

MangoXPPNet takes as input an RGB image of size 227×227×3. Its backbone includes Ghost modules, channel attention (Squeeze-and-Excitation (SE) and Efficient Channel Attention (ECA)), and MobileNetV3-like bottleneck layers, achieving high-level feature representation efficiently. Batch normalization and rectified linear operation (ReLU) stabilize optimization and support non-linear changes for robust gradient movement.

1. Ghost stem block (7×7, 64 channels): Wraps up low-level visualities like leaf outlines, line divisions, and texture demarcations. Squeeze-and-excitation (SE) block recalibrates channel responses, supplementing informative features and reducing background noise.
2. Ghost block with SE and downsampling (5×5, 128 channels): Applies 128 filters, decreases spatial resolution, and uses max-pooling. SE module enhances middle-range disease and pest features.
3. Ghost block with ECA (3×3, 256 channels): Captures complex texture patterns and local color variation. ECA module improves channels sensitive to disease-relevant structures.

Stage / Layer group	**Filter size / operation**	**Filters / units**	**Stride**	**Output size**	**Activation / Attention**
Input	–	–	–	227×227×3	–
Ghost Group 1	Conv (7×7) + depthwise 3×3	64	2	114×114×64	ReLU + SE
Ghost Group 2	Conv (5×5) + depthwise 3×3	128	1	114×114×128	ReLU + SE
Max Pooling 1	MaxPool (3×3)	–	2	57×57×128	–
Ghost Group 3	Conv (3×3) + depthwise 3×3	256	1	57×57×256	ReLU + ECA
Bottleneck Block (rb1)	1×1 expand → DW 3×3 → 1×1 proj	512	1	57×57×512	ReLU + SE
Conv4	Conv (3×3)	512	1	57×57×512	ReLU
Max Pooling 2	MaxPool (2×2)	–	2	29×29×512	–
Conv5	Conv (3×3)	256	1	29×29×256	ReLU
GAP	Global Average Pooling	–	–	256	–
FC1	Dense	256	–	256	GELU + Dropout (0.3)
Output Layer	Dense	16	–	16	Softmax

Table 3.2: Feature maps used in the proposed MangoXPPNet architecture.

4. Residual Bottleneck Block (MobileNetV3, 512 channels): Expands channels, applies depth-wise convolution, and projects back to 512 channels. Internal SE block recalibrates channels for expressive and efficient feature learning.

5. Conv4 stage (3×3, 512 channels + pooling): Further enriches representations, batch normalization and ReLU activation, followed by max-pooling to reduce spatial dimension and grow receptive field.

6. Conv5 stage (3×3, 256 channels): Compresses deep and discriminative features for the classification module.

In general, MangoXPPNet backbone is efficient and expressive. Ghost modules remove redundant calculations, and SE/ECA attention mechanisms increase feature sensitivity to disease-relevant areas, enabling sharp and robust accuracy with a small parameter footprint.

3.3.2 Classification Layers

At the end of the convolutional hierarchy, feature maps are converted into class-specific probability distributions by the classification head. Each of the 256 channels in the 29×29×256 tensor is aggregated into one feature description layer (Global Average

Pooling (GAP)), resulting in a feature space of 256 dimensions. This increases interpretability and enables Grad-CAM-style post-hoc analysis. The aggregated features are input to a fully connected Dense layer of 256 neurons, using GELU activation for smooth non-linearity and extensive feature interaction. Dropout (rate 0.3) alleviates overfitting. The final softmax Dense layer of 16 neurons gives predicted probabilities for the 16 mango disease and pest classes.

MangoXPPNet has approximately 4.11 million trainable parameters (15.68 MB in 32-bit floating-point representation), providing enough capability to model complex disease patterns in mango leaf images.

3.4 Comparative Analysis on Pretrained Models

The comparative analysis was conducted with various established pretrained convolutional neural networks (CNNs), such as AlexNet, VGG16, VGG19, and ResNet50. These architectures were selected based on their diversity, historical value, and performance in image-classification tasks. They include early CNN models like AlexNet and VGG, as well as more modern, parameter-efficient models such as ResNet and EfficientNet.

The comparisons between MangoXPPNet and these benchmarks provide an overall view of the performance and highlight the benefits of MangoXPPNet in accuracy, computational efficiency, and scalability. Such a comparison makes it possible to objectively evaluate how the model achieves state-of-the-art performance with a significantly reduced parameter footprint and computational cost compared to traditional deep-learning models.

3.4.1 AlexNet

AlexNet has eight learnable layers, including five convolutional layers and three fully connected layers. It introduced several groundbreaking features that have become standard in modern deep learning, such as Rectified Linear Unit (ReLU) activation, Local Response Normalization (LRN), overlapping max-pooling, and dropout regularization to curb overfitting [44].

Network structure:

- Conv1 → Max-Pooling
- Conv2 → Max-Pooling
- Conv3 → Conv4 → Conv5 → Max-Pooling
- Fully Connected: FC1 → FC2 → FC3

3.4.2 VGG16

VGG16 has thirteen convolutional layers and three fully connected layers, organized into five consecutive convolutional blocks. All convolutions use a 3×3 kernel with a stride of one, and a 2×2 max-pooling layer is used at the end of each block to gradually decrease spatial dimensions.

Network structure:

- Block 1: Conv ×2 (64 filters) → Max-Pooling
- Block 2: Max-Pooling → Conv ×2 (128 filters)
- Block 3: Conv ×3 (256 filters) → Max-Pooling
- Block 4: Max-Pooling → Conv ×3 (512 filters)
- Block 5: Conv ×3 (512 filters) → Max-Pooling
- Fully Connected: FC1 → FC2 → FC3

VGG16's deep and regular architecture, with small 3×3 filters, enables feature extraction at different scales. Its simplicity and balanced depth make it a strong baseline for evaluating compact architectures like MangoXPPNet.

3.4.3 VGG19

VGG19 is a variant of VGG16, adding extra convolutional layers for increased depth and fine-grained feature extraction. The design ethos remains the same, with 3×3 convolutions and 2×2 max-pooling, but later blocks are deeper.

Network structure:

- Block 1: Conv ×2 (64 filters) → Max-Pooling
- Block 2: Max-Pooling → Conv ×2 (128 filters)
- Block 3: Conv ×4 (256 filters) → Max-Pooling
- Block 4: Max-Pooling → Conv ×4 (512 filters)
- Block 5: Conv ×4 (512 filters) → Max-Pooling
- Fully Connected: FC1 → FC2 → FC3

VGG19 builds on VGG16 by providing more abstract representations due to greater hierarchical depth. Comparing MangoXPPNet and VGG19 highlights trade-offs between depth, computational cost, and model performance, especially in disease-classification tasks.

3.4.4 ResNet50

ResNet50 is a fifty-layer convolutional network that introduced residual learning, a key advance enabling much deeper networks without vanishing gradients. Shortcut connections allow identity mappings, efficient gradient propagation, and feature reuse across layers.

Network structure:

- First Round: Conv → Max-Pooling
- Conv2_x Block: 3 residual units
- Conv3_x Block: 4 residual units
- Conv4_x Block: 6 residual units
- Conv5_x Block: 3 residual units
- Global Average Pooling → Dense Layer

ResNet50 is a deep architecture used as a benchmark for scalable models. Its residual connections contrast with the sequential feature-extraction nature of MangoXPP-Net, allowing performance comparisons between residual-based depth optimization and lightweight attention-enhanced feature learning.

Chapter 4

Experimental Setup

4.1 Experimental Setup

4.1.1 Hyperparameter Settings

The mango XPPNet architecture was used to identify both types of mango leaf disease and healthy leaves with three datasets, namely MangoLeafBD[45], Mango Pest Classification[42], and Mango Leaf Disease Identification Dataset (MLDID)[43]. The model was trained in 100 epochs on the MangoLeafBD and MLDID datasets, and in 50 epochs on the Mango Pest dataset. MangoLeafBD and MangoPest were trained on a batch size of 12, whereas MLDID was trained on a batch size of 16, depending on the memory used and the size of the dataset. All experiments were based on the Stochastic Gradient Descent (SGD) optimiser with an initial learning rate of 0.001 in the case of MangoLeafBD and MangoPest, and 0.0005 in the case of MLDID to maintain a steady convergence rate. All the pretrained CNN architectures (AlexNet[44], VGG16, VGG19, and ResNet50) were fine-tuned under the same experimental conditions in order to offer a consistent basis of comparison. All the models were trained with the SGD algorithm and a learning rate of 0.001, with 32 inputs in a batch, and 100 epochs. Such a homogenous design allows an equal comparison, with the disparities in performance due to an architectural difference but not to the hyper-parameter difference.

4.1.2 Callback setup

Along the main optimisation control settings, three call back mechanisms were also added in all experiments to make the training of the model stable and efficient. Validation accuracy was monitored using a model-checkpointing callback and only the model weights with the best performance were saved so that the final model would be the model with the maximum validation accuracy in training. Early stopping was used where the value of patience was fifteen epochs and the loss at validation was checked and the training was stopped when there was no observable improvement which therefore prevented the execution of extra epochs and minimized over-fitting. Learning-rate reduction strategy was used also, where the validation loss was observed instead and the learning rate was halved when the validation loss did not decrease in five consecutive epochs. The learning rate was kept at least at the minimum value of 0.0000001. All these settings of the call backs contributed to stabilisation of the optimisation, better convergence in the later stages of training and consistency and reliability across all experiments. This provides a detailed summary of the training settings and configuration-specific parameters and details the most important hyper-parameters and settings used in all the experiments.

4.2 Hyperparameter Tuning

The set of hyper-parameters used to create the proposed MangoXPPNet model were identified by both trial and error and the experience of the earlier studies of the CNN-based plant disease recognition. The aim was to find environments with compromise of stability of training, generalisation ability and computational efficiency. The key hyper-parameters that have been fine-tuned in this paper will involve the batch size, dropout rate, and learning rate as follows.

4.2.1 Batch Size

The choice of 12 and 16 as the batch size is determined by the nature of datasets and access to the hardware. In particular, batch size 12 was applied in the case of MangoLeafBD and MangoPest, and 16 was applied in the case of MLDID. The experimental analysis showed that smaller batches (e.g., 8) led to larger validation-accuracy variance because of unstable gradient update, but larger batches (e.g., 32) took longer to converge without significant improvement in performance.

4.2.2 Dropout Rate

The dropout was added in two levels (0.3 and 0.4) to reduce the over-fitting and increase the model generalisation. A dropout rate of 0.3 produced the most consistent regularisation effect in shallower layers and 0.4 produced a better regularisation effect in deeper layers through systematic testing in the range of 0.2 to 0.5. The dual dropout structure was used to make sure that learning features was balanced and also avoids over-dependence on particular neurons.

4.2.3 Learning Rate

The learning rate of MangoLeafBD and MangoPest was set at 0.001 which as well as MLDID was established through controlled experiments and was empirically determined. Greater values (e.g. 0.01) produced an unstable convergence and oscillating losses, and smaller values (e.g 0.0001) produced too slow optimisation. The determined learning rates established a good balance between the rate of convergence and the smoothness of the training without facing gradient divergence.

4.2.4 Optimization Strategy

The hyper-parameters have not been optimised automatically by using grid search or Bayesian optimisation but by trial and error. Since the models have a lightweight architecture and training can be effectively tuned manually, it offered a viable and computationally efficient method of comparing various configurations with the datasets.

Chapter 5

Results

5.1 Quantitative Assessment

This part shows the experimental data of the proposed MangoXPPNet model and its performance against long-established pretrained CNN architectures and earlier literature. The model was trained and evaluated separately on three benchmark datasets, namely, MangoLeafBD, Mango Pest Classification, and Mango Leaf Disease Identification Dataset (MLDID) and to test its generalisation performance in relation to various mango leaf imagery.

A standard MangoXPPNet architectural topology was adopted in every test for equity and uniformity. Under nonintrusive changes to hyperparameters, including batch size, and learning rate, only slight changes to nonintrusive changes were undertaken to enable dataset-specific properties and maximise training stability. This methodology shows the strength, flexibility, and scalability of the suggested architecture, thus indicating its potential to ensure the high performance without the necessity of structural changes depending on the dataset. Detailed performances of the models on each dataset, and comparisons with conventional pretrained models (AlexNet, VGG16, VGG19 and ResNet50) in both classification accuracy and precision, recall, F1-score, and computational efficiency are presented in the following subsections. All these analyses demonstrate the ability of MangoXPPNet to find a trade off between accuracy and efficiency to be applied practically in agriculture.

5.1.1 Model Training and Evaluation Overview

The entire learning behaviour of the assessed deep learning models has been depicted in Figure 5.1, Figure 5.2, Figure 5.3, Figure 5.4, and Figure 5.5, in which the accuracy of training and loss of the joint training and validation of the models in respect to the epochs have been shown. These numbers enable one to directly compare the convergence, the generalization behaviour and the stability of optimization of AlexNet, VGG16, VGG19, ResNet50, and the proposed MangoXPPNet architecture. Baseline models of AlexNet, VGG16, and VGG19 all exhibit continuous trends of accuracy as the training process progresses even though the trends tend to exhibit smooth transitions of direction as the more the epochs, the more the transitions. These models provide stable learning with the validation curve shows random variation and that means that there are some regions where the process of generalization is not so stable and still the process recovers the training curve. ResNet50 is more robust and exhibits overblown oscillations in its validation performance as indicated by the accuracy and loss curves. The latter, especially during the initial and intermediate training phases, point to the fact that ResNet50s is prone to the impact of classes and that it overfits in the short-term between training sessions. Conversely, convergence behaviour of MangoXPPNet model proposal is the most stable and smooth than other models. It possesses high rates of accuracy curve and is almost perfect throughout the training period (in training and validation). In the same way, its loss curves are negative but not much curves exist between the training loss and the validation loss. The behaviour proves the fact that MangoXPPNets has an efficient discriminative feature extraction and can preserve a stable performance even in case of further learning progress.

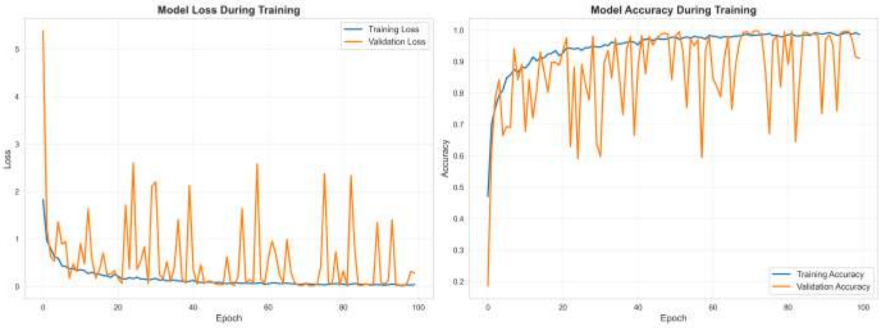


Figure 5.1: Training/validation accuracy for AlexNet.

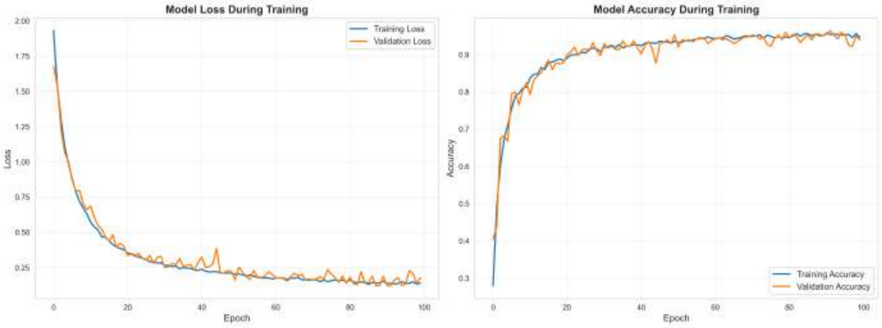


Figure 5.2: Training/validation accuracy for VGG16.

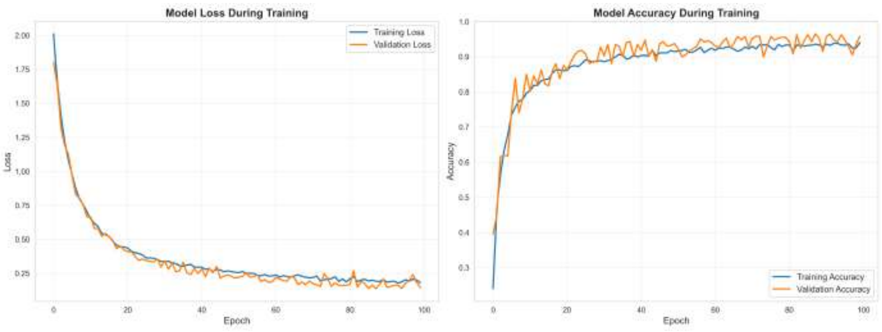


Figure 5.3: Training/validation accuracy for VGG19.

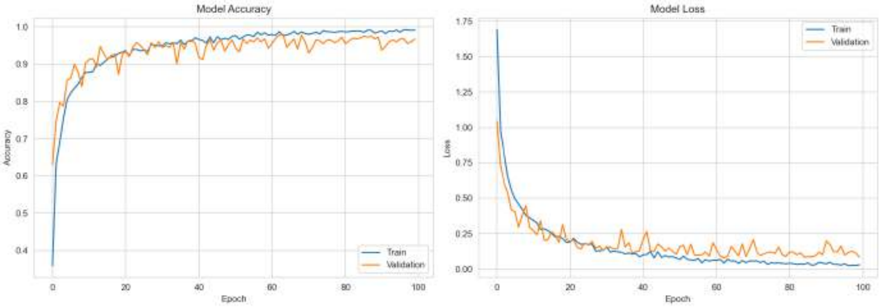


Figure 5.4: Training/validation accuracy for ResNet50.

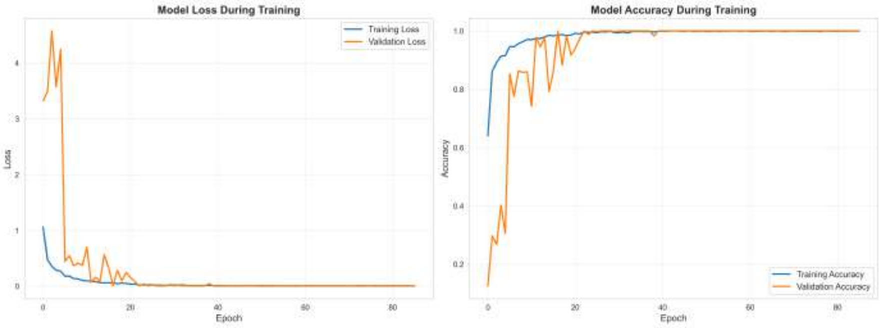


Figure 5.5: Training/validation accuracy for MangoXPPNet.

5.1.2 Cross-Dataset Performance

Figure 5.6 and Figure 5.7 illustrate the cross-dataset evaluation and are helpful to illustrate the flexibility and robustness of MangoXPPNet to the MangoLeafBD data only. Having been trained on MangoPest dataset (Figure 5.6), it is expected that the model would initially undergo a small oscillation in the validation accuracy in the first few epochs, as would be normal due to the variability of the datasets and the presence of different pest species having slight difference between classes. Nonetheless, the more the training is done, the better the validation is determined and also it follows the training pattern and its generalization is high. The same tendency can be noticed in case the model is trained on MLDID dataset (Figure 5.7). The reason of the first fluctuation in the validation accuracy is that, when the original data of MLDID is described by the fact that the diversity and complexity of the disease categories increase, MangoXPPNet tends to achieve a certain and high validation accuracy approach as far as the training performance is concerned. The above outcomes suggest the strength of the models and the reason why they can accommodate the specific distribution of sets of data despite not necessarily tuning to sets of data. The cross-dataset consistency provides the recommended models with the high chances of being applied into real-life situations in different agricultural settings.

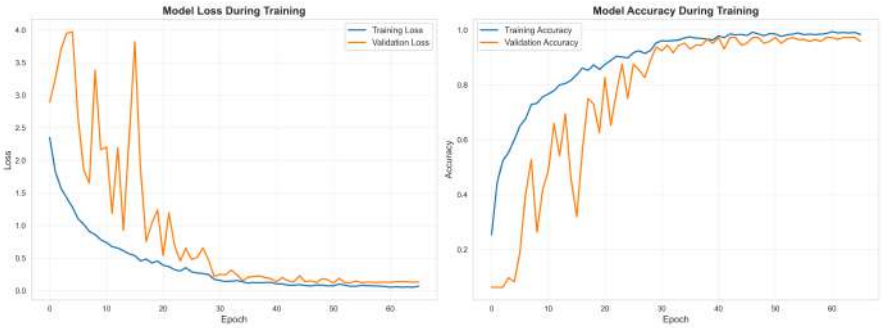


Figure 5.6: Cross-dataset evaluation: MangoPest.

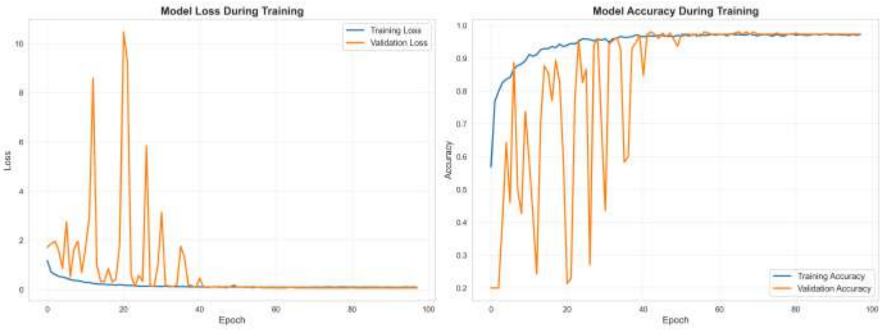


Figure 5.7: Cross-dataset evaluation: MLDID.

5.1.3 Loss and Optimization Trends

The loss per dataset and the joint accuracy is also helpful in providing valuable information of optimization processes of the models. As it can be observed in Figure 5.1, Figure 5.2, Figure 5.3, Figure 5.4, and Figure 5.5, AlexNet, VGG16, and VGG19 training loss curves are relatively smooth, and the validation loss curve can contain spikes in some cases; this can be a sign of instability of the learning process or the inability to adapt to the previously unknown samples at this stage. VGG16 and VGG19 are among them, lower controlled behaviour, and loss curve of their validation is well followed by training loss curve in most of the epochs. Once again, ResNet50 contains more drastic variations and the especially wide spikes in the curves of its validation loss can be utilized to understand the observation of instability in its accuracy trend. This indicates that ResNet50 is competent enough to minimize training loss although, in certain instances, it can be erratic with unfamiliar information. However, MangoXPPNet trend is far more different: the loss during training and validation are minimized and kept at the highest rate and minimal divergence, which indicate that the learning process is very balanced. The agreement of the accuracy and loss of the primary and secondary data sets (Figure 5.6 and Figure 5.7) is the reason supporting the good generalization without overfitting property of the models.

5.1.4 ROC Curve Analysis

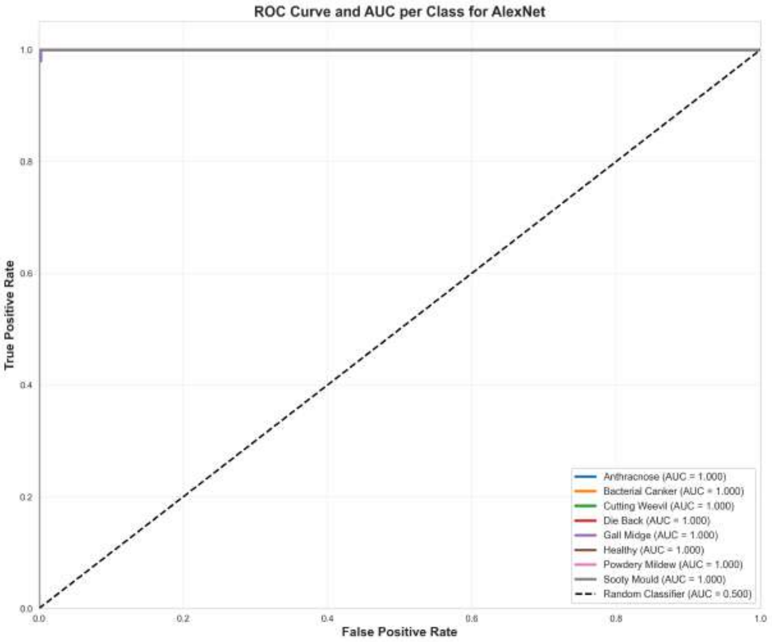


Figure 5.8: ROC curve for AlexNet on MangoLeafBD.

One more insight regarding the capabilities of all models to classify at the level of classes can be gathered by the ROC curves of all models in the dataset MangoLeafBD provided in Figures 5.8–5.12. There is also high separability of the classes, as well as the ROC curves are very close to perfection meaning that the architecture can separate individual patterns of the disease classes despite its relatively shallow architecture. VGG16 and VGG19 are quite comparable in that, high performance is high, and all the classes of the disease exhibit ROC curves, which increase up to the upper-left corner, which signifies high sensitivity and specificity. The ResNet50 is also successful in the test even though some classes are slightly different with VGG models which means that there is slight difference in confidence of discrimination. The model titled MangoXPPNet (Figure 5.12) was the only model that was suggested to achieve a perfect score on AUC (1.00) at all of the disease categories and can be interpreted as the decision showing perfect discrimination at the level of classes. This outcome confirms the quality

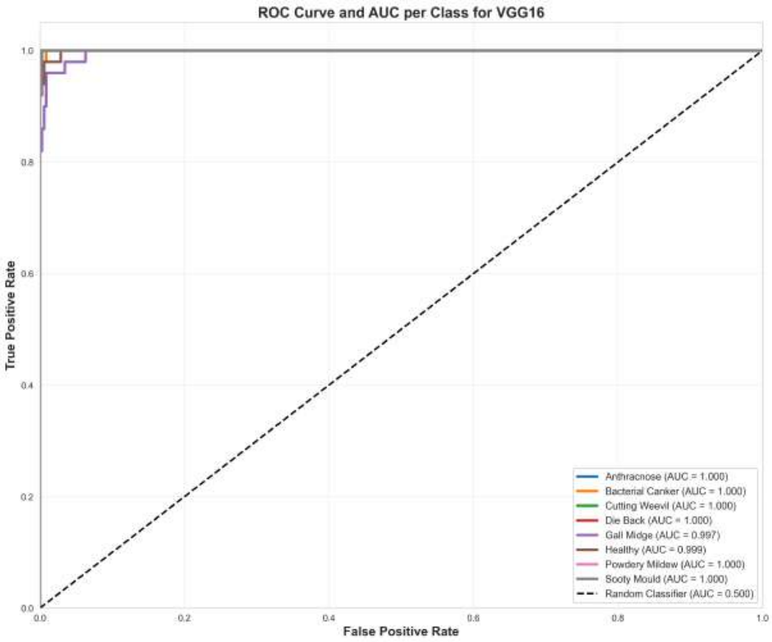


Figure 5.9: ROC curve for VGG16 on MangoLeafBD.

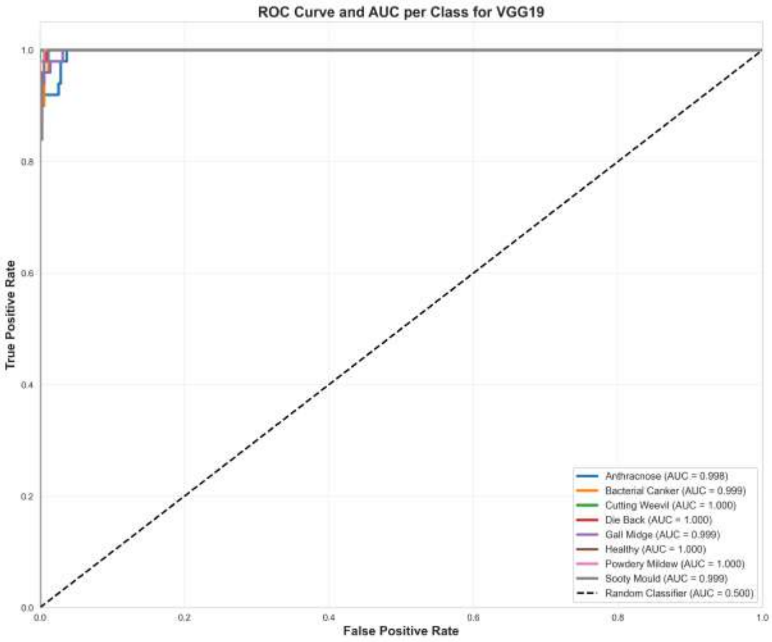


Figure 5.10: ROC curve for VGG19 on MangoLeafBD.

of the suggested architecture regarding the training of the most peculiar features even among the similar patterns of diseases to get the same exact prediction.

5.1.5 Cross-Dataset ROC Performance

Other ROC tests in Figures 5.13 and 5.14 are yet again asserting that MangoXPPNets cross-dataset are performing. In the MangoPest dataset (Figure 5.13), even then MangoXPPNet can still give near-perfect ROC curves to all the classes of pests most of

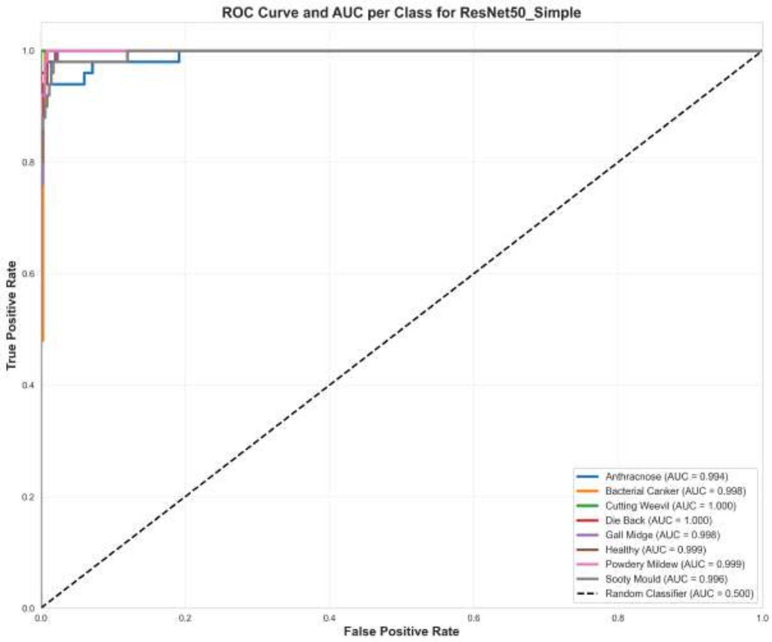


Figure 5.11: ROC curve for ResNet50 on MangoLeafBD.

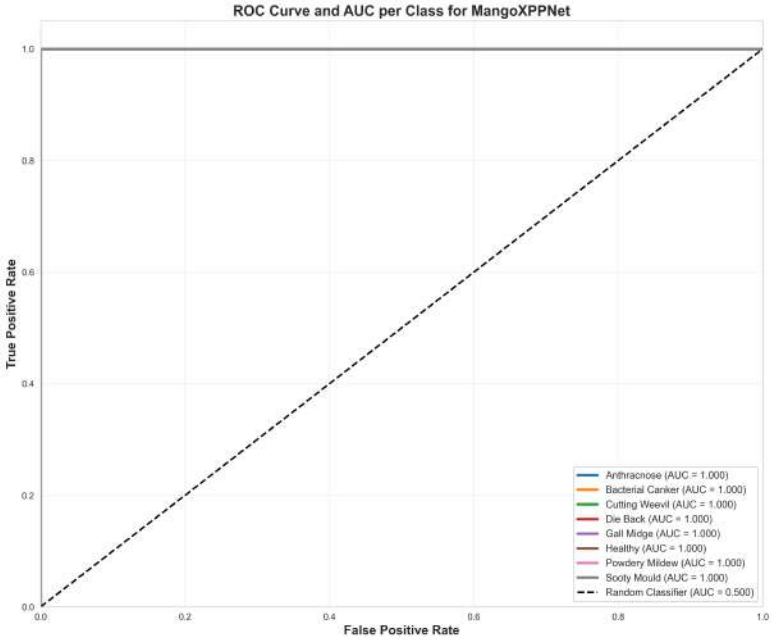


Figure 5.12: ROC curve for MangoXPPNet on MangoLeafBD.

which have an AUC of 1.00 and only one which has a very small decline to 0.99. This proves the fact that the models are most discriminating even in relation to various biological conditions and environmental differences. This is evident in the case of the ML-DID dataset (Figure 5.14) where MangoXPPNet beats high AUC in all the classes of diseases, however, most prominently, complex, including Bacterial Canker, Die Back, Healthy leaves. Even the small but much less reliable values of AUC of Anthracnose and Gall Midge indicate inconsistency in natural data, and not the deficiencies of the

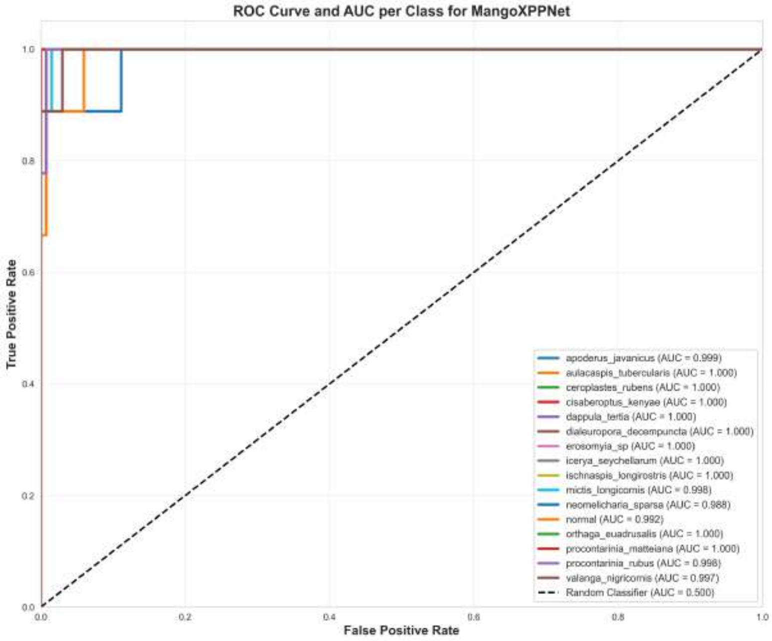


Figure 5.13: ROC curve for MangoXPPNet on MangoPest dataset.

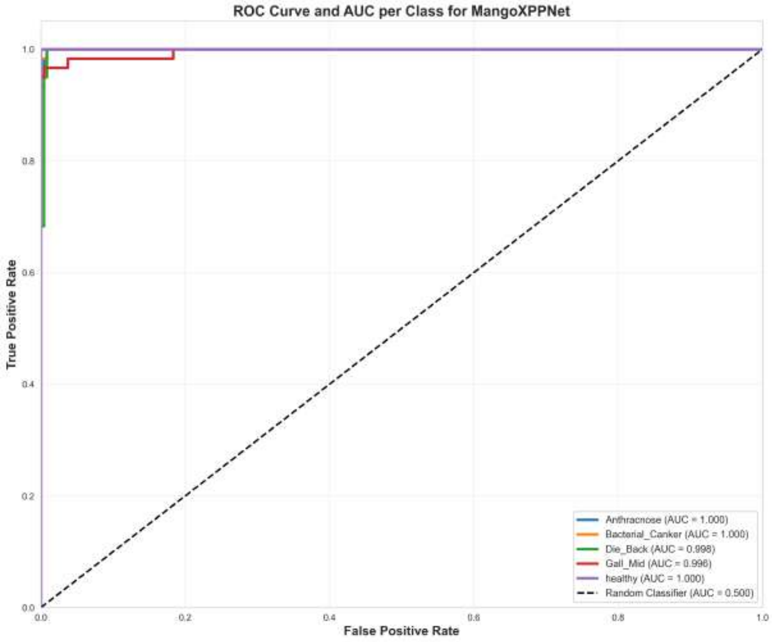


Figure 5.14: ROC curve for MangoXPPNet on MLDID dataset.

models. Such cross-dataset ROC outcomes are in line with the generality and robustness of MangoXPPNets in detecting leaf state and disease cues using different datasets.

5.1.6 Confusion Matrix Insights

Lastly, Figures 5.15–5.19 also present the confusion matrices of the experimented pretrained models, and Figures 5.20–5.21 also present the cross-dataset confusion matrices of MangoXPPNet. The AlexNet and the VGG16 and VGG19 can classify the major-

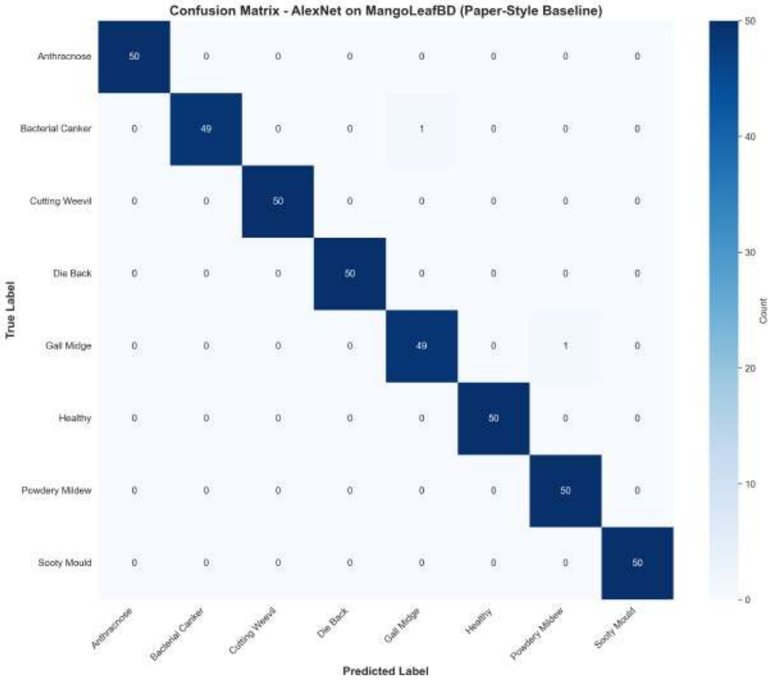


Figure 5.15: Confusion matrix for AlexNet.

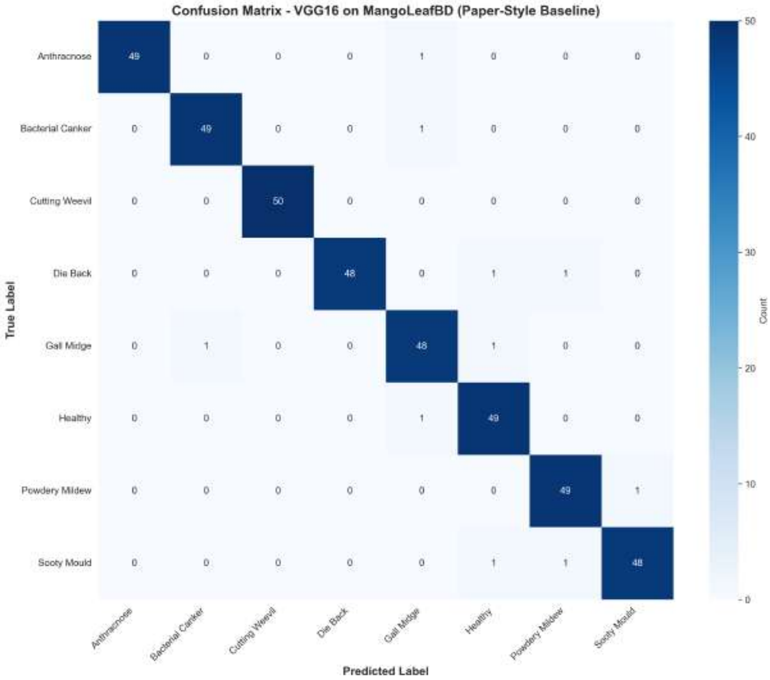
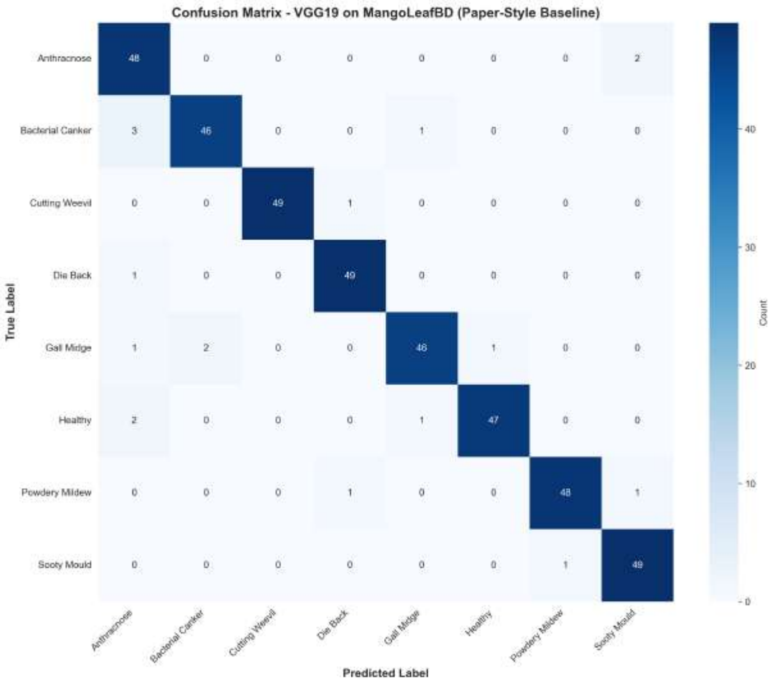


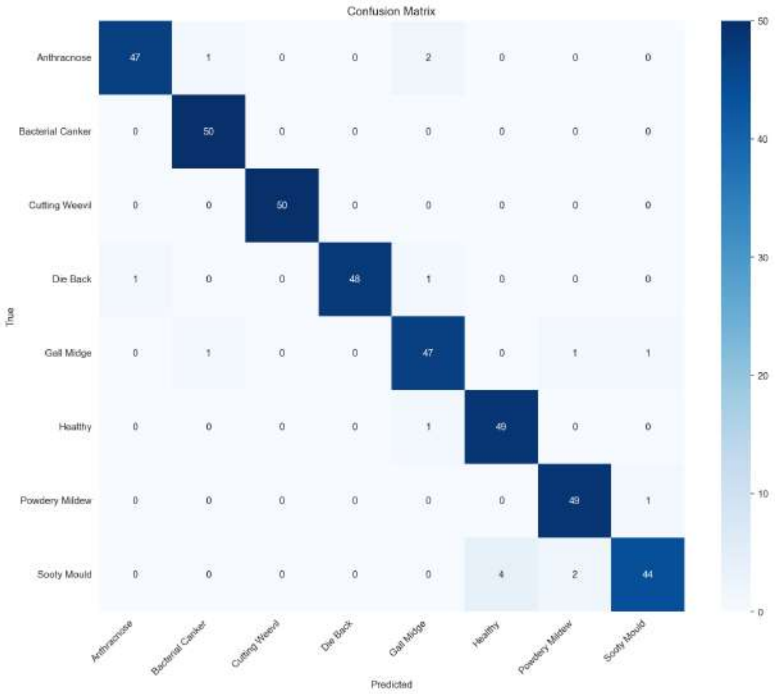
Figure 5.16: Confusion matrix for VGG16.

ity of the classes of diseases properly but may in some cases incorrectly classify even more similar images, i.e. categories of Sooty Mould or Gall Midge. The confusion matrix of resnet50s shows that it has more scattered errors, as well as it coincides with its turning errors of various levels of validation at the initial training stages. However, MangoXPPNet shows very high classification accuracy, and it has only two misclassifications alongside all the classes of MangoLeafBD set. The cross-dataset confusion



True Label \ Predicted Label	Anthracnose	Bacterial Canker	Cutting Weevil	Die Back	Gall Midge	Healthy	Powdery Mildew	Sooty Mould
Anthracnose	48	0	0	0	0	0	0	2
Bacterial Canker	3	46	0	0	1	0	0	0
Cutting Weevil	0	0	49	1	0	0	0	0
Die Back	1	0	0	49	0	0	0	0
Gall Midge	1	2	0	0	46	1	0	0
Healthy	2	0	0	0	1	47	0	0
Powdery Mildew	0	0	0	1	0	0	48	1
Sooty Mould	0	0	0	0	0	0	1	49

Figure 5.17: Confusion matrix for VGG19.



True \ Predicted	Anthracnose	Bacterial Canker	Cutting Weevil	Die Back	Gall Midge	Healthy	Powdery Mildew	Sooty Mould
Anthracnose	47	1	0	0	2	0	0	0
Bacterial Canker	0	50	0	0	0	0	0	0
Cutting Weevil	0	0	50	0	0	0	0	0
Die Back	1	0	0	48	1	0	0	0
Gall Midge	0	1	0	0	47	0	1	1
Healthy	0	0	0	0	1	49	0	0
Powdery Mildew	0	0	0	0	0	0	49	1
Sooty Mould	0	0	0	0	0	4	2	44

Figure 5.18: Confusion matrix for ResNet50.

matrices (Figures 5.20 and 5.21) also reveal that the error is insignificant and data is extremely predominant at the diagonal. All these findings confirm that it is more consistent in class discriminative features extraction and performance when there is a change in the dataset.

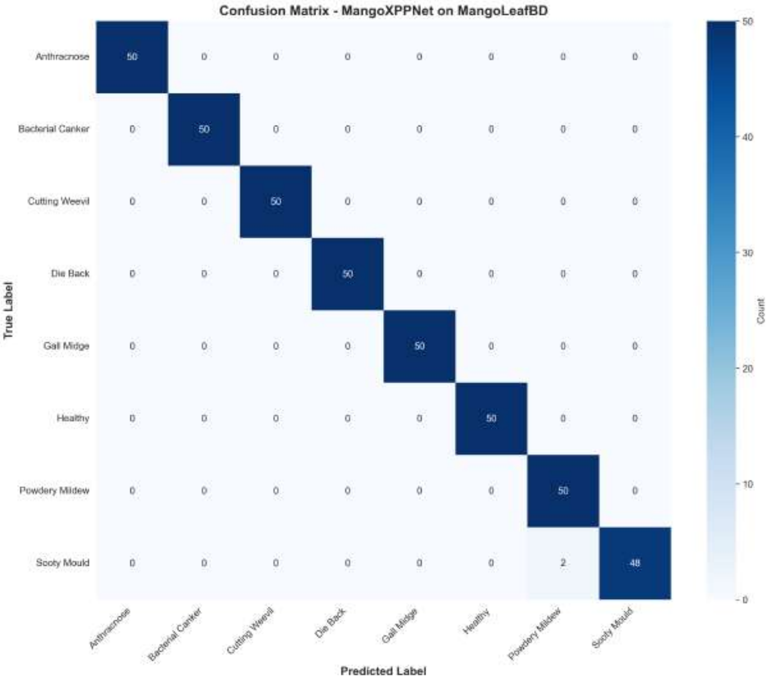


Figure 5.19: Confusion matrix for MangoXPPNet.

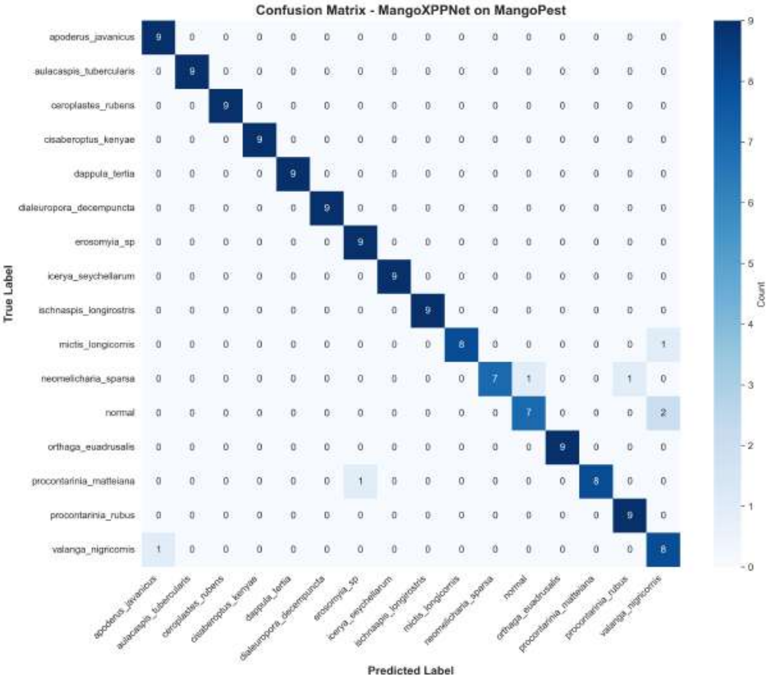


Figure 5.20: Cross-dataset confusion matrix 1 for MangoXPPNet.

5.1.7 Class-Level Performance on MangoLeafBD (Table 5)

Table 5.1 shows the full comparison of the classification performance of AlexNet, VGG16, VGG19, ResNet50, and the presented MangoXPPNet on the MangoLeafBD dataset. In all the models, MangoXPPNet shows the most stable and good performance with a perfect precision, recall and F1-score of most disease classes (1.00), such as An-

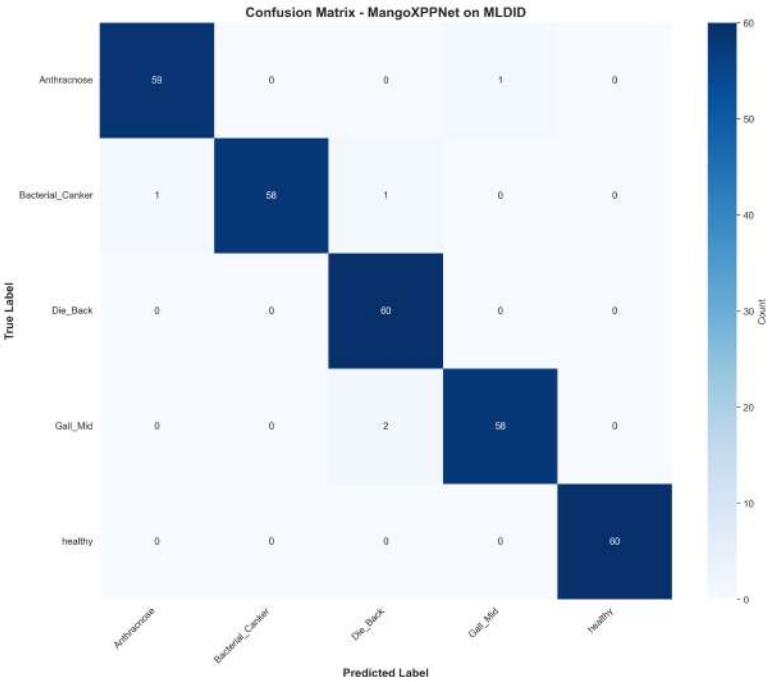


Figure 5.21: Cross-dataset confusion matrix 2 for MangoXPPNet.

thracnose, Bacterial Canker, Cutting Weevil, Die Back, Gall Midge and Healthy leaves. The only slight decreases are seen in Powdery Mildew and Sooty Mould where the model scores F1 of 0.98. Comparatively, the baseline models have different degrees of inconsistency. AlexNet is relatively high performing and exhibits minor drops with Gall Midge and Powdery Mildew. VGG16 has a good overall performance but a f1-score of less than 0.96 on Gall Midge and Healthy leaves. VGG19 shows greater variation especially in the classes involving Anthracnose and Bacterial Canker. Although ResNet50 is competitive in various categories, it displays instability in case of Gall Midge, Powdery Mildew and Sooty Mould. In comparison to these models, MangoXPPNet is evidently more stable in classes, and it is resilient even in categories that are difficult with traditional architectures.

5.1.8 Overall Metrics Comparison

In accordance with these results at the class level, Table 5.2 gives the general evaluation metrics of each of the models on the dataset of MangoLeafBD. The accuracy of MangoXPPNet is 99.50 with precision, recall and F1-scores that are close to 99.50, which signifies its outstanding balance of all measurements. AlexNet is also a highly performer in terms of the accuracy of 99.50 but its variation by the classes does not allow it to stay at par with MangoXPPNets consistency. VGG16 and VGG19 come second and third with accuracies of 97.50 and 95.50, respectively with moderate losses because of their sensitivity to certain disease categories. ResNet50 has a better performance than

Model	**Predicted Label**	**Precision**	**Recall**	**F1-Score**
AlexNet	Anthracnose	**1.00**	**1.00**	**1.00**
	Bacterial Canker	**1.00**	0.98	0.99
	Cutting Weevil	**1.00**	**1.00**	**1.00**
	Die Back	**1.00**	**1.00**	**1.00**
	Gall Midge	0.98	0.98	0.98
	Healthy	**1.00**	**1.00**	**1.00**
	Powdery Mildew	0.98	**1.00**	0.99
	Sooty Mould	**1.00**	**1.00**	**1.00**
VGG16	Anthracnose	**1.00**	0.98	0.99
	Bacterial Canker	0.98	0.98	0.98
	Cutting Weevil	**1.00**	**1.00**	**1.00**
	Die Back	**1.00**	0.96	0.98
	Gall Midge	0.94	0.96	0.95
	Healthy	0.94	0.98	0.96
	Powdery Mildew	0.96	0.98	0.97
	Sooty Mould	0.98	0.96	0.97
VGG19	Anthracnose	0.87	0.96	0.91
	Bacterial Canker	0.96	0.92	0.94
	Cutting Weevil	**1.00**	0.98	0.99
	Die Back	0.96	0.98	0.97
	Gall Midge	0.96	0.92	0.94
	Healthy	0.98	0.94	0.96
	Powdery Mildew	0.98	0.96	0.97
	Sooty Mould	0.94	0.98	0.96
ResNet50	Anthracnose	0.98	0.94	0.96
	Bacterial Canker	0.96	**1.00**	0.98
	Cutting Weevil	**1.00**	**1.00**	**1.00**
	Die Back	**1.00**	0.96	0.98
	Gall Midge	0.92	0.94	0.93
	Healthy	0.92	0.98	0.95
	Powdery Mildew	0.94	0.98	0.96
	Sooty Mould	0.96	0.88	0.92
MangoXPPNet (Proposed)	Anthracnose	**1.00**	**1.00**	**1.00**
	Bacterial Canker	**1.00**	**1.00**	**1.00**
	Cutting Weevil	**1.00**	**1.00**	**1.00**
	Die Back	**1.00**	**1.00**	**1.00**
	Gall Midge	**1.00**	**1.00**	**1.00**
	Healthy	**1.00**	**1.00**	**1.00**
	Powdery Mildew	0.96	**1.00**	0.98
	Sooty Mould	**1.00**	0.96	0.98

Table 5.1: Class-level performance comparison of models on MangoLeafBD.

Models	**Accuracy**	**Precision**	**Recall**	**F1-score**
AlexNet	0.9950	0.9950	0.9950	0.9950
VGG16	0.9750	0.9755	0.9750	0.9751
VGG19	0.9550	0.9564	0.9550	0.9552
ResNet50	0.9600	0.9607	0.9600	0.9598
MangoXPPNet	0.9950	0.9952	0.9950	0.9950

Table 5.2: Overall metrics comparison of models on MangoLeafBD.

VGG19 but still, its accuracy of 96.00 is lower in comparison to MangoXPPNet. These comparison findings reiterate the effectiveness and strength of MangoXPPNet with regard to processing the complicated feature distributions, as in MangoLeafBD dataset.

5.1.9 MangoPest Dataset Results

Table 5.3: Classification Report of MangoXPPNet on the MangoPest Dataset

Predicted Labels	**Precision**	**Recall**	**F1-Score**
Apoderus Javanicus	0.9000	1.0000	0.9474
Aulacaspis Tubercularis	1.0000	1.0000	1.0000
Ceroplastes Rubens	1.0000	1.0000	1.0000
Cisaberoptus Kenyae	1.0000	1.0000	1.0000
Dappula Tertia	1.0000	1.0000	1.0000
Dialeuropora Decempuncta	1.0000	1.0000	1.0000
Erosomyia Sp	0.9000	1.0000	0.9474
Icerya Seychellarum	1.0000	1.0000	1.0000
Ischnaspis Longirostris	1.0000	1.0000	1.0000
Mictis Longicornis	1.0000	0.8889	0.9412
Neomelicharia Sparsa	1.0000	0.7778	0.8750
Normal	0.8750	0.7778	0.8235
Orthaga Euadrusalis	1.0000	1.0000	1.0000
Procontarinia Matteiana	1.0000	0.8889	0.9412
Procontarinia Rubus	0.9000	1.0000	0.9474
Valanga Nigricornis	0.7273	0.8889	0.8000

Table 5.3 presents the performance of MangoXPPNets on the MangoPest dataset, which has a high generalization capability. Many species of pests, such as Aulacaspis Tubercularis, Cisaberoptus Kenyae, Ceroplastes Rubens, Dialeuropora Decempuncta and Orthaga Euadrusalis, are perfectly predictable by the model with no errors in precision, recall or F1-scores. Also high performance is noted in Apoderus Javanicus and Erosomyia sp. classes which continue to possess F1-scores exceeding 0.94. Minimal decreases are experienced in the categories of Neomelicharia Sparsa, Normal and Valanga Nigricornis and F1-scores vary between 0.82 and 0.90 because of intricate visual similarities in these classes. However, the overall stability of the models in a wide range of pest species proves that it is able to successfully classify real-world agricultural pests.

5.1.10 MLDID Dataset Results

On the same note, Table 5.4 presents performance of MangoXPPNets on Mango Leaf Disease Identification Dataset (MLDID). The model still shows high accuracy, recall, and F1-scores of all categories and reaches the highest values of 1.00 in the case of Healthy leaves and Bacterial Canker. There are also diseases which have high F1-scores between 0.97 and 0.98 i.e., Anthracnose, Die Back and Gall Midge. These findings prove that MangoXPPNet can be successfully adjusted to new datasets and other

Table 5.4: Classification Report of MangoXPPNet on the MLDID Dataset

Predicted Labels	Precision	Recall	F1-Score
Anthracnose	0.9833	0.9833	0.9833
Bacterial Canker	1.0000	0.9667	0.9831
Die Back	0.9524	1.0000	0.9756
Gall Midge	0.9831	0.9667	0.9748
Healthy	1.0000	1.0000	1.0000

imaging conditions and classes, which supports its applicability as a robust disease classification system.

5.1.11 Cross-Dataset Consistency

Datasets	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
MangoLeafBD [25]	99.50	99.52	99.50	99.50
MangoPest [26]	95.14	95.64	95.14	95.14
MLDID [27]	98.33	98.38	98.33	98.34

Table 5.5: Cross-dataset consistency metrics for MangoXPPNet.

Table 5.5, as well as the visualizations of Figure 5.6 and Figure 5.7, demonstrate the cross-dataset consistency of MangoXPPNet. The model is the highest-performing on MangoLeafBD, where its high performances on the class level are combined with a total accuracy of 99.50. The model on the MangoPest data still keeps an accuracy of 95.14 with precision and recall rates of more than 95, which underscores its versatility to the pest classification task. The MLDID data is also well performed in the model with accuracy of `(98.33%)` and balanced precision and recall scores. All these findings prove that MangoXPPNet does not change its predictive performance as the characteristics of the dataset change greatly. Figure 5.6 visually compares the models evaluated on MangoLeafBD and it is evident that the MangoXPPNets is more accurate, precise, recall, and F1-score compared to AlexNet, VGG16, VGG19, and ResNet50. Besides, Figure 5.7 demonstrates the generalization performance of the models within the context of MangoLeafBD, MangoPest and MLDID which once again proves that it is very robust and stable with the diverse data.

5.1.12 State-of-the-Art Comparison

5.1.13 Summary of Quantitative Findings

Altogether, the MangoXPPNet model proposed is shown to be highly effective in terms of performance in various datasets, being superior to traditional frameworks and state-of-the-art models in the past. The high level of generalization, consistency at the class

Ref.	**Model**	**Accuracy (%)**	**Precision**	**Recall**	**F1-score**	**XAI**
Rizvee et al. [15]	LeafNet	99.55	99.5	99.45	99.47	✗
Mahbub et al. [28]	LCNN	98.00	97.6	97.5	97.5	✗
Singh et al. [29]	MCNN	97.13	–	–	–	✗
Vijay et al. [30]	EfficientNetB4 + CNN	93.01	93.23	94.0	93.07	✗
This paper	**MangoXPPNet (MangoLeafBD)**	**99.50**	**99.52**	**99.50**	**99.50**	✓
This paper	**MangoXPPNet (MangoPest)**	**95.14**	**95.64**	**95.14**	**95.14**	✓
This paper	**MangoXPPNet (MLDID)**	**98.33**	**98.38**	**98.33**	**98.34**	✓

Table 5.6: Comparison of MangoXPPNet with state-of-the-art models.

level, and the combination of explainability make it an extremely competent and trustworthy instrument to be used in real-life agricultural settings.

5.2 Qualitative Assessment

5.2.1 Grad-CAM Visualizations

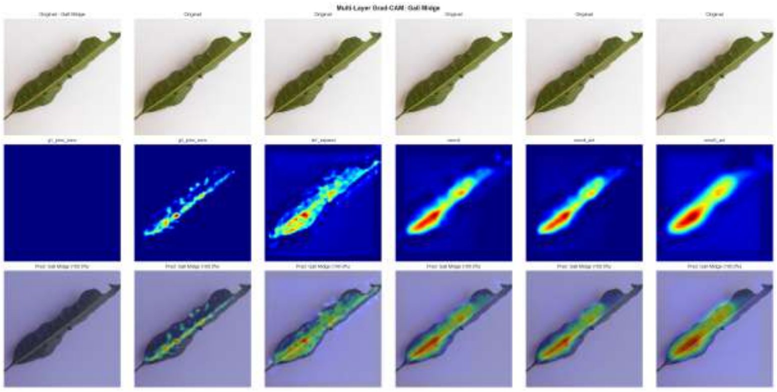


Figure 5.22: Grad-CAM visualization for Gall Midge.

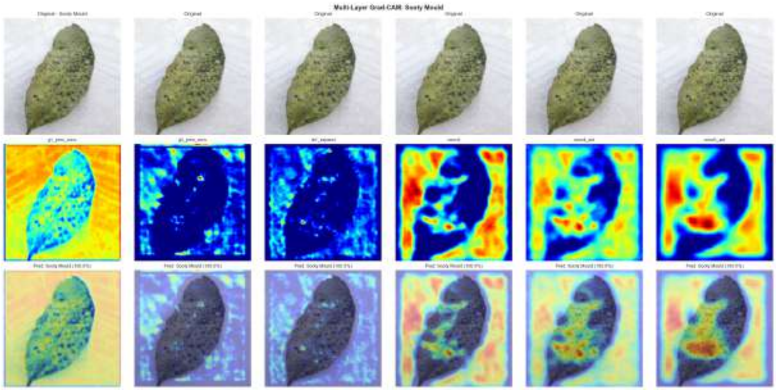


Figure 5.23: Grad-CAM visualization for Sooty Mould.

Detailed performances of the models on each dataset, and comparisons with conventional pretrained models (AlexNet[44], VGG16, VGG19, and ResNet50) in both

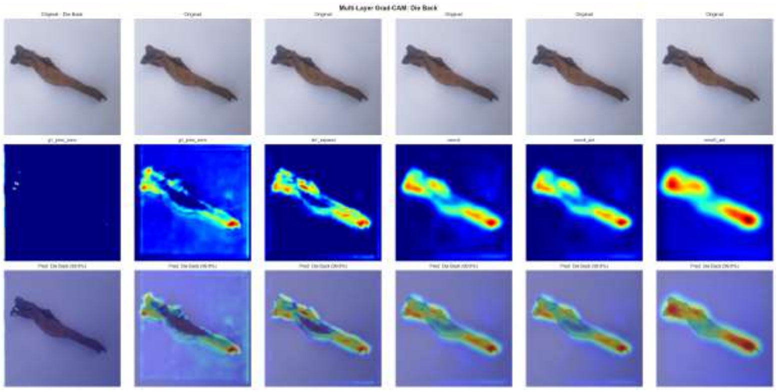


Figure 5.24: Grad-CAM visualization for Die Back.

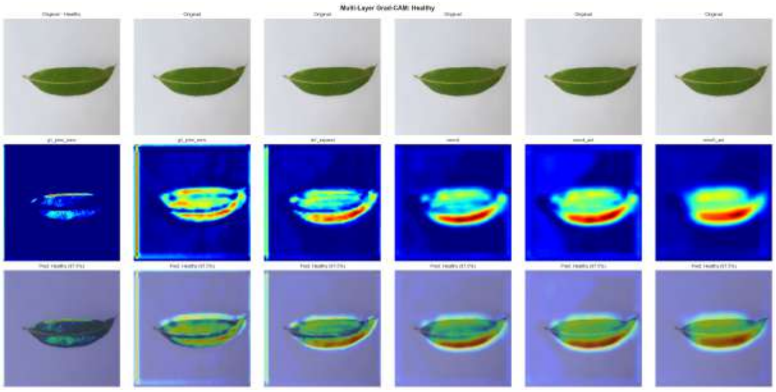


Figure 5.25: Grad-CAM visualization for Healthy leaves.

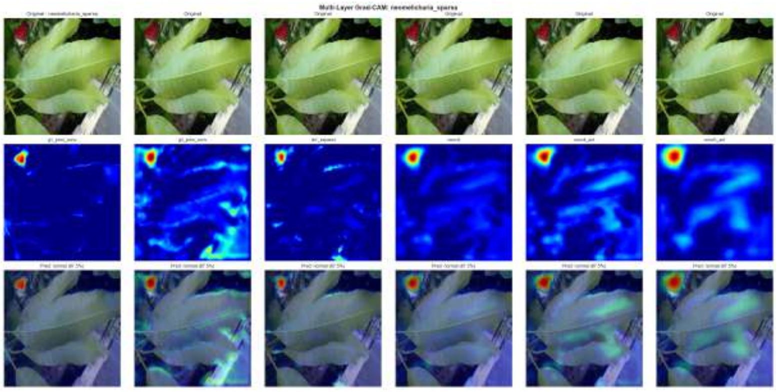


Figure 5.26: Grad-CAM visualization for Neomelicharia Sparsa.

classification accuracy and precision, recall, F1-score, and computational efficiency are presented in the following subsections. All these analyses demonstrate the ability of MangoXPPNet to find a trade off between accuracy and efficiency to be applied practically in agriculture.

The Grad-CAM visualizations of Gall Midge given in Figure 5.22 can be used to observe how the models attention becomes more and more localized to the elongated, textured regions of the infestation as the models approach the latter layers. This development underscores the ability of the models to isolate small-scale morphological

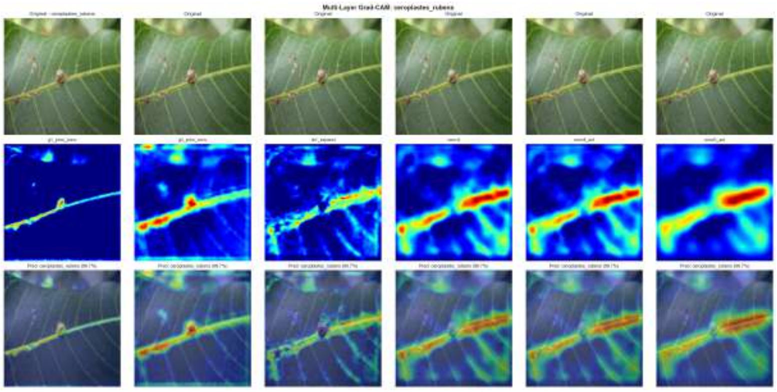


Figure 5.27: Grad-CAM visualization for Ceroplastes Rubens.

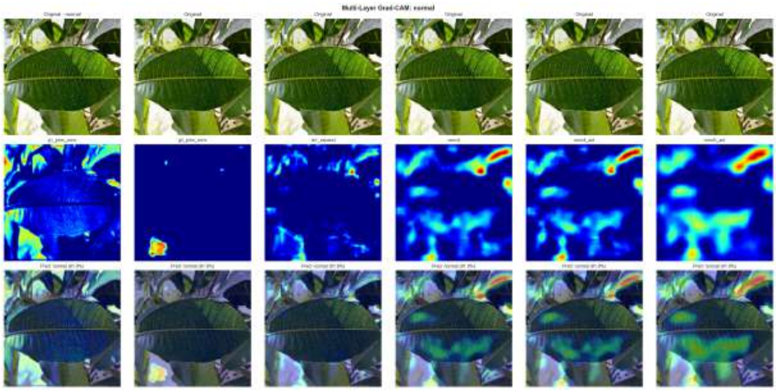


Figure 5.28: Grad-CAM visualization for Normal leaves.

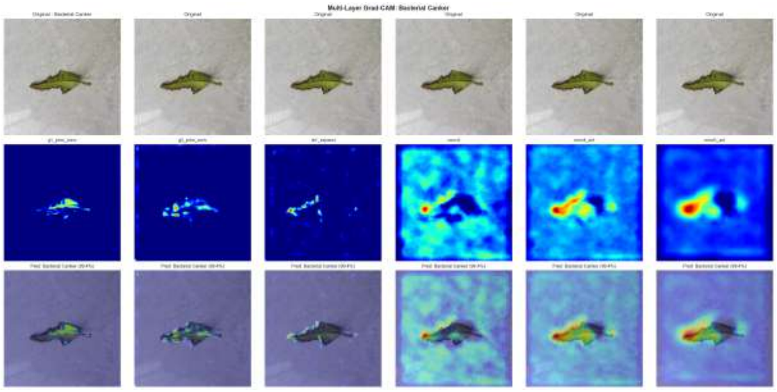


Figure 5.29: Grad-CAM visualization for Bacterial Canker.

deformities that are linked with Gall Midge. The outputs of Grad-CAM in Figure 5.23 display the results of Sooty Mould with the deeper layers highlighting the dark clustered areas of the fungi. The growing distinctness of the regions noted in all layers highlights the localization capacity of the MangoXPPNets to this disease, whose distribution is irregular and noisy.

Figure 5.24 shows the Grad-CAM flow of Die Back in which the most severely affected areas of the leaf are highlighted, and it is clear that the model will always focus on the worst-affected parts of the leaf in the network. On the contrary, Figure 5.25

shows the Grad-CAM activation of Healthy leaves, when the attention is widely and evenly distributed, the lack of separate pathological indicators and the support of the correctness of the classification of Healthy.

Figure 5.26 emphasizes the Grad-CAM output when using Neomelicharia Sparsa, the model scans through the textures layers, slowly identifying small textual abnormalities and light reflective structures deeper into the body-textures that are often disregarded when using modest feature extraction algorithms. Figure 5.27 indicates the Grad-CAM maps of Ceroplastes Rubens, high-density activations indicate the locations of the scale-like pest deposits along the line or vein on the leaf, indicating that the networks can localize small and concentrated infestations. Figure 5.28 illustrates the Grad-CAM development of the Normal leaves that, like in the healthy group, exhibit a diffused pattern of activation, meaning that there are no significant disease indicators.

Lastly, Figure 5.29 has the Grad-CAM analysis of Bacterial Canker, and in this case, the results of deep-layer activations are well-focused on the lesion area, and this outcome is exceptionally clear. The fact that the localization has been consistent across the layers confirms that the models are sound in determining this disease despite its relatively small and compact footprint of symptoms.

Together, the Grad-CAM visualizations indicate that MangoXPPNet is highly interpretable and the predictions of MangoXPPNet are based on the actual pathological or structural characteristics shown by every leaf image. This visual information can be used by agricultural professionals to confirm the behavior of the models so that it fits with the diagnostic characteristics. To farmers and field practitioners, Grad-CAM heatmaps provide a clearer illustration as to why a particular leaf has been determined as diseased or healthy, which makes them more inclined to believe the outputs of the models and take decisions when working in a real agricultural application.

5.2.2 Saliency Map Analysis

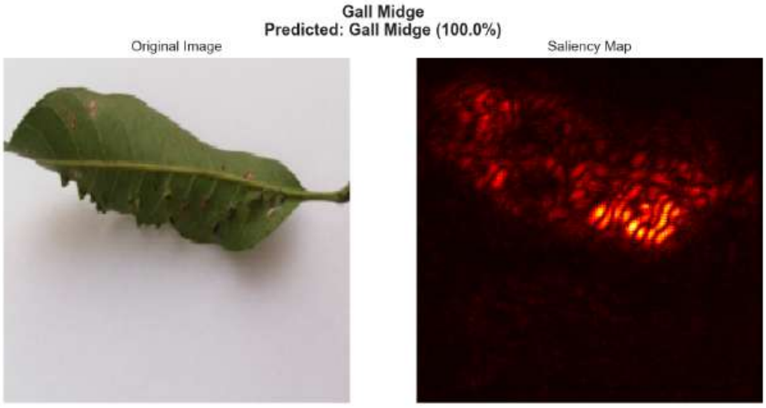


Figure 5.30: Saliency map for Gall Midge.

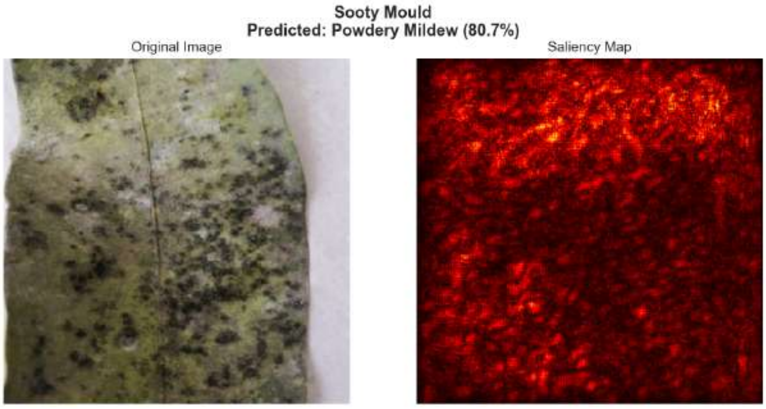


Figure 5.31: Saliency map for Sooty Mould.

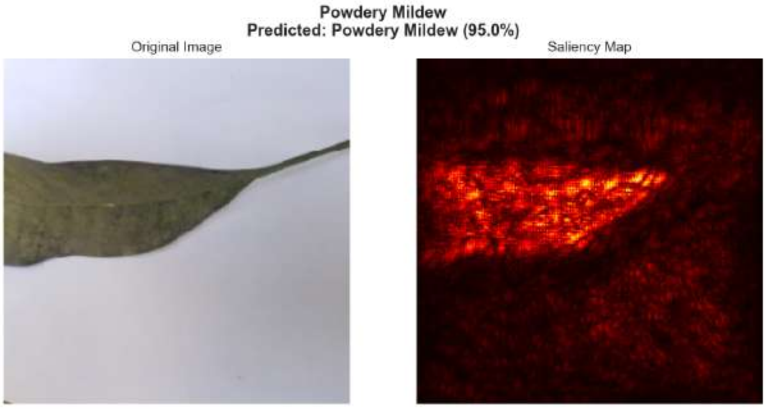


Figure 5.32: Saliency map for Powdery Mildew.

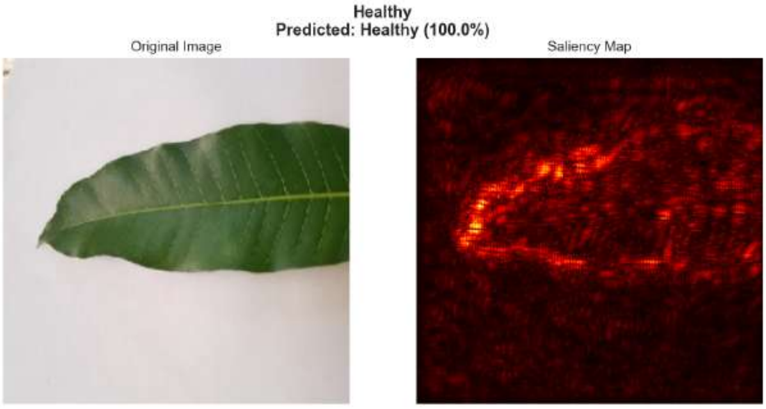


Figure 5.33: Saliency map for Healthy leaves.

To complement the Grad-CAM, saliency maps were also used to offer a supplemental explanation of the predictions of the models by pointing out the most important pixel intensities. Figure 5.30 summarizes the saliency visualization for Gall Midge, Figure 5.31 for Sooty Mould, Figure 5.32 for Powdery Mildew, and Figure 5.33 for Healthy leaves. In the case of Gall Midge, we can highlight the saliency map which highlights the central distorted area which represents the visible infestation locations. As in the case of Sooty Mould, the model focuses on randomly distributed high-intensity clusters of fungi, which are very similar to the diseases typical black patches. Figure 5.32, which is a representation of Powdery Mildew, shows that there are thick powder-coated places on the leaf surface, which proves that the model focuses on the right places of the symptomatic areas. Conversely the Healthy leaf saliency map (Figure 5.33) has a uniform distribution with no hotspots, which re-enforces the lack of disease indicators.

The interpretability of these saliency analyses is useful in ensuring that the decisions that the model makes are always informed by the most informative visual features. They can also be used with Grad-CAM to explain the model in a transparent and credible way that will help in expert validation and its practical implementation. The integrated interpretability enables MangoXPPNet to not just be a black-box system but a system that is explainable, reliable, and is practical to deploy in the field to diagnose mango leaf disease via automated means.

Chapter 6

Discussion and Limitations

6.1 Discussion

The emergence of deep learning in agriculture imaging has accelerated due to the concern of proper and punctual disease detection in crop management. This work had suggested MangoXPPNet as a single, dataset-independent CNN that can be used to diagnose a variety of mango leaf diseases and pest infestations. The MangoXPPNet is a stable design, unlike other standard pretrained networks, and can be applied to datasets with significantly small adjustments to hyperparameters, with experimental reproducibility. This does not require fine-tuning or extremely unbalanced convergence.The overall results suggest that MangoXPPNet is very stable, performs better than known CNN baselines, and can generalise well otherwise across datasets of varying properties of images.

The learning curves on MangoLeafBD demonstrate one of the most important benefits of the model its steady and smooth convergence behaviour. Unlike AlexNet, VGG16 and VGG19 which exhibit moderate variations in the validation accuracy, and ResNet50 which exhibits severe oscillatory effects and short-term overfitting, MangoXPPNet has near-perfect alignment in training and validation curves over the entire training period. This trend indicates how a balanced optimization process operates where the model keeps on narrowing down discriminative features without moving outward with unknown samples. The fact that the difference between the training and validation loss is minimal further supports the fact that MangoXPPNet has good generalization ability even in the long run of training.

Cross-dataset experimentation also indicates this stability. Interactions with MangoPest at training The model starts to oscillate a bit when trained on MangoPest, and this is natural as the pest species are diverse biologically and morphologically. These fluctuations decrease however as training progresses and there is a steady increase in the validation performance and the validation performance and training behaviour are in agreement. The same can be said about MLDID, in which the variation and the complexity of the disease manifestations initially cause small discrepancies in the accuracy of the validation. Nevertheless, MangoXPPNet in the end realizes high and stable validation rates and shows the capacity to adjust itself to datasets sharing varying proportions of classes and visual complexity without changing its architectural framework. This flexibility enhances the generalizability of the models to be implemented under heterogeneous conditions of the field in the actual field scenario in agriculture.

The ROC analyses also can suggest that MangoXPPNets discriminative ability is high. Classes have a UA of 1.00 on MangoLeafBD, which implies that they are perfectly separable and the decision boundaries are well-known to be confident. These results are much better than those of the baseline models which despite their performance are inconsistent across challenging classes like Gall Midge, Sooty Mould or Powdery Mildew. The fact that the AUC values in MangoPest showed a near-perfect value with slight decrease to 0.99 in one class only is another demonstration of the ability of the models to recognize minor pest-related visual clues. All classes also achieve high AUC scores on MLDID, although there are slight variations that can be explained by inherent variation in the expression of diseases but not due to structural constraints of the models. Combined, these AUC findings confirm the reliability of MangoXPPNets at class level with different datasets.

The confusion matrices provide further support to the strength of the models. In MangoLeafBD, MangoXPPNet makes two misclassifications compared to the pretrained models which exhibit wider scattering of the confusion matrices, especially in visually similar classes. The MangoPest and MLDID cross-dataset matrices also present few off-diagonal values, which data confirms a high level of generalisation despite variations in image distribution, light, shape of the leaf and the presence of the symptom. These findings can be attributed to the fact that such models are capable of capturing fine-grained spatial and textual information using its convolutional hierarchy.

In addition to quantitative measures, the qualitative analyses demonstrate noticeable interpretation of the models by displayed gradient patterns of the long infestations (Gall Midge), the solid masses of fungal elements (Sooty Mould), the necrotic spots (Die Back), or the compact foci (Bacterial Canker) with more specific layers receiving the more discriminative attention. The observations and activities in the diffuse patterns of the case of the healthy or normal leaves are effective in confirming the absence of local disease indications that give perceptual confirmation of accurate classifications. Just like saliency maps, saliency maps can always target the regions that are specific to pests or diseases without introducing variance in healthy samples, saliency maps identify the pixel intensities that have the largest influence on the model predictions. The findings of these interpretability can be useful in overcoming the gap between automated classification and expert validation as they offer transparency which is imperative to the practical application.

6.2 Limitations and Future Work

MangoXPPNet has limitations although it is performing very well. The misclassifications are minimal, however some of the visually similar categories (see Neomelicharia Sparsa, Normal leaves, or Valanga Nigricornis in the MangoPest dataset, and Powdery Mildew or Sooty Mould in MangoLeafBD) appear to have slightly lower scores than other classes. This implies that classification has been difficult at fine grains when the symptoms are either overlapping in terms of texture or distribution. Moreover, any experiment uses only image data. In the field, disease presence is affected by other factors such as environmental conditions, nutrient imbalances and co-occurring pest attacks. Thus, such a system might not be capable of catching contextual information that could enhance the accuracy of diagnoses. Lastly, although the architecture is stable and effective compared to more fully trained models, it is computationally costly to train high-resolution models and deploy it in low-resource devices, unless optimized further.

The research on the future will center on the improvement of the flexibility, effectiveness, and functionality of MangoXPPNet. The use of multimodal data, including weather data, soil quality indicators, or pest density reports, can be useful in enhancing the predictive reliability during field situations, when the symptoms of the weeds alone are invalid. Additional developments of hard-to-separate classes by focusing on augmentation or class-specific sampling methods might also decrease residual misclassifications. Deployment wise, it will be necessary to come up with light-weight variations of MangoXPPNet by pruning, quantization, or simplifying the architecture to support real-time performance on edge computers or mobile systems that have become common in agricultural systems. Also, the further validation of models on new field data sets might reveal more information about real-life variability and long-term stability of models. Continuing with the interpretability tools presented in the current research, it is also possible to develop future research that will evaluate the incorporation of these visual explanations into the actual farmer oriented applications to enable informed decision making and add more confidence in the automated systems.

All in all, this paper emphasizes that MangoXPPNet is a very trustworthy, interpretable, and generalisable architecture in mango disease and mango pest classification and has a high potential to be included in the precision agriculture systems and field-ready diagnostics devices.

Chapter 7

Conclusion

This paper presented a convolutional neural network, MangoXPPNet, which is an integrated diagnosis network of mango leaf diseases and pest-related abnormalities. It was tested with three benchmark datasets, (MangoLeafBD, MangoPest and MLDID) with a fixed architectural structure and a few hyperparameters varied. The findings reveal that MangoXPPNet has shown superior performance over popular pretrained networks, and attains high accuracy on MangoLeafBD with 99.50 percent and still has good performance on the MangoPest and MLDID with 95.14 and 98.33 percent respectively. These results support the assertion that the ability of a small, domain-directed CNN to achieve high discrimination in a wide variety of visual tasks and maintain training stability. Qualitative interpretability analyses also help in the support of the models effectiveness. Grad-CAM and Saliency maps indicate that MangoXPPNet concentrates on the regions that bear the most symptoms and it confirms that the features learned by the model correspond to pertinent biological indicators. The paramount benefit of the proposed architecture is that it provides consistency at the level of classes, especially differentiating closely related types of diseases that are traditionally difficult to the standard pretrained model. Despite the overall high competition performance, there is a small group of classes that had visual overlaps and showed slight declinations in classification scores. These examples imply that enhancement can be implemented with increased data diversity or class-specific augmentation measures. Moreover, since all experiments were based solely on image data, future developments can examine other sources of information, such as environmental or contextual, to increase predictive consistency in the field. Wider validation based on field-captured images and creation of interactive diagnostic instruments will also be taken into consideration in order to allow real-time use by farmers and agricultural extension employees.

Overall, MangoXPPNet provides a powerful, interpretable and dataset-independent health monitoring platform of mango leaves. Its stability on various datasets can be used as a sign of its possible application as a useful part of intelligent crop-monitoring systems and as a promising step in the development of AI-based precision agriculture.

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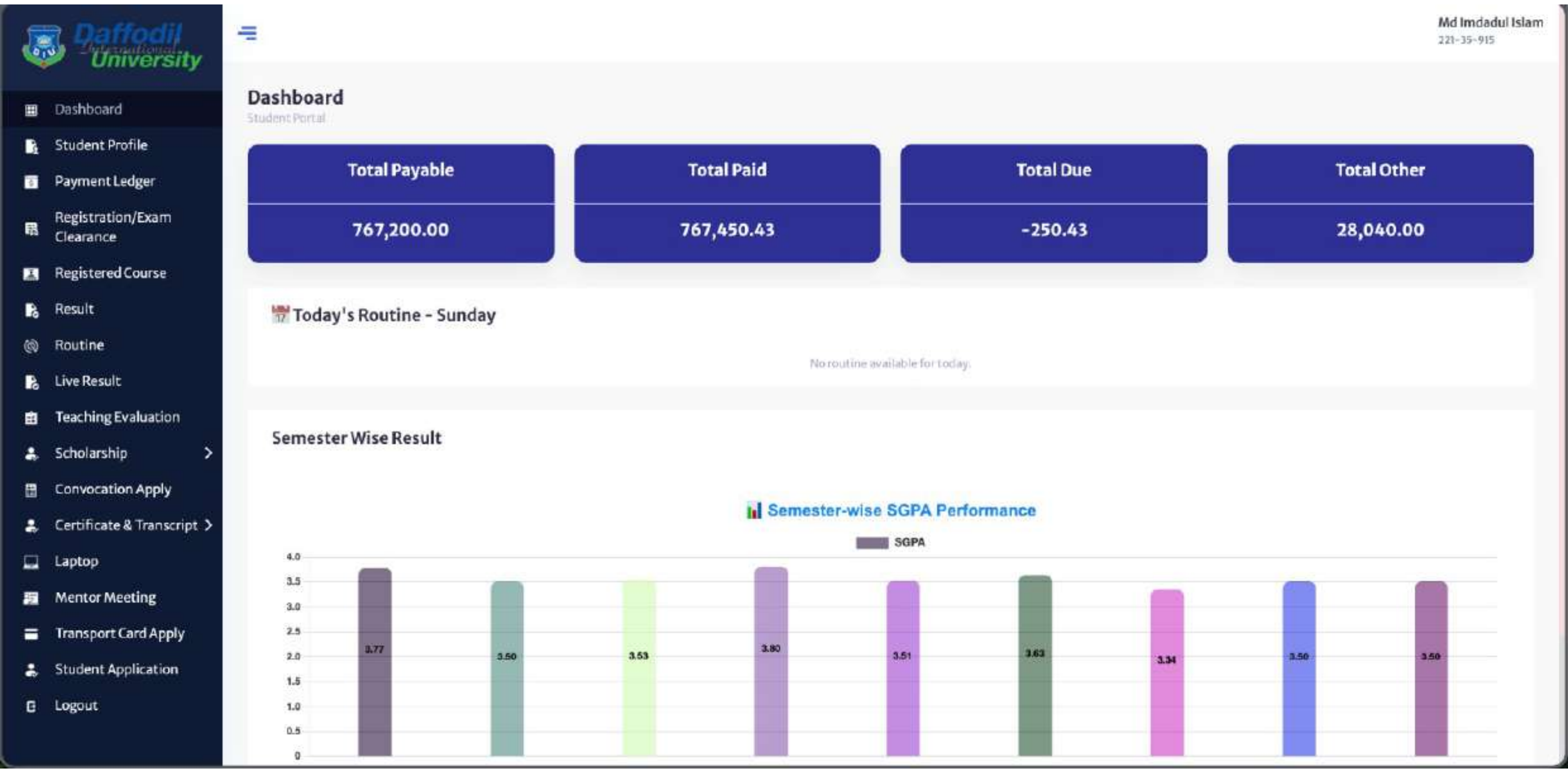

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