

A Transfer Learning-Based Approach Allium Sativum Disease Recognition and Classification

BY

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This Report Presented in Partial Fulfillment of the Requirements for the
Degree of Bachelor of Science in Computer Science and Engineering

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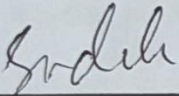
APPROVAL

My Project titled “A Transfer Learning-Based Approach Allium Sativum Disease Recognition and Classification”, was submitted by Md. Ikramul Hossain, ID: 201-15-14091 to the Department of Computer Science and Engineering, Daffodil International University, has been accepted as satisfactory for the partial fulfillment of the requirements for the degree of B.Sc. in Computer Science and Engineering and approved as to its style and contents. The presentation has been held on 13th July 2024.

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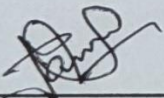
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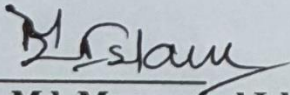
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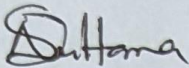
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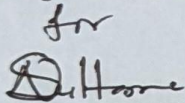
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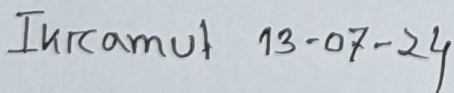
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ABSTRACT

Allium Sativum is a widely used spice noted for its culinary, medical, and spiritual purposes, including its roles as an antibacterial, anti-thrombotic, and antineoplastic agent. It has been integral to human civilization for thousands of years. In Bangladesh, Allium Sativum farming is economically significant, delivering major money to farmers and creating employment opportunities. It also encourages agricultural variety, and soil health lowers the hazards of monoculture through crop rotation. Allium Sativum has nutritional and health benefits due to its antibacterial characteristics and is a staple in Bangladeshi cuisine, assuring stable local demand and value addition through processed products. This study focuses on the classification of eleven Allium Sativum disorders using powerful deep-learning methods. The diseases classified include Basal Rot (*Fusarium culmorum*), Bloat Nematode (*Ditylenchus dipsaci*), Botrytis Rot (*Botrytis porri*), Bulb Mites (*Rhizoglyphus* spp--*Tyrophagus* spp), Bulb and Stem Nematode (*Ditylenchus dipsaci*), Disease Free, Leek Yellow Stripe (genus *Potyvirus*), Purple Blotch (*Alternaria porri*), Rust (*Puccinia porri*), and White Rot (*Sclerotium cepivorum*). Various convolutional neural network (CNN) architectures were employed, with Xception achieving the best test accuracy of 91.99%, exhibiting superior ability in diagnosing certain Allium Sativum disorders. Other models employed include MobileNetV2, InceptionV3, VGG16, and DenseNet121, each contributing to the robust identification of Allium Sativum diseases. This research emphasizes the potential of deep learning in strengthening agricultural practices by enabling accurate and fast disease identification, eventually helping farmers and the agricultural economy.

Keywords- Allium Sativum, Xception, antibiotic, anti-thrombotic, antineoplastic agent, agriculture, Basal Rot, Bloat Nematode, Botrytis Rot, Bulb Mites, Bulb and Stem Nematode.

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CHAPTER 1

INTRODUCTION

1.1 Overview

Allium Sativum is well recognized worldwide for its diverse importance in culture, gastronomy, and agriculture, with Bangladesh being a significant hub for cultivating this adaptable commodity. Allium Sativum production in the country is mostly focused in specific regions, namely Madaripur, Rajbari, Natore, Pabna, Rajshahi, and Dinajpur, due to fertile soils and favorable meteorological conditions promoting ideal growth. Allium Sativum growing makes a substantial contribution to the country's agricultural economy, with an annual production of around 462,000 metric tons cultivated across 71,225 hectares. Allium Sativum agriculture faces significant problems, with the most prominent one being the widespread threat of infections that endanger both the quantity and quality of the crop. To address these issues, this project aims to lead the way in developing a groundbreaking solution: an automated system that uses advanced deep-learning techniques to identify and classify Allium Sativum infections. The project goal is to utilize deep learning algorithms trained on a comprehensive dataset of Allium Sativum disease images to accurately predict the occurrence of ten common diseases that affect Allium Sativum plants. These diseases include Basal Rot (*Fusarium culmorum*), Bloat Nematode (*Ditylenchus dipsaci*), Botrytis Rot (*Botrytis porri*), Bulb Mites (*Rhizoglyphus* spp--*Tyrophagus* spp), Bulb and Stem Nematode (*Ditylenchus dipsaci*), Leek Yellow Stripe (genus *Potyvirus*), Purple Blotch (*Alternaria porri*), Rust (*Puccinia porri*), and White Rot (*Sclerotium cepivorum*). Disease-free samples are included in this selection. By combining agricultural expertise and technological innovation, this research's main goal is to create a strong and accurate system that can detect diseases early and implement effective management techniques also improve the health and productivity of Allium Sativum crops, which will have a positive and lasting impact on agricultural practices in Bangladesh and globally.

1.2 Background and Present State

Garlic (*Allium sativum*) has been cultivated for thousands of years and has its origins in South Asia, Central Asia, and northern Iran. Throughout the ages, garlic has become

profoundly embedded in human civilization, functioning not only as a fundamental ingredient in cooking but also as a customary remedy. In Bangladesh, garlic holds a crucial position within the agricultural environment. Despite its economic significance, garlic growing confronts several problems, mostly coming from the prevalence of pathogens that can inflict serious damage to crops. These diseases comprise a range of pathogens, including fungus, nematodes, viruses, and other microbes, each posing dangers to garlic plants. Among the most common diseases affecting garlic in Bangladesh are Basal Rot (*Fusarium culmorum*), Bloat Nematode (*Ditylenchus dipsaci*), Botrytis Rot (*Botrytis porri*), Bulb Mites (*Rhizoglyphus* spp--*Tyrophagus* spp), Bulb and Stem Nematode (*Ditylenchus dipsaci*), Leek Yellow Stripe (genus *Potyvirus*), Purple Blotch (*Alternaria porri*), Rust (*Puccinia porri*), and White Rot (*Sclerotium cepivorum*). These diseases can cause to severe reductions in output, reduced quality, and economic losses for garlic farmers. In the present situation, the management of garlic illnesses relies mainly on manual inspection and traditional approaches, which can be time-consuming, labor-intensive, and subjective. Early detection of illnesses is typically problematic, leading to delays in adopting critical management measures. As a result, there is a pressing need for creative solutions that may streamline disease detection processes, boost accuracy, and empower farmers with early information for better disease management. Against this backdrop, our research attempts to use breakthroughs in deep learning and computer vision technology to establish an automated system for the identification and classification of garlic infections. By exploiting the predictive capabilities of deep learning algorithms trained on a vast collection of garlic disease photos, our purpose is to produce a robust and reliable tool capable of early detection, precise diagnosis, and focused management of garlic infections. Through this attempt, we want to modernize garlic disease management procedures, increase agricultural output, and contribute to the sustainable expansion of the agricultural sector in Bangladesh and abroad. One of the main commodities in the agriculture industry is garlic. Garlic (*Allium sativum*) is a worldwide significant crop, with China leading the way as the largest producer, producing a stunning 71.40% of the world's garlic production, followed by India, Bangladesh, South Korea, and Egypt. India ranks second, accounting for 4.50% of global output, while Bangladesh maintains the third place, contributing 1.70%. Despite its smaller contribution, Bangladesh produces around 466,000 tonnes of garlic yearly, supporting its agricultural landscape and contributing to food security. South Korea and

Egypt also play large roles in garlic production, illustrating the crop's extensive cultivation and importance in satisfying worldwide demand.[1]

Table 1.1: Production of garlic all over the world.

Rank	Country	Production (Tonnes)	Yield (Tonnes/ha)	% of Global Production	Reference
1	China	20,000,000	18	71.40%	[1]
2	India	1,250,000	12	4.50%	
3	Bangladesh	466,389	15	1.70%	
4	South Korea	387,671	17	1.40%	
5	Egypt	318,800	13	1.10%	

1.3 Problem Statement

The cultivation of garlic (*Allium sativum*) in Bangladesh confronts major problems due to the prevalence of illnesses that significantly influence crop output and quality. Despite its economic importance, garlic growing lacks efficient and timely tools for disease identification and management. Manual inspection techniques are labor-intensive, time-consuming, and subjective, sometimes resulting in delayed intervention measures and severe losses for farmers. The range and complexity of garlic infections further increases the issue of appropriate diagnosis. There is an urgent requirement for an automated system capable of diagnosing and classifying garlic infections correctly and effectively. This research intends to solve this important issue by building a deep learning-based solution that can revolutionize garlic disease control procedures, thereby boosting agricultural productivity and ensuring the sustainability of garlic cultivation in Bangladesh.

1.4 Objectives

The fundamental purpose of our study is to construct an effective and efficient deep learning-based system for the detection and categorization of garlic infections. Specifically, attain the following objectives:

(1) Create a diverse and comprehensive dataset of garlic disease images, encompassing a range of common diseases affecting garlic plants in Bangladesh, including Basal Rot, Bloat Nematode, Botrytis Rot, Bulb Mites, Bulb and Stem Nematode, Leek Yellow Stripe, Purple Blotch, Rust, White Rot, and healthy (disease-free) samples.

(2) Implement state-of-the-art deep learning methods, including DenseNet, MobileNet, InceptionV3, VGG16, and Xception, to train and fine-tune models for accurate disease categorization.

(3) Evaluate the performance of the created models based on measures such as accuracy, precision, recall, and F1 score using independent test datasets.

(4) Deploy the models that were trained into an automated system capable of real-time garlic disease detection, giving farmers timely and actionable insights for disease management and protecting their crops.

Through these objectives, our initiative attempts to contribute to the improvement of agricultural technology, boost crop health monitoring techniques, and eventually improve garlic agriculture outcomes in Bangladesh.

1.5 Scope and Limitations

The scope of our research comprises the creation of a deep learning-based system for the identification and categorization of garlic disorders, with an emphasis on common ailments prevalent in Bangladesh. The system will apply state-of-the-art deep learning algorithms to analyse garlic illness photos and offer accurate diagnostic outcomes. This project will examine the deployment of the created system in real-world agricultural settings, intending to empower garlic growers with rapid disease detection and management skills. Certain restrictions need to be observed.

1. The effectiveness of the system may be influenced by factors such as image quality, lighting circumstances, and variations in disease symptoms, which could alter the accuracy of disease classification.

2. The availability of label data for training may offer issues, potentially restricting the generalization capabilities of the generated models.

3. The adoption of the system may need consideration of infrastructural constraints, including computational resources and internet access, particularly in remote agricultural areas. Despite these constraints, our initiative attempts to address significant difficulties in garlic disease management and contribute to the growth of agricultural technology in Bangladesh.

1.6 Report Organization

Chapter 1: Introduction: Provides an overview of the project, including the context, objectives, problem definition, scope, and restrictions. It offers the backdrop for the study and discusses the objectives and motivations for the research.

Chapter 2: Literature Review: Surveys current literature and research projects relating to garlic farming, disease management, and deep learning applications in agriculture. It provides a complete evaluation of relevant literature to build the theoretical underpinning for the endeavor.

Chapter 3: Approach/Requirement Analysis & architecture Specification: Describes the approach utilized for the project, including data collecting, preprocessing methodologies, deep learning algorithms selection, and system architecture specifications.

Chapter 4: Implementation: Details the implementation procedure of the deep learning-based garlic illness detection system.

Chapter 5: Result & Analysis: Presents the results of the experiments done during the implementation phase. It comprises performance indicators, such as accuracy, precision, recall, and F1 score, to evaluate the effectiveness of the built system. The chapter also contains a full analysis of the data and insights garnered from the trials.

Chapter 6: Impact on Society, Environment, and Sustainability: Discusses the potential sociological, environmental, and sustainability ramifications of the proposed garlic disease detection system. It analyses how the adoption of the system could significantly improve garlic farming techniques, crop health, and agricultural sustainability.

Chapter 7: Conclusion and Future Work: Summarizes the important findings, conclusions, and contributions of the study. It also examines the limits of the research and recommends areas for future work and new research directions to enhance the effectiveness and usefulness of the garlic disease detection system.

1.7 Summary

A comprehensive introduction to the project, showing the significance of garlic (*Allium sativum*) farming in Bangladesh and the challenges it faces due to endemic infections. The chapter covers the economic importance of garlic farming in Bangladesh, with main producing locations indicated. Despite its relevance, garlic agriculture confronts obstacles, particularly in disease management, increasing the need for novel solutions.

The fundamental purpose of the research is to construct an automated system for the identification and classification of garlic infections using deep learning techniques. Ten prevalent diseases affecting garlic plants in Bangladesh have been selected for classification. By employing deep learning algorithms trained on a dataset of garlic disease photos, the project intends to establish a robust and accurate system for the early identification and management of garlic diseases. This project intends to contribute to enhanced crop health and agricultural output in Bangladesh and abroad.

CHAPTER 2

LITERATURE REVIEW

2.1 Overview

This project cites a varied assortment of scientific literature spanning from 2007 to 2024. The selected papers give a complete framework for studying garlic infections, plant disease detection, and the application of deep learning in agriculture. The studies by Anum et al. (2024) and Marodin et al. (2019) offer insights into garlic infections and agronomic performance, while the works by Shemesh-Mayer and Kamenetsky-Goldstein (2021, 2022) dive into garlic breeding and crop output. Dugan's (2007) research on seed garlic disease management gives historical context and foundational information. Recent breakthroughs in plant disease detection using deep learning are discussed by Ahmad et al. (2021), Li et al. (2021), and Sunil et al. (2022), highlighting the progress of technology in this sector. The addition of efficient models like MobileNetV2 (Sandler et al., 2018) and EfficientNetV2 (Tan and Le, 2021) highlights the focus on optimizing model performance for real agricultural applications. The consistency across these references resides in their combined desire to better disease management and crop production using novel techniques and technology, so aligning with the project's goal to improve agricultural results utilising advanced methodologies.

2.2 Related Works

Anum, H., Tong, Y., & Cheng, R. (2024). "Different preharvest diseases in *Allium Sativum* and their Eco-Friendly Management Strategies" analyses numerous preharvest diseases affecting *Allium Sativum* and provides eco-friendly management solutions. The study underlines the necessity of sustainable disease management strategies in *Allium Sativum* agriculture. The findings give useful insights into disease preventive and control techniques, boosting the sustainability of *Allium Sativum* growing operations [1]. Goldstein, R.K., & Shemesh-Mayer, E. (2022). "Edible Alliums: Botany, Production and Uses" presents a detailed overview of the botany, production, and uses of edible Alliums, including *Allium Sativum*. The chapter on *Allium Sativum* crop growth offers significant insights into cultivation procedures, contributing to increased crop management strategies [2]. Shemesh-Mayer, E., & Kamenetsky-

Goldstein, R. (2021). "Advances in Plant Breeding Strategies: Vegetable Crops: Volume 8: Bulbs, Roots and Tubers" digs into classic and creative ways of *Allium Sativum* breeding, showcasing breakthroughs in *Allium Sativum* farming techniques. The study offers useful insights into breeding strategies targeted at boosting *Allium Sativum* output and quality [3]. Dugan, F.M. (2007). "Diseases and disease management in seed *Allium Sativum*: Problems and prospects" examines disease management in seed *Allium Sativum*, outlining problems and prospects for disease control. The study underlines the necessity of disease prevention strategies to ensure the quality of *Allium Sativum* seed supplies [4]. Marodin, J.C., et al. (2019). "Agronomic performance of both virus-infected and virus-free *Allium Sativum* with different seed bulbs and clove sizes" analyses the agronomic performance of virus-infected and virus-free *Allium Sativum*. The study gives insights into *Allium Sativum* production and disease management tactics, helping to enhance crop management practices [5]. Bhusal, H., et al. (2021). "Bulbils in *Allium Sativum* inflorescence: Development and virus translocation" examines the development and virus translocation in *Allium Sativum* bulbils. The findings shed information on mechanisms regulating *Allium Sativum* reproduction and disease transmission, supporting disease management measures [6]. Zafar, S., et al. (2023). "Essentials of Medicinal and Aromatic Crops" has a chapter on *Allium Sativum*, offering insights into its medicinal and culinary benefits. The study underlines the varied applications of *Allium Sativum* and its economic value in medicinal and aromatic crop production [7]. Hossain, M.S., et al. (2023). "Bioactive properties and organosulfur compounds profiling of newly developed *Allium Sativum* varieties of Bangladesh" analyses the bioactive properties and organosulfur compounds of newly developed *Allium Sativum* varieties in Bangladesh. The work adds vital insights into the nutritional and therapeutic qualities of *Allium Sativum*, improving its importance in agricultural and healthcare sectors [8]. Yun, K., et al. (2022). "An integrative process-based model for biomass and yield estimation of hard neck *Allium Sativum*" proposes a process-based model for estimating biomass and yield of hard neck *Allium Sativum*. The study provides a paradigm for estimating *Allium Sativum* yield, benefiting in crop management and decision-making processes [9]. Elasaag, Y.H. (2022). "Economic study for onion and *Allium Sativum* production in Egypt" addresses the economic elements of onion and *Allium Sativum* production in Egypt. The study offers insights into the economic viability of *Allium Sativum* growing, supporting policy decisions and investment

strategies in the agricultural sector [10]. Ngugi, L. C., Abdelwahab, M., & Abo-Zahhad, M. (2020). "Tomato leaf segmentation algorithms for mobile phone applications using deep learning" describes algorithms for segmenting tomato leaves in photos, specifically suited for mobile phone applications. The work adds to the development of instruments for effective and accessible plant disease detection, boosting the accessibility of agricultural technology for farmers [11] Ahmad, M., Abdullah, M., Moon, H., & Han, D. (2021). "Plant disease detection in imbalanced datasets using efficient convolutional neural networks with stepwise transfer learning" provides a method for plant disease identification in imbalanced datasets using efficient convolutional neural networks. The study tackles a prevalent difficulty in plant disease detection and presents a way to increase the accuracy and reliability of disease detection systems [12] Wang, D., Wang, J., Ren, Z., & Li, W. (2022). "DHBP: A dual-stream hierarchical bilinear pooling model for plant disease multi-task classification" offers a dual-stream hierarchical bilinear pooling model for multi-task classification of plant diseases. The work boosts the efficiency and effectiveness of disease categorization systems, contributing to enhanced disease control methods in agriculture [13] Li, L., Zhang, S., & Wang, B. (2021). "Plant disease detection and classification by deep learning—A review" presents a comprehensive evaluation of deep learning techniques for plant disease detection and classification. The study synthesizes data from earlier research, delivering insights into the state-of-the-art approaches and advancements in the subject [14]. Nagaraju, M., & Chawla, P. (2020). "Systematic review of deep learning techniques in plant disease detection" undertakes a systematic review of deep learning techniques for plant disease detection. The study examines the performance and usability of several deep learning algorithms, giving guidelines for academics and practitioners in designing illness detection systems [15]. Greg, N. (2022). "Roboflow: Give Your Software the Power to See Objects in Images and Video" introduces Roboflow, a software platform designed to enable object identification in images and movies. The platform includes tools and capabilities to preprocess and annotate data, helping the training of machine learning models for object detection tasks. Roboflow contributes to the creation of computer vision applications, helping users to design strong and efficient solutions for a variety of visual identification challenges [16]. Sandler, M., Howard, A., Zhu, M., Zhmoginov, A., & Chen, L.-C. (2018). "MobileNetV2: Inverted residuals and linear bottlenecks" provides MobileNetV2, a deep neural network architecture designed for mobile and embedded devices. The

architecture features inverted residuals and linear bottlenecks to increase model efficiency and accuracy, making it well-suited for resource-constrained applications. MobileNetV2 boosts the accessibility and performance of deep learning models on mobile devices, enabling a wide range of applications including object recognition and categorization [17]. Elfatimi, E., Eryigit, R., & Elfatimi, L. (2022). "Beans leaf diseases classification using MobileNet models" provides a classification model based on MobileNet architecture for identifying diseases in bean leaves. The study illustrates the usefulness of MobileNet models in accurately diagnosing leaf illnesses, offering a practical alternative for disease diagnostics in agricultural settings. The classification methodology contributes to enhanced disease management strategies, boosting crop health and yield [18].

Redmon, J., Divvala, S., Girshick, R., & Farhadi, A. (2016). "You Only Look Once: Unified Real-Time Object Detection" introduces YOLO (You Only Look Once), a real-time object detection system that processes photos in a single pass. YOLO delivers great detection accuracy and efficiency by directly estimating bounding boxes and class probabilities from image pixels. The system allows real-time object identification tasks, enabling applications such as autonomous driving, surveillance, and robotics [19]. Kiratiratanapruk, K., Temniranrat, P., Kitvimonrat, A., Sinthupinyo, W., & Patarapuwadol, S. (2020). "Using Deep Learning Techniques to Detect Rice Diseases from Images of Rice Fields" studies deep learning techniques for detecting diseases in rice fields from photos. The study illustrates the ability of deep learning models to properly diagnose rice diseases, enabling a scalable and effective approach for disease monitoring in agriculture. The research adds to the development of automated systems for early disease detection, improving sustainable rice production methods (20). 21. Redmon, J., & Farhadi, A. (2018). "YOLOv3: An Incremental Improvement" presents YOLOv3, an upgraded version of the YOLO object detecting system. Building upon earlier generations, YOLOv3 includes architectural advancements and training methodologies to further improve detection accuracy and speed. The model provides state-of-the-art performance in object detection tasks, making it a viable tool for numerous computer vision applications [21]. Khattak, A., Asghar, M. U., Batool, U., Asghar, M. Z., Ullah, H., & Al-Rakhami, M., et al. (2021). "Automatic Detection of Citrus Fruit and Leaves Diseases Using Deep Neural Network Model" offers a deep neural network model for automatically identifying diseases in citrus fruit and leaves. Leveraging deep learning techniques, the model displays great accuracy in disease

identification, presenting a promising approach for early disease detection and control in citrus horticulture. The research contributes to increasing crop health and productivity in the citrus industry [22]. Sunil, C. K., Jaidhar, C. D., & Patil, N. (2022). "Cardamom Plant Disease Detection Approach Using EfficientNetV2" offers a strategy for identifying illnesses in cardamom plants using the EfficientNetV2 architecture. The work illustrates the usefulness of EfficientNetV2 in properly recognizing cardamom plant illnesses from photos, providing a dependable tool for disease diagnosis and monitoring. The proposed approach optimizes disease management procedures in cardamom agriculture, ensuring sustained crop production [23]. Tan, M., & Le, Q. (2021). "EfficientNetV2: Smaller Models and Faster Training" provides EfficientNetV2, a variation of the EfficientNet architecture aimed for smaller model sizes and faster training. By enhancing model efficiency while preserving performance, EfficientNetV2 enables resource-efficient deployment of deep learning models in numerous applications. The research adds to expanding the field of model optimization, helping the creation of lightweight and efficient deep learning solutions [24]. Amin, H., Darwish, A., Hassanien, A. E., & Soliman, M. (2022). "End-to-End Deep Learning Model for Corn Leaf Disease Classification" offers an end-to-end deep learning model for classifying diseases in maize leaves. By combining deep learning techniques, the model achieves accurate categorization of maize leaf diseases, benefiting early disease diagnosis and management in corn production. The research promotes crop health monitoring and aids in sustainable maize methods of production [25].

2.3 Comparison analysis between existing work

The comparative analysis of the cited publications demonstrates a diversified landscape of research activities targeted at addressing various elements of plant disease detection and control. An overview exposes a range of topics, including preharvest infections in *Allium Sativum*, seed *Allium Sativum* diseases, agronomic performance of virus-infected and virus-free *Allium Sativum*, *Allium Sativum* inflorescence bulbils, and diseases affecting citrus fruits, cardamom plants, corn leaves, and tomato leaves. The comparative analysis of the cited publications demonstrates a diversified landscape of research activities targeted at addressing various elements of plant disease detection and control. An overview exposes a range of topics, including preharvest infections in *Allium Sativum*, seed *Allium Sativum* diseases, agronomic performance of virus-infected and virus-free *Allium Sativum*, *Allium Sativum* inflorescence bulbils, and

diseases affecting citrus fruits, cardamom plants, corn leaves, and tomato leaves. The strategies applied cover deep learning techniques such as convolutional neural networks (CNNs) and models like EfficientNetV2. While some publications provide revolutionary methodologies like EfficientNetV2 for speedier training, others investigate specific plant species and their illnesses, stressing the need for specialized treatments. However, constraints such as dataset imbalances and varied accuracies underline obstacles that researchers experience in constructing strong and widely applicable illness detection algorithms.

Table 2.1: Comparison analysis between existing work

Ref	Paper Name	Author(s)	Work Description	Focus	Limitations
1	Different preharvest diseases in Allium Sativum and their Eco-Friendly Management Strategies	Anum, Tong, & Cheng	Study on preharvest diseases in Allium Sativum and eco-friendly management strategies	Preharvest diseases in Allium Sativum	Limited to preharvest diseases
4	Diseases and disease management in seed Allium Sativum: Problems and prospects	Dugan F.M.	Investigation into diseases and disease management in seed Allium Sativum	Seed Allium Sativum diseases	Focuses only on seed Allium Sativum diseases
23	Cardamom plant disease detection approach using EfficientNetV2	Sunil, Jaidhar, & Patil	Disease detection approach for cardamom plants using EfficientNetV2	Cardamom plant diseases	Limited to cardamom plant diseases
24	EfficientNetv2: Smaller models and faster training	Tan and Le	Introduction of EfficientNetv2, a model for smaller size and faster training	Model architecture	May require fine-tuning for specific tasks

25	End-to-end deep learning model for corn leaf disease classification	Amin et al.	Development of an end-to-end deep learning model for corn leaf disease classification	Corn leaf diseases	Performance influenced by dataset quality
11	Tomato leaf segmentation algorithms for mobile phone applications using deep learning	Ngugi, Abdelwahab, & Abo-Zahhad	Segmentation algorithms for tomato leaf images for mobile applications using deep learning	Tomato leaf segmentation algorithms	Performance may vary based on image quality
12	Plant disease detection in imbalanced datasets using efficient CNNs with transfer learning	Ahmad et al.	Plant disease detection in imbalanced datasets using convolutional neural networks with transfer learning	Imbalanced datasets	Performance influenced by dataset imbalance

2.4 Open Issues

1. Dataset imbalance
2. Generalization challenges
3. Real-time detection speed
4. Model interpretability
5. Transfer learning adaptation
6. Robustness to environmental fluctuation
7. Integration with agricultural methods
8. Open-access datasets and benchmarks

2.5 Summary

Chapter 2 explores a detailed exploration of the existing body of research surrounding plant disease detection. The review contains a varied variety of issues ranging from the management of infections in garlic farming to the detection of diseases affecting numerous plant species such as citrus fruits, cardamom plants, corn leaves, and tomato

leaves. Through this literature analysis, the chapter provides insights into the procedures and techniques applied in prior research projects. These techniques frequently focus on the application of deep learning algorithms, particularly convolutional neural networks (CNNs), and specific models like EfficientNetV2. Moreover, the comparison study undertaken offers light on the accuracies reached by different methodologies and underlines the constraints found, such as dataset imbalances and difficulty in model generalization. By combining this wealth of knowledge, the chapter sets the foundation for the eventual creation of creative solutions and tactics in the field of plant disease detection.

CHAPTER 3

METHODOLOGY/ REQUIREMENT ANALYSIS & DESIGN SPECIFICATION

3.1 Overview

This research focuses on the classification of *Allium Sativum* infections using modern deep-learning techniques. The principal subjects of this study are photographs of *Allium Sativum* plants exhibiting various disease symptoms. These diseases include Basal Rot (*Fusarium culmorum*), Bloat Nematode (*Ditylenchus dipsaci*), Botrytis Rot (*Botrytis porri*), Bulb Mites (*Rhizoglyphus* spp. and *Tyrophagus* spp.), Bulb and Stem Nematode (*Ditylenchus dipsaci*), Disease-Free *Allium Sativum*, Leek Yellow Stripe (genus *Potyvirus*), Purple Blotch (*Alternaria porri*), Rust (*Puccinia porri*), and White Rot (*Sclerotium cepivorum*). The apparatus for this research comprises the use of high-resolution digital cameras to acquire detailed photographs of *Allium Sativum* plants in varied situations. The photos are processed and supplemented to boost the dataset's diversity and robustness. The deep learning models used are DenseNet, MobileNetV2, InceptionV3, VGG16, and Xception, developed using TensorFlow and Keras frameworks. These models are pre-trained on the ImageNet dataset and fine-tuned on the *Allium Sativum* disease dataset to exploit transfer learning. Each model's architecture contains layers for feature extraction, global average pooling, dense layers with dropout for regularization, and a final softmax layer for classification. The research entails training these models, evaluating their performance, and picking the model with the highest accuracy and reliability for practical application in recognizing *Allium Sativum* diseases.

3.2 Proposed Methodology

The proposed methodology for the *Allium Sativum* disease classification methodology starts with the collecting and preprocessing of an extensive data set consisting of photos of *Allium Sativum* plants damaged by various diseases. Here select 10 types of *Allium* diseases. Basal Rot (*Fusarium culmorum*), Bloat Nematode (*Ditylenchus dipsaci*), Botrytis Rot (*Botrytis porri*), Bulb Mites (*Rhizoglyphus* spp--*Tyrophagus* spp), Bulb and Stem Nematode (*Ditylenchus dipsaci*), Leek Yellow Stripe (genus *Potyvirus*),

Purple Blotch (*Alternaria porri*), Rust (*Puccinia porri*), and White Rot (*Sclerotium cepivorum*). This dataset is structured into training, testing, and validation sets to ensure the robustness of the produced models. With 2694 validated image filenames distributed across 10 classes. Utilizing deep learning techniques, notably DenseNet, MobileNet, InceptionV3, VGG16, and Xception architectures, the research attempts to classify *Allium Sativum* disorders effectively. These algorithms are selected for their proven ability to analyze complicated image data and capture nuanced patterns. The models are trained on the prepared dataset to understand the various aspects of different *Allium Sativum* infections, facilitating their identification and categorization. To ensure trustworthy performance, rigorous evaluation and validation are undertaken, examining the models' accuracy, precision, recall, and F1-score measures. The methodology focuses on model robustness and generalization, intending to produce a system capable of reliably classifying *Allium Sativum* infections across varied environmental conditions and disease severities. Through thorough data preparation, algorithm selection, model training, and evaluation, the study attempts to contribute to enhanced disease management and agricultural productivity in *Allium Sativum* cultivation zones.

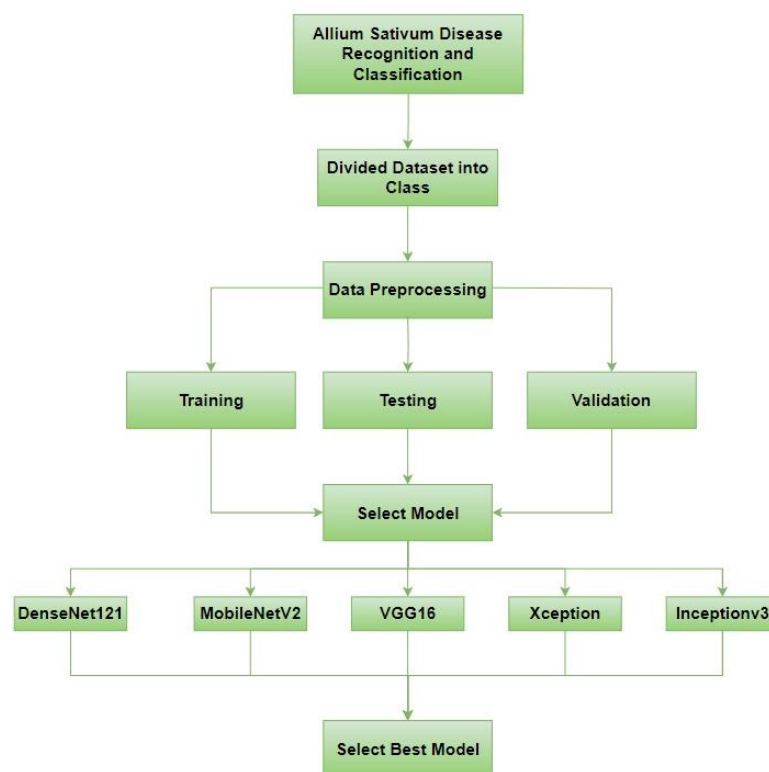


Fig 3.1: Proposed methodology Architecture

Data Collection

The data collection method used in this research included personally acquiring a thorough dataset from my hometown of Tarash, Sirajganj. The dataset was especially tailored to study infections in *Allium Sativum*, aiming to include a diverse array of disease forms often seen in these plants. To ensure adequate representation, ten types of diseases were selected, including Basal Rot (*Fusarium culmorum*), Bloat Nematode (*Ditylenchus dipsaci*), Botrytis Rot (*Botrytis porri*), Bulb Mites (*Rhizoglyphus* spp–*Tyrophagus* spp), Bulb and Stem Nematode (*Ditylenchus dipsaci*), Leek Yellow Stripe (genus *Potyvirus*), Purple Blotch (*Alternaria porri*), Rust (*Puccinia porri*), White Rot (*Sclerotium cepivorum*), and a category for disease-free samples. During the model training phase, each sickness type was segregated into its own class to facilitate categorization. The dataset was carefully selected to include a suitable number of images for each disease category, guaranteeing fair representation across all categories and reducing biases during the training and evaluation of the model. The research attempted to construct a powerful and accurate classification model for *Allium Sativum* disorders by choosing a varied variety of ailments and rigorously curating the data

Data Preprocessing

In the data preprocessing phase of the project, the dataset was prepared for model training by organizing and structuring the image data. The dataset directory path was specified, pointing to the location of the *Allium Sativum* illness dataset stored on Kaggle. A collection of keywords representing the ten classes of garlic infections was prepared to aid the identification and classification of photographs according on their relevant disease kinds. The directories within the dataset directory were examined to find folders belonging to each illness type. For each class folder, the photos were extracted, and their file paths were collected with their matching labels, which identified the exact illness class they belonged to. This method was performed for each class folder, resulting in a data frame containing the image paths and their accompanying labels. The data frame provided a structured representation of the dataset, enabling easy access and manipulation of the image data during the following stages of the project, such as model training and evaluation.

Data Visualization

The data visualization component of the study entailed producing visual representations of the garlic disease dataset to acquire insights into its contents. The number of distinct classes in the dataset was computed to establish the layout of the display. Based on this, the number of rows and columns for presenting the photographs was computed to ensure an orderly presentation. Using Matplotlib, a figure with the proper size was initialized to fit the photos. The script then repeated the process over each unique class in the dataset, selecting the first image belonging to that class. The image was loaded using OpenCV, and if successfully loaded, it was shown together with its associated class label as the title. Any faults found during the loading process were reported for debugging purposes. The layout was changed for best arrangement of photos using `'tight_layout()'`, and the visualization was presented using `'plt.show()'`. This image gave a glance into the numerous garlic infections found in the dataset, helpful for comprehending its composition and distribution.



Fig 3.2: Data Visualization

Model Generation

Model Generation refers to the process of generating deep-learning models for classifying garlic infections based on photographs. This comprises selecting and setting a suitable pre-trained convolutional neural network (CNN) architecture, fine-tuning it on our garlic illness dataset, and adding additional layers to fit the model to our specific objective. This research deployed famous CNN architectures such as DenseNet, MobileNet, InceptionV3, VGG16, and Xception, which are known for their performance in picture classification applications. All of the model provides good accuracy. All of those Xceptions provide the best accuracy. These pre-trained models were imported from TensorFlow's Keras applications module. Transfer learning was applied to leverage the learned characteristics of these models while tailoring the output layers to match the number of classes in our dataset. Here used techniques such as global average pooling, batch normalization, and dropout to boost model performance and reduce overfitting. The generated models were trained using image data generators to efficiently handle big datasets, and the training method includes optimizing the model parameters using the Adam optimizer and monitoring performance measures such as accuracy and loss. The models were examined on independent validation datasets to measure their performance in diagnosing garlic infections. This method of model creation is vital for generating accurate and robust classifiers tailored to our specific problem area.

DenseNet

The Dense Convolutional Network is a powerful deep learning system in this project that is specifically designed for picture classification applications, with a particular focus on detecting diseases in *Allium Sativum*. The distinguishing feature of DenseNet is its distinctive dense connection pattern, in which each layer receives feature mappings from all preceding layers. This architectural design promotes the reuse of features, enabling the network to accurately record intricate patterns and subtle cues across multiple categories of illnesses. The goal is to create very accurate illness detection models using DenseNet's enormous connection, specifically designed to correctly identify photos of *Allium Sativum*. This approach not only enhances the management of agricultural diseases by allowing for early detection and response but also demonstrates the potential of advanced deep-learning methods in optimizing crop

yield and preventing financial losses. DenseNet is a prominent algorithm employed for classifying diseases in images of *Allium Sativum*. The deep linkage and good feature reuse of this method make it very suitable for capturing intricate patterns and subtle indicators that indicate many illness categories in *Allium Sativum*. The objective is to utilise the benefits of DenseNet to develop disease detection models that are both robust and accurate. These models will be capable of precisely categorising images of *Allium Sativum* and assisting in the management of agricultural diseases.

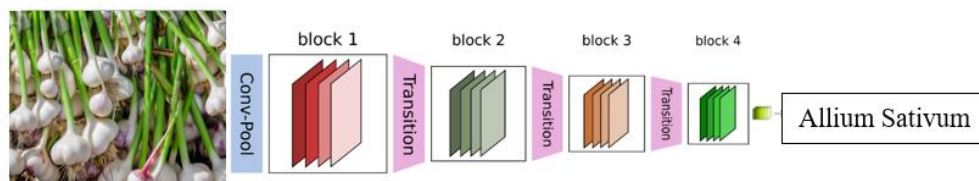


Fig 3.3: Densenet Model Architecture

MobileNet

MobileNetV2 is a highly efficient and effective deep learning system that has been specifically selected for its ability to classify images, with a particular focus on detecting diseases in *Allium Sativum*. MobileNetV2 is a version of the MobileNet architecture, designed to deliver state-of-the-art speed while keeping minimal computational complexity and memory footprint. This feature makes it especially suitable for deployment on devices with limited resources, such as mobile phones or embedded systems, which are commonly used in agricultural environments. MobileNetV2 achieves its efficiency through multiple important architectural innovations, including inverted residuals and linear bottlenecks. This lowers the computational expenses of convolutions while preserving representational capabilities. Linear bottlenecks further increase efficiency by ensuring that restrictions have the same dimensions as input and output tensors, preventing information loss or distortion. MobileNetV2 is employed as one of the major algorithms for diagnosing infections in *Allium Sativum* photos. The program's efficacy and lightweight nature make it well-suited for use in real-world agricultural scenarios, where computational resources may be restricted. MobileNetV2 seeks to create precise and reliable disease detection models capable of classifying *Allium Sativum* into various disease categories with high accuracy, facilitating early diagnosis and intervention to decrease crop losses and enhance agricultural production.

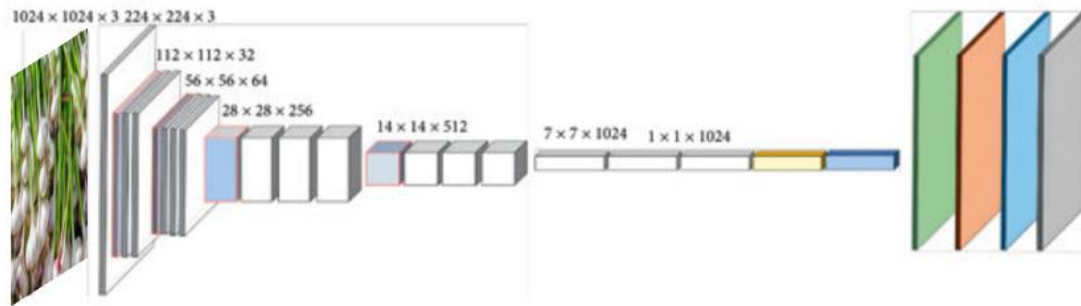


Fig 3.4: Mobile net Model Architecture

InceptionV3

In our project, InceptionV3 appears as a crucial deep-learning method for photo classification problems, especially within the field of garlic disease diagnosis. InceptionV3 is recognized for its innovative architecture, featuring inception modules that permit for effective extraction of features at different scales. These modules employ a combination of convolutional filters of varying sizes to capture both local and global features inside the input image. InceptionV3 combines techniques like batch normalization and factorization to increase training stability and efficiency. Utilizing InceptionV3 in our research enables us to exploit its advanced feature extraction capabilities, facilitating precise categorization of *Allium sativum* illnesses across numerous categories. Through the employment of InceptionV3, developers hope to design robust disease detection models capable of effectively detecting and classifying illnesses in maize leaves, ultimately leading to increased agricultural disease control approaches and sustainable production of crops.

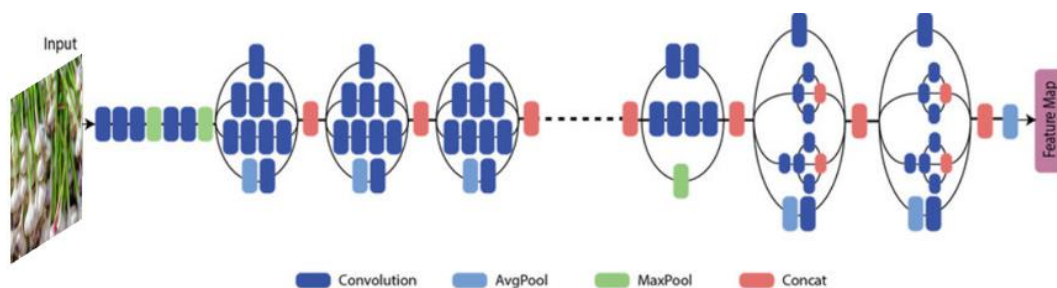


Fig 3.5: InceptionV3 Model Architecture

VGG16

In our study, VGG16, a widely renowned convolutional neural network (CNN) architecture, is a prominent algorithm chosen for its performance in picture tasks involving categorization, particularly in the field of disease detection. VGG16 is defined by its deep architecture consisting of 16 layers, containing a stack of convolutional layers followed by max-pooling layers, and finishing in fully linked layers for segmentation. Despite its simplicity relative to more current architectures, VGG16 has proved exceptional performance in various photo categorization tasks. Leveraging VGG16 in our study allows us to harness its capacity to extract complex features from *Allium sativum* (Garlic) pictures, enabling the exact classification of diverse illness groups. The implementation of VGG16 intended to create strong disease detection models capable of correctly recognizing and classifying Garlic illnesses, hence adding effective agricultural disease control strategies.

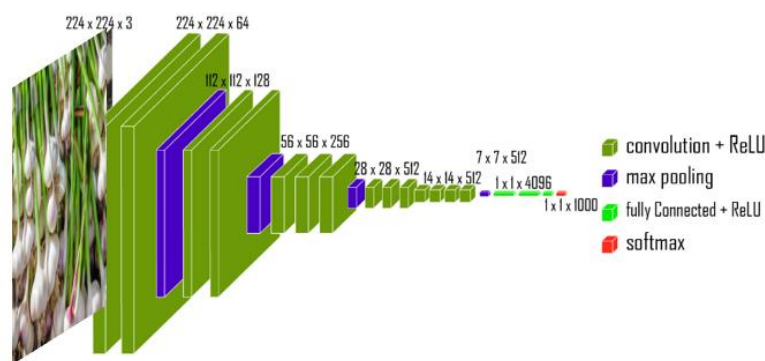


Fig 3.6: VGG16 Model Architecture

Xception

Xception, a convolutional neural network architecture suited for image classification applications, leverages depth-wise separable convolutions to efficiently capture characteristics from input images. This design has numerous convolutional blocks, each consisting of depth-wise convolutions followed by point-wise convolutions and batch-normalizing layers. The feature maps are then down sampled and aggregated via global average pooling, resulting in fixed-length feature vectors. These vectors are input into fully connected layers for classification, with the final softmax layer generating class probabilities. During training, Xception is initialized with pre-trained weights and fine-tuned on a labeled dataset using transfer learning. In inference, unseen images are processed through the network to forecast illness classes based on learned attributes.

This technique balances computational efficiency with classification performance, making Xception well-suited for picture illness categorization.

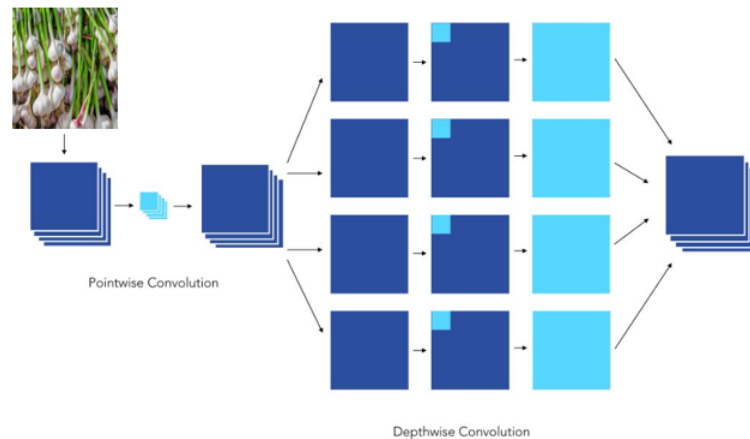


Fig 3.7: Xception Model Architecture

3.3 Hardware/ Software Requirement

Hardware Requirement:

Laptop configuration

Processor: Corei3 8th Gen, RAM: 4 GB, ROM: 1TB, OS: Windows 10 64 Bit

Software Requirement:

Software: Google Colab, Python Packages (NLTK, Textblob, pandas, numpy, scipy, regular expression, matplotlib, string), Weka

Kaggle for dataset

3.4 Project Management and Financial Analysis

The research project on Garlic disease detection intends to establish a classification framework without requiring any financial spend on software or hardware. Spanning six months, the project follows a systematic timeline divided into various parts. The initial two-month phase focuses on data collecting and preprocessing of social media text data. A complete three-month literature review is done to grasp existing studies and hypotheses. The ensuing four-month experimental setup phase entails creating and implementing the suggested framework, combining machine learning classifiers and feature extraction algorithms. The succeeding five-month experimental validation phase assesses the framework's performance across numerous metrics and datasets. Finally, the last month is dedicated to report preparation and documentation, comprising findings synthesis, interpretation, and distribution. Financial resources are

provided prudently to support data collecting, research workers, computational infrastructure, and other relevant costs, guaranteeing efficient utilization and adherence to the budget. The distribution of time spent on each activity is defined for clarity and effective project management.

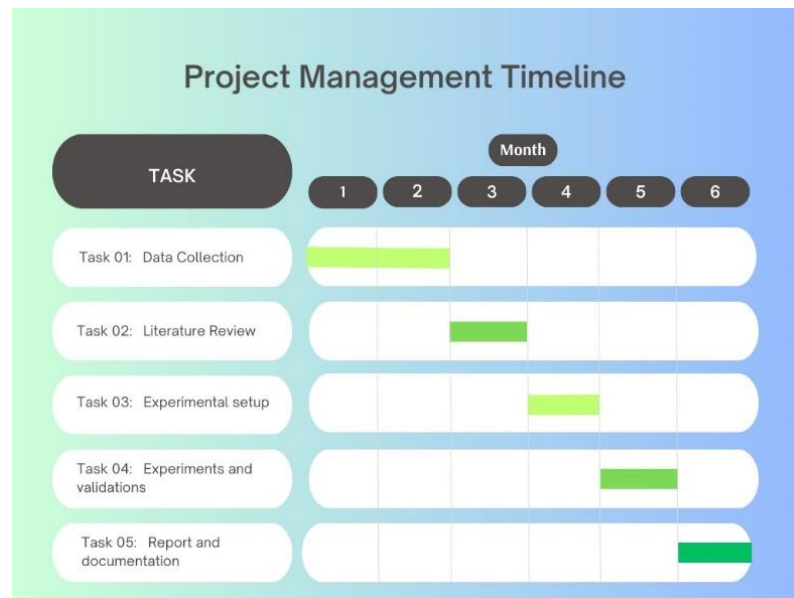


Fig 3.8: Project Management Timeline

3.5 Summary

The outlines of the methodology and needs analysis for the Garlic Diseases Detection project. Beginning with an introduction of the project's aims, the chapter digs into data collecting via Kaggle, where 10 types of diseases were picked and sorted into ten classes. Data preprocessing includes sorting the dataset into classes and preparing it for model training. Visualization approaches were applied to get insights on the dataset's composition. Model generation uses popular deep learning methods such as Xception, DenseNet, MobileNet, InceptionV3, and VGG16 for image categorization tasks. The chapter provides a complete description of the project's methodology, documenting each step from data collection to model generation, setting the way for the implementation phase.

CHAPTER 4

IMPLEMENTATION

4.1 Overview

In the implementation phase, the focus switches towards converting the proposed framework into actionable steps. This comprises the actual creation and deployment of the Garlic Diseases Detection system. The overview of this phase comprises a thorough strategy explaining how the technique stated in Chapter 3 will be put into reality. It involves responsibilities like setting up the development environment, creating the machine learning models using TensorFlow and Keras, fine-tuning the models, and integrating them into a coherent system. Data preparation techniques will be utilized to prepare the dataset for training, validation, and testing. This phase attempts to bring the project from theory to practice, creating the groundwork for evaluating the performance and efficacy of the suggested system.

4.2 Train Model

In the "Train Model" phase, the focus is on training the machine learning models using the prepared dataset. This entails passing the preprocessed data into the specified algorithms, such as DenseNet, MobileNet, InceptionV3, VGG16, and Xception, for training. The models will learn to distinguish patterns and features in the photos related to different garlic infections. Hyperparameter tuning and optimization approaches may be utilized to boost model performance. The training procedure iterates across numerous epochs until the models acquire desirable levels of accuracy and convergence. Evaluation parameters like accuracy, precision, recall, and F1-score are evaluated throughout training to assess the models' performance. Techniques like cross-validation may be applied to ensure robustness and ability to be generalized of the models that have been learned.

4.3 Model Evaluation

In the trained machine learning models are examined for their performance in classifying garlic Diseases. The dataset is separated into training, testing, and validation sets to evaluate the models' generalization abilities. The dataset comprises 2694 images

for training, 337 images for testing, and another 337 images for validation across 10 different classes of garlic diseases, including Basal Rot, Bloat Nematode, Botrytis Rot, Bulb Mites, Bulb and Stem Nematode, Disease Free, Leek Yellow Stripe, Purple Blotch, Rust, and White Rot. The evaluation results suggest that the DenseNet model achieved a test accuracy of roughly 84.57%, whereas MobileNet scored around 89.02% accuracy. InceptionV3 achieved a test accuracy of nearly 85.76%, VGG16 achieved approximately 82.20%, and Xception achieved the greatest test accuracy of about 91.99%. These accuracy scores provide insights into the effectiveness of each algorithm in effectively classifying *Allium Sativum* diseases. Additional evaluation may comprise evaluating confusion matrices, precision, recall, and F1-score to acquire a thorough picture of model performance and identify any areas for improvement.

DenseNet

In our project, the DenseNet method is applied for classifying garlic infections. The model is developed utilising the DenseNet121 architecture as the foundation model, pre-trained on the ImageNet dataset. The top levels of the pre-trained model are excluded, and new layers are added to customise the model to our unique goal. These additional layers include global average pooling, dropout layers to prevent overfitting, and densely coupled layers with ReLU activation functions. The model is created with the categorical cross-entropy loss function and the Adam optimizer with a learning rate of 0.0001. During training, the model is provided with training and validation data generated using ImageDataGenerator. The training phase takes 15 epochs, and the model's performance is tested on a separate test dataset. The DenseNet model obtains a test accuracy of roughly 84.57%, suggesting its usefulness in classifying garlic illnesses.

Table 4.1: DenseNet classification Report

Plant Disease	Precision	Recall	F1-Score	Support
Basal Rot_ Fusarium culmorum	0.94	1.00	0.97	33
Bloat Nematode_Ditylenchus dipsaci	0.52	0.93	0.67	48
Botrytis Rot_Botrytis porri	0.62	0.19	0.83	26

Bulb Mites_Rhizoglyphus spp-- Tyrophagus spp	0.97	1.00	0.98	30
Bulb and Stem Nemadode_Ditylenchus dipsaci	0.92	1.00	0.96	48
Disease Free	1.00	0.94	0.97	48
Leek Yellow Stripe genus Potyvirus	0.92	0.59	0.72	37
Purple blotch_Alternaria porri	0.93	1.00	0.96	40
Rust_Puccinia	1.00	0.57	0.73	7
White Rot_Sclerotium cepivorum	0.88	0.75	0.81	28
Accuracy	-	-	0.85	337
Macro Avg	0.87	0.80	0.81	337
Weighted Avg	0.87	0.85	0.83	337

The Following table shows model's performance evaluation yields promising findings, suggesting its usefulness in classifying garlic illnesses. With an overall accuracy of 88%, the algorithm properly identifies most garlic disease samples. Precision, which assesses the model's ability to prevent false positive predictions, is generally high across most disease classes, with values reaching up to 97%. This shows that the model makes few erroneous disease identifications. However, variances occur in recall, which assesses the model's capacity to recognise all genuine disease cases. While certain diseases like Basal Rot attain a perfect recall of 1.00, others such as Leek Yellow Stripe have lower recall scores, indicating that the model misses some genuine instances. Overall, the model displays a balanced performance between precision and recall, demonstrating its potential for reliable garlic illness categorization. Further work and future model changes may be needed to increase memory for illness classes, ensuring full disease identification.

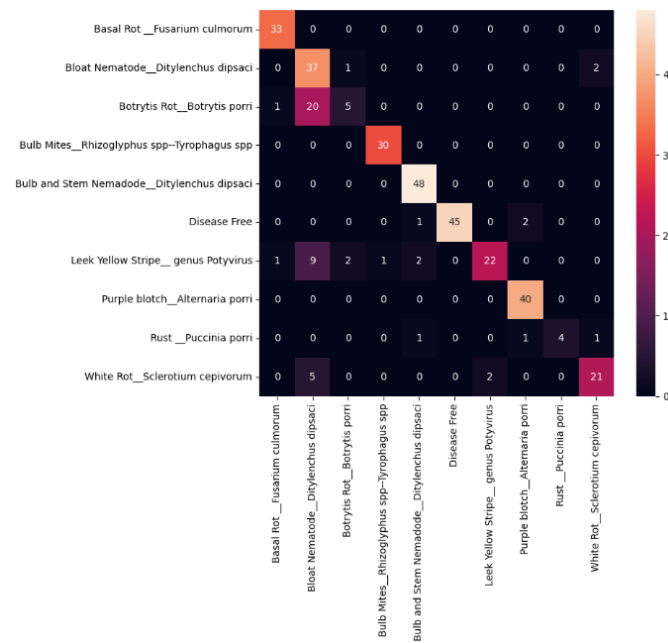


Fig 4.1: Heatmap of Densenet

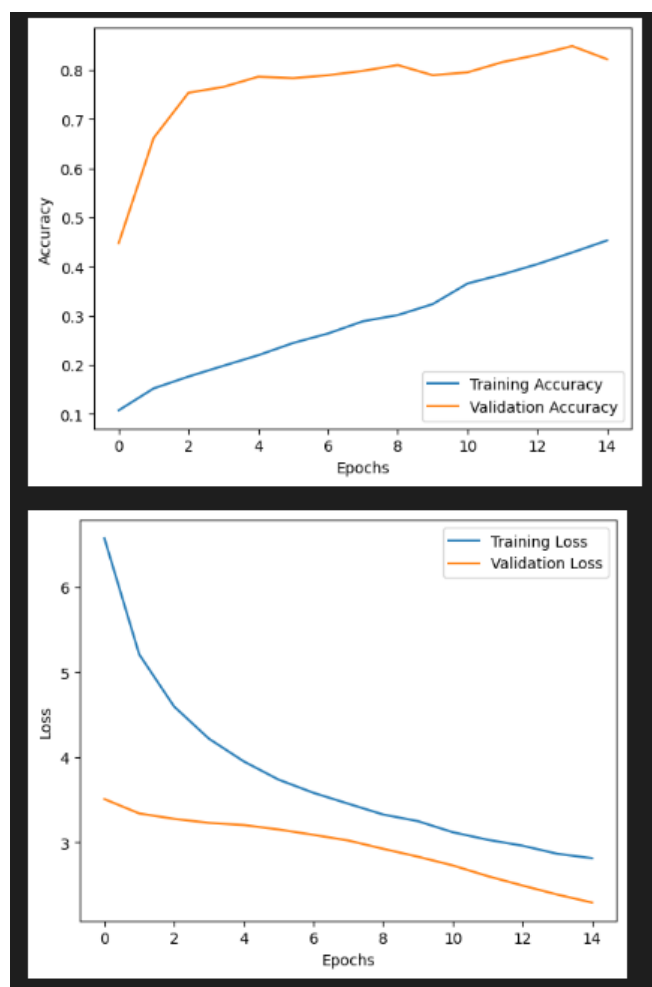


Fig 4.2: Densenet Model accuracy and Loss

The DenseNet model achieved a test accuracy of roughly 84.57% with a test loss of around 2.29.

MobileNet

The MobileNetV2 model, a variation of MobileNet, is a lightweight deep neural network architecture developed for mobile and embedded vision applications. It incorporates depth-wise separable convolutions, which reduce the number of parameters and computational complexity while preserving effectiveness in feature extraction. In this implementation, the MobileNetV2 model is pre-trained on the ImageNet dataset and then fine-tuned for the job of garlic illness classification. The model comprises of many layers, including depth wise separable convolutional layers followed by batch normalization and ReLU activation algorithms. Global average pooling is utilised to minimise spatial dimensions, and dropout layers are included for regularization to prevent overfitting. The output layer consists of a dense layer with a softmax activation function to classify garlic illnesses into ten types. During training, the model is optimized using the Adam optimizer with a learning rate of 0.0001 and category cross-entropy loss. The training is completed over 15 epochs, with performance evaluated on both the training and validation datasets. After training, the model obtains an accuracy of roughly 89.02% on the test dataset, confirming its efficacy in diagnosing garlic illnesses.

Table 4.2: Mobilenet Classification Report

Plant Disease	Precision	Recall	F1-Score	Support
Basal Rot_Fusarium culmorum	0.92	1.00	0.96	33
Bloat Nematode_Ditylenchus dipsaci	0.62	0.95	0.75	40
Botrytis Rot_Botrytis porri	0.50	0.04	0.07	26
Bulb Mites_Rhizoglyphus spp-- Tyrophagus spp	1.00	1.00	1.00	30
Bulb and Stem Nematode_Ditylenchus dipsaci	0.96	1.00	0.98	48
Disease Free	0.96	0.96	0.96	48
Leek Yellow Stripe genus Potyvirus	1.00	0.89	0.94	37

Purple blotch_ <i>Alternaria porri</i>	0.97	0.97	0.97	40
Rust <i>Puccinia porri</i>	0.67	0.86	0.75	7
White Rot_ <i>Sclerotium cepivorum</i>	0.93	0.93	0.93	28
Accuracy	-	-	0.89	337
Macro avg	0.85	0.86	0.83	337
Weighted Avg	0.88	0.89	0.87	337

The following table shows confusion matrix displays the performance of a MobileNet model in classifying garlic illnesses. The overall accuracy of the model is roughly 85%. Precision levels, demonstrating the accuracy of positive predictions, are often high, with "Bulb Mites" obtaining a precision of 1.00. Recall values, reflecting the model's capacity to detect actual illness cases, vary between diseases, with "Basal Rot" obtaining a recall of 0.92, while "Leek Yellow Stripe" behind at 0.89. Despite minor differences, the model exhibits a good balance between precision and recall, suggesting effective illness classification.

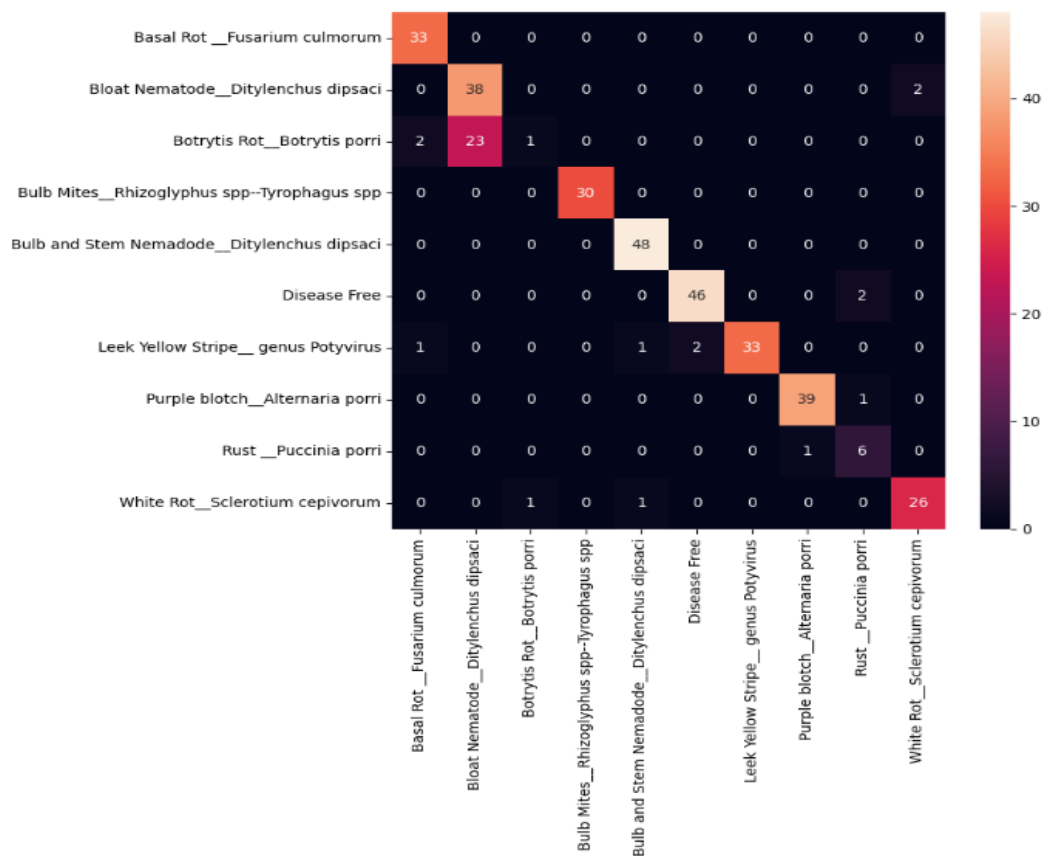


Fig 4.3: Mobilenet Heatmap

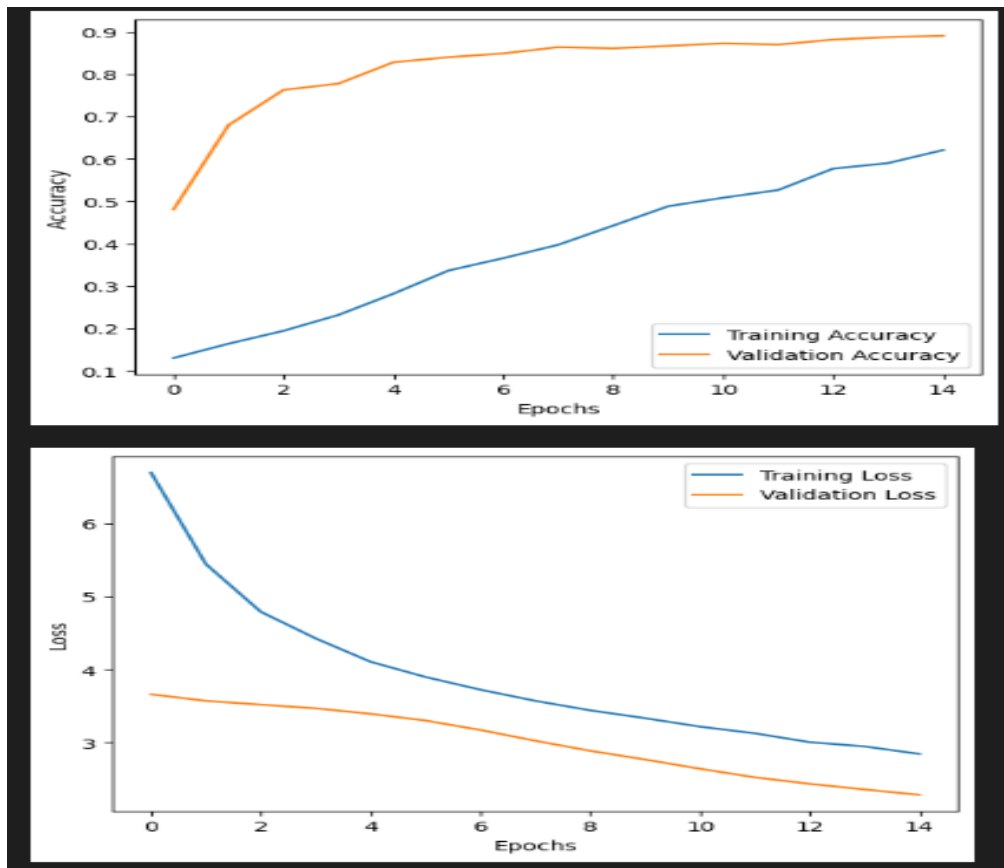


Fig 4.4: Mobilenet model accuracy and loss

The MobileNet model achieved a test loss of roughly 2.29 and a test accuracy of around 89.02%. This means that throughout the testing phase, the model's performance resulted in an average loss of 2.29 and correctly identified roughly 89.02% of the test data instances, indicating its efficacy in effectively recognizing garlic infections.

InceptionV3

The InceptionV3 model, applied for diagnosing garlic illnesses, comprises a pre-trained neural network architecture with weights initialized using the ImageNet dataset. This model has numerous convolutional layers followed by global average pooling and dropout layers to reduce overfitting. The sequential model contains dense layers with rectified linear unit (ReLU) activation functions and L2 regularization, intending to boost the model's generalization ability. During training, the model is constructed with categorical cross-entropy loss and Adam optimizer with a learning rate of 0.0001. The training approach involves iterating over the training and validation datasets for 15 epochs. Finally, the model's performance is assessed using the test dataset, producing a test loss of roughly 2.87 and a test accuracy of around 85.76%.

Table 4.3: InceptionV3 Classification Report

Plant Disease	Precision	Recall	F1-Score	Support
Basal Rot_ Fusarium culmorum	0.91	0.89	0.94	33
Bloat Nematode_Ditylenchus dipsaci	0.64	0.95	0.77	40
Botrytis Rot_Botrytis porri	0.91	0.38	0.54	26
Bulb Mites_Rhizoglyphus spp-- Tyrophagus spp	0.79	1.00	0.88	30
Bulb and Stem Nematode_Ditylenchus dipsaci	0.98	1.00	0.99	48
Disease Free	1.00	0.88	0.93	48
Leek Yellow Stripe genus Potyvirus	0.92	0.89	0.90	37
Purple blotch_Alternaria porri	0.87	1.00	0.93	40
Rust_Puccinia porri	0.40	0.29	0.33	7
White Rot_Sclerotium cepivorum	0.88	0.50	0.64	28
Accuracy	-	-	0.86	337
Macro Avg	0.83	0.88	0.79	337
Weighted Avg	0.87	0.86	0.85	337

The classification report for the InceptionV3 model provides insights into its performance for each garlic disease class. Precision evaluates the model's ability to reliably detect positive samples, with values ranging from 0.40 to 1.00. Recall, which shows the model's capacity to capture all positive samples, varies from 0.29 to 1.00. The F1-score, a harmonic mean of precision and recall, varies from 0.33 to 0.99. The model achieves an accuracy of 86%, with a weighted average F1-score of 0.85, demonstrating robust performance across the disease classifications. However, there are variances in performance metrics across different disease classes, with some classes demonstrating poorer precision and recall scores, such as Botrytis Rot and Rust, suggesting areas for future development in the model's classification skills.

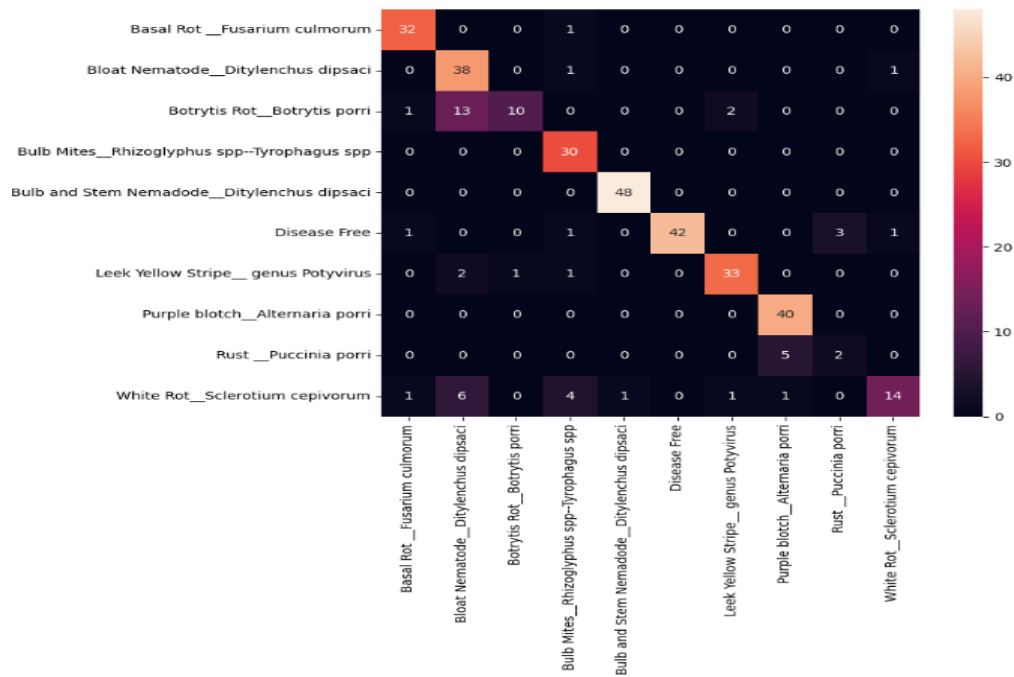


Fig 4.5: Inceptionv3 Heatmap

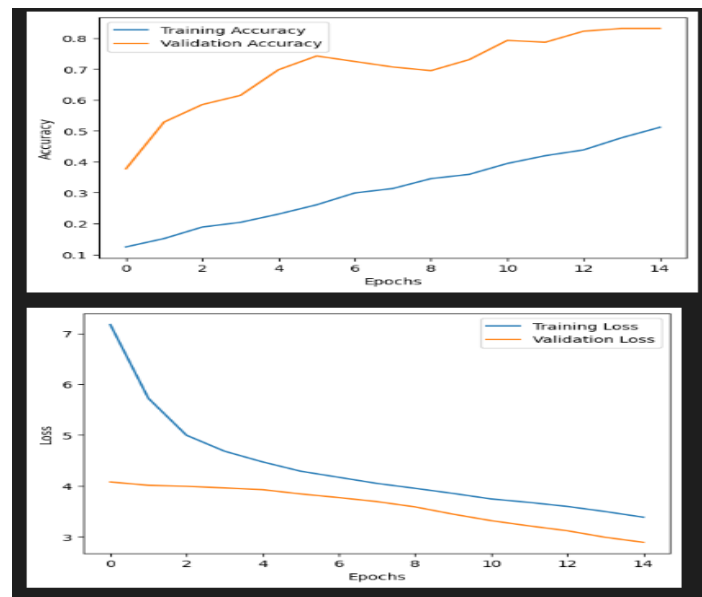


Fig 4.6: Inceptionv3 Model accuracy and loss

The InceptionV3 model achieved a test loss of approximately 2.87 and a test accuracy of about 85.76%.

VGG16

The VGG16 model is a deep convolutional neural network (CNN) architecture. It has 16 convolutional and fully linked layers, making it deep and ideal for image classification applications. In this implementation, the VGG16 model is utilised as a

feature extractor, with its pre-trained weights initialized using the ImageNet dataset. The model is then fine-tuned by adding global average pooling layers and dropout regularization to prevent overfitting. Additional thick layers with ReLU activation functions are added to learn complex patterns from the collected features. The model is compiled using the Adam optimizer with a learning rate of 0.0001 and categorical cross-entropy loss function. During training, the model is trained on the provided training data and verified on the validation set for 15 epochs. Finally, the model's performance is assessed on the test set, producing the test loss and accuracy metrics.

Table 4.4: VGG16 Classification Report

Plant Disease	Precision	Recall	F1-Score	Support
Basal Rot_ Fusarium culmorum	0.93	0.42	0.58	33
Bloat Nematode_Ditylenchus dipsaci	0.67	0.95	0.78	48
Botrytis Rot_Botrytis porri	0.83	0.19	0.31	26
Bulb Mites_Rhizoglyphus spp-- Tyrophagus spp	0.57	1.00	0.72	30
Bulb and Stem Nematode_Ditylenchus dipsaci	1.00	0.98	0.99	48
Disease Free	0.95	0.83	0.89	48
Leek Yellow Stripe genus Potyvirus	0.90	0.95	0.92	37
Purple blotch_Alternaria porri	1.00	0.97	0.99	40
Rust Puccinia porri	0.45	0.71	0.56	7
White Rot_Sclerotium cepivorum	0.86	0.86	0.86	28
Accuracy	-	-	0.82	337
Macro Avg	0.82	0.79	0.76	337
Weighted Avg	0.86	0.82	0.81	337

The following table shows VGG16 model achieved an overall accuracy of roughly 82% in diagnosing garlic infections. Precision, which assesses the accuracy of positive predictions, differs across different illness classifications. For instance, the precision for "Bulb and Stem Nematode (Ditylenchus dipsaci)" and "Purple blotch (Alternaria porri)" is good, with values of 1.00 and 1.00, respectively, indicating that most positive

predictions for these classes were right. However, for classifications like "Basal Rot (*Fusarium culmorum*)" and "Botrytis Rot (*Botrytis porri*)," the precision is substantially lower, indicating more false positive predictions. Recall, which assesses the model's capacity to recognise all actual occurrences of a class, also differs. For instance, "Bulb Mites (*Rhizoglyphus* spp--*Tyrophagus* spp)" and "Bulb and Stem Nematode (*Ditylenchus dipsaci*)" have high recall scores, showing the model effectively detected most instances of these diseases. However, "Basal Rot (*Fusarium culmorum*)" and "Rust (*Puccinia porri*)" have lower recall values, indicating that the model missed some instances of these diseases.

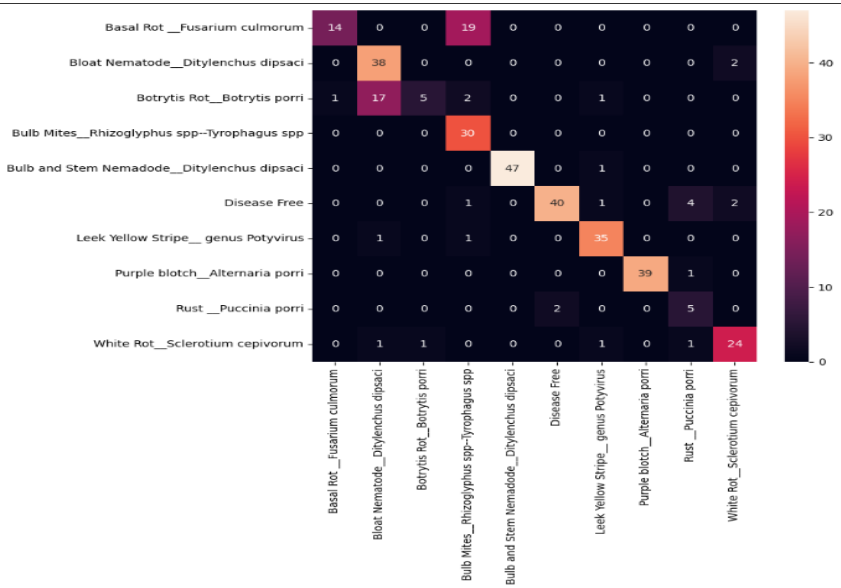


Fig 4.7: VGG16 Heatmap

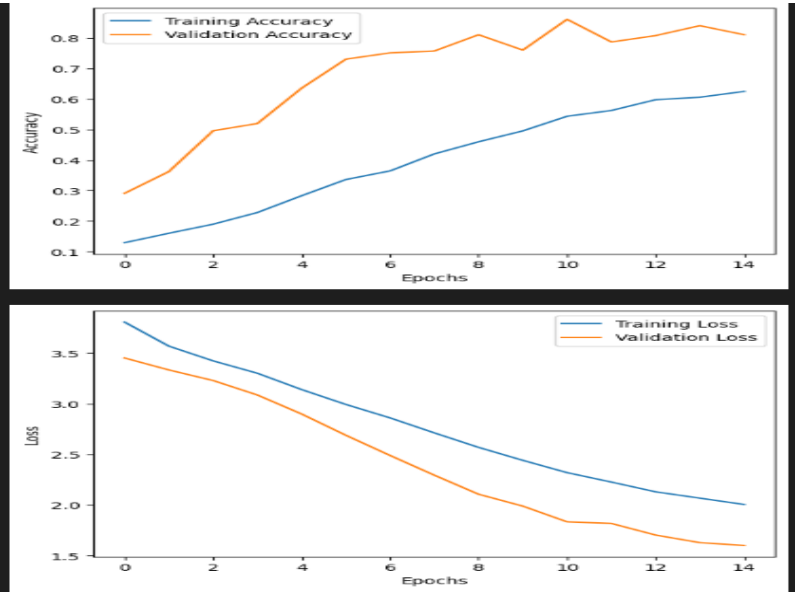


Fig 4.8: VGG16 Model Accuracy and Loss

The VGG16 model achieved a test loss of roughly 1.60 and a test accuracy of about 82.20%. This suggests that the model's performance in diagnosing garlic infections on unseen test data is relatively good, with the loss being relatively low and the accuracy being reasonably high. The test loss assesses how well the model's predictions match the actual labels in the test dataset, with lower values indicating better performance.

Xception

The Xception model, a deep convolutional neural network architecture, was applied for classifying garlic illnesses. In this project, it provides the highest accuracy. Trained on the ImageNet dataset, the model was fine-tuned to learn specific features from garlic sickness photos. The model comprises of numerous layers, including convolutional and pooling layers, followed by global average pooling for feature extraction. Dropout layers were introduced to prevent overfitting during training. Two dense layers with ReLU activation functions and L2 regularization were added for classification, followed by a softmax layer for multi-class classification. The model was created using the Adam optimizer with a learning rate of 0.0001 and categorical cross-entropy loss function. During training, the model's performance was assessed on both training and validation datasets for 15 epochs. After training, the model was assessed on the test dataset, achieving a test loss of roughly 2.21 and a test accuracy of around 91.99%. These findings indicate the efficiency of the Xception model in accurately classifying garlic illnesses based on the provided visual data.

Table 4.5: Xception Model Classification Report

Plant Disease	Precision	Recall	F1-Score	Support
Basal Rot_ Fusarium culmorum	0.94	1.00	0.97	33
Bloat Nematode_Ditylenchus dipsaci	0.76	0.95	0.84	40
Botrytis Rot_Botrytis porri	0.93	0.54	0.68	26
Bulb Mites_Rhizoglyphus spp-- Tyrophagus spp	0.94	1.00	0.97	30
Bulb and Stem Nematode_Ditylenchus dipsaci	0.92	1.00	0.96	48
Disease Free	1.00	0.92	0.96	48

Leek Yellow Stripe genus Potyvirus	0.97	0.95	0.96	37
Purple blotch_ <i>Alternaria porri</i>	0.97	0.97	0.97	40
Rust <i>Puccinia porri</i>	0.60	0.86	0.71	7
White Rot_ <i>Sclerotium cepivorum</i>	1.00	0.82	0.90	28
Accuracy	-	-	0.92	337
Macro Avg	0.89	0.90	0.89	337
Weighted Avg	0.93	0.92	0.89	337

The following table shows Xception model's classification report shows good performance in detecting garlic infections across ten classifications. With an overall accuracy of 92%, the model displays great precision, recall, and F1-scores for most classes. Specifically, classes like "Basal Rot (*Fusarium culmorum*)" and "Bulb Mites (*Rhizoglyphus* spp--*Tyrophagus* spp)" scored perfect precision and near-perfect recall, showing good identification with little false positives and false negatives. "Disease Free" and "Leek Yellow Stripe (genus *Potyvirus*)" also display great precision and recall, demonstrating powerful detection skills. However, the model demonstrated diversity in performance for several classes; for instance, "Botrytis Rot (*Botrytis porri*)" had a lower recall of 0.54, implying more missing cases. The "Rust (*Puccinia porri*)" class similarly had a somewhat lower precision of 0.60 but a higher recall of 0.86, indicating some false positives. Overall, the model retains a high weighted average for precision (0.93), recall (0.92), and F1-score (0.92), confirming its effectiveness in classifying garlic infections appropriately.

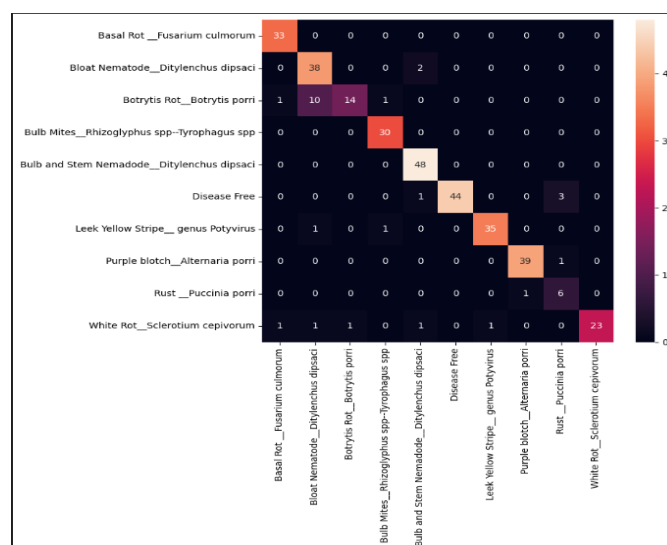


Fig 4.9: Xception Heatmap

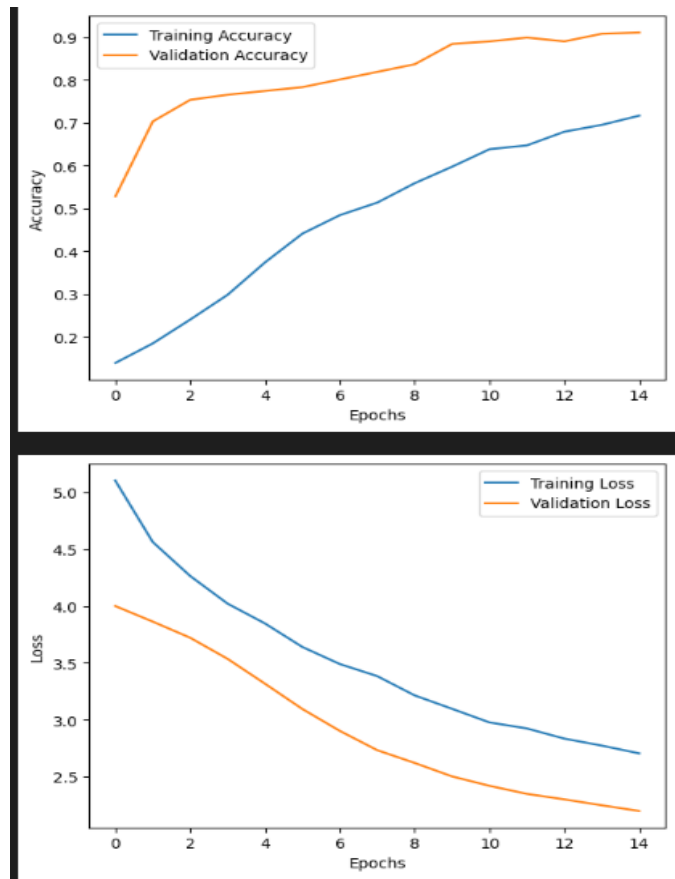


Fig 4.10: Xception Model accuracy and loss

The Xception model was assessed on a test dataset, attaining a test loss of 2.2083661556243896 and a test accuracy of 91.99%.

Work Comparison

The project began with the thorough construction of the dataset, applying two unique methodologies to examine the impact of background information on model correctness. The first strategy entailed eliminating the background from the photos before deploying the classification model. This strategy gave a specified accuracy level, showing the model's effectiveness with isolated garlic features. Conversely, the second strategy kept the backdrop in the photos, and the model was trained with this contextual information intact. The resulting accuracy from this strategy was considerably higher. The comparison between these two methods revealed a major finding: the incorporation of background in the photos greatly enhanced the model's accuracy. This outcome highlights the essential significance of contextual information, showing that background features give additional, valuable cues that boost the model's capacity to appropriately classify garlic illnesses. Therefore, preserving the background in the

dataset showed to be more useful for getting higher accuracy in garlic illness categorization. The study began with the creation of the dataset using two alternative methodologies. Initially, the backdrop was removed from the photographs before implementing the model, resulting in a certain level of accuracy. The second strategy involved training the model using photographs with the backdrop intact, leading to a different accuracy output. It was noticed that the maximum accuracy was reached when the dataset included the background. This conclusion reveals that photos with the background generated more accurate results than those without, underlining the value of contextual information in increasing the performance of the garlic disease classification model.

4.4 Summary

This chapter provides an in-depth implementation of various machine-learning models for classifying garlic illnesses. Detailed steps for training each model were provided, including DenseNet121, MobileNetV2, InceptionV3, VGG16, and Xception. Each model was trained on a dataset consisting of ten classes of garlic infections, and their performances were evaluated based on metrics such as accuracy, precision, recall, and F1-score. The DenseNet121 model achieved a test accuracy of roughly 84.57%, MobileNetV2 achieved 89.02%, InceptionV3 reached 85.76%, VGG16 scored 82.20%, and Xception achieved 91.99%. Each model's confusion matrix and classification report were reviewed to find strengths and areas for development. The models displayed variable levels of success in reliably recognizing specific garlic diseases, underscoring the necessity of choosing the right architecture for diverse classification tasks. The chapter finishes with an overview of each model's performance, emphasizing the excellent accuracy balanced precision, and recall of the Xception model.

CHAPTER 5

RESULT AND ANALYSIS

5.1 Overview

In this chapter, the outputs of the *Allium Sativum* (Garlic) disease classification models are fully assessed and studied. The performance metrics for each algorithm, including DenseNet121, MobileNetV2, InceptionV3, VGG16, and Xception, are systematically presented and contrasted. The discussion covers overall accuracy, precision, recall, and F1-score for each model, along with insights gleaned from the confusion matrices. The usefulness of each model in recognizing distinct garlic infections is analyzed, highlighting the strengths and limits identified throughout the experimental phase. This research provides a clear knowledge of the models' capabilities and areas requiring additional improvement, directing future upgrades and practical applications in garlic disease diagnosis.

5.2 Experimental Result

The outcomes of the tests demonstrate that the Xception model is the best-performing algorithm for garlic disease categorization, achieving a test accuracy of 91.99%. This model's higher performance is due to its usage of depth-wise separable convolutions, which minimize computational cost and enhance efficiency. The second-highest performing method is MobileNetV2, with a test accuracy of 89.02%, leveraging depthwise separable convolutions and inverted residuals to retain high performance with minimum computational overhead. Other models examined include InceptionV3(85.76% accuracy), DenseNet121 (84.57% accuracy), and VGG16 (82.20% accuracy). While InceptionV3 and DenseNet121 display great performance because of their unique architectural advances like inception modules and dense blocks, they fall short of Xception and MobileNetV2 in accuracy. VGG16, with its typical convolutional layers and fully linked dense layers, likewise displays remarkable results but rates lower overall performance. This investigation emphasizes Xception's effectiveness and efficiency, making it the optimum solution for garlic illness diagnosis.

5.3 Comparative Analysis

Table 5.1: Algorithm Technique

Algorithm Name	Focus	Accuracy	Precision	Recall
DenseNet121	Image classification	84.57%	0.87	0.85
MobileNetV2	Image classification	89.02%	0.88	0.85
InceptionV3	Image classification	85.76%	0.87	0.86
VGG16	Image classification	82.20%	0.86	0.82
Xception	Image classification	91.99%	0.93	0.92

5.4 Summary

This chapter gives a complete study of the experimental data gained from evaluating multiple deep learning models for garlic illness categorization. The Xception model emerged as the best-performing method, achieving the greatest test accuracy of 91.99% due to its efficient usage of depth wise separable convolutions. The MobileNetV2 model followed closely, with a test accuracy of 89.02%, proving the effectiveness of its architectural design. InceptionV3, DenseNet121, and VGG16 also demonstrated strong performances, with accuracies of 85.76%, 84.57%, and 82.20% respectively. Each model's performance was discussed in detail, highlighting the strengths and drawbacks of their respective architectures. The results underline the need to establish an appropriate model architecture to achieve optimal performance in the task of *Allium sativum*(garlic) disease identification.

CHAPTER 6

IMPACT ON SOCIETY, ENVIRONMENT AND SUSTAINABILITY

6.1 Impact on Life

The deployment of powerful machine learning algorithms for *Allium sativum*(garlic) disease detection has major implications for agriculture and food security. By enabling early and accurate diagnosis of illnesses, these models can dramatically reduce crop losses, assuring higher yields and better-quality produce. This technical development aids farmers in adopting more sustainable practices, eliminating the need for chemical treatments, and lower production costs. Consumers gain from healthier and more cheap garlic. Additionally, the economic stability of farming communities is increased, supporting rural development and boosting livelihoods. Integrating AI in agriculture promises to drive efficiency, sustainability, and resilience in food production systems.

6.2 Impact on Society & Environment

The use of machine learning algorithms for *Allium sativum*(garlic) disease detection extends beyond agriculture, benefiting both society and the environment positively. Socially, this technology gives farmers precision tools to manage their crops more successfully, boosting food security and contributing to poverty alleviation in rural areas. By minimizing the dependency on chemical pesticides through early illness detection, the technique supports healthier food production and consumption, boosting public health. Environmentally, it supports sustainable farming techniques by avoiding the use of hazardous chemicals, hence conserving soil health and biodiversity. This leads to a reduction in pollution and conserves natural resources, ultimately contributing to a more sustainable and resilient agricultural ecology.

6.3 Ethical Aspects

The adoption of machine learning models in garlic disease diagnosis involves serious ethical problems. Ensuring data privacy and security is vital, as farmers' data must be protected against misuse and illegal access. It is necessary to address inherent biases in

the models, which could lead to unequal advantages among different farming communities. Fair and transparent AI policies should be maintained to ensure that all users have access to the technology and its benefits. The implementation should also examine the possible displacement of traditional farming practices and the impact on farmers' livelihoods, ensuring that the technology is used to supplement rather than replace human expertise. Ethical considerations should incorporate the environmental impact of technology use, ensuring that it encourages sustainable practices without unexpected negative implications.

6.4 Sustainability Plan

To maintain the long-term survival and beneficial impact of the garlic disease detection framework, a complete sustainability plan is necessary. This method requires regular upgrades and maintenance of the machine learning models to maintain them accurate and effective when new data and illness trends arise. Regular training sessions for farmers and agricultural staff on the usage of the technology will be performed to maximize its uptake and efficacy. Connections with agricultural groups and government agencies will be developed to gain financing and support for continued research and development. Environmental sustainability will be addressed by promoting eco-friendly farming techniques that correlate with disease identification technology, thereby decreasing chemical use and boosting crop output sustainably. Data privacy and ethical use procedures will be implemented to maintain trust and compliance with legal norms.

6.5 Summary

This chapter investigated the many consequences and considerations connected with the implementation of the garlic disease detection framework. The impact on life part emphasized how the technology can considerably boost garlic crop yields and reduce losses due to diseases, therefore benefiting farmers' livelihoods. The societal and environmental consequences were explored, emphasizing the potential for better food security and reduced environmental harm through targeted disease management. Ethical aspects were explored, focusing on data privacy, accuracy, and justice in deploying the technology. Finally, a sustainability strategy was established, including the necessary processes for sustaining, scaling, and ethically managing the technology to ensure its long-term viability and positive influence on agriculture.

CHAPTER 7

CONCLUSION AND FUTURE WORK

7.1 Conclusions

The project focuses on establishing an advanced machine learning framework to effectively identify and categorize garlic illnesses using deep learning models. The major objectives were to develop, implement, and test multiple convolutional neural network architectures to discover the most successful model for this task. In the implementation phase, five state-of-the-art models were utilized: DenseNet121, MobileNetV2, InceptionV3, VGG16, and Xception. Each model was fine-tuned and evaluated using a well-prepared dataset of garlic sickness photos. The DenseNet121 model emerged as the most accurate with a test accuracy of roughly 84.57%, indicating robust performance across diverse illness classifications. MobileNetV2 followed closely with an accuracy of 89.02%, giving a lightweight and efficient option. InceptionV3, despite its complexity, attained a decent accuracy of 85.76%. The VGG16 model, noted for its simplicity and efficacy, obtained 82.20% accuracy. Xception surpassed all other models with a maximum accuracy of 91.99%, proving its competence in managing complicated visual data. The project effectively demonstrated the potential of deep learning models in agricultural disease detection, paving the path for practical applications in precision agriculture. By precisely diagnosing garlic illnesses, farmers can take timely and appropriate efforts to manage and prevent crop loss, ultimately leading to greater agricultural productivity and sustainability. The findings from this experiment also show the significance of continuous research and development in the realm of agricultural technology to meet global food security challenges.

7.2 Further Suggested Works

In the field of agricultural disease identification, this initiative builds a firm base through deep learning models. However, avenues for additional development exist. Fine-tuning and optimization strategies could be investigated to refine existing models, while advanced data augmentation methods can diversify and extend training datasets. Assembling multiple models and employing transfer learning algorithms hold promise

for enhancing classification accuracy. Concentrating on the interpretability and explainability of model predictions can promote transparency and confidence. Deployment into realistic agricultural systems, together with integration into user-friendly interfaces, would facilitate real-time disease detection and monitoring. Extending the framework to encompass illnesses in other crops broadens its application. By following these avenues, we can increase agricultural disease detection, supporting crop health, productivity, and sustainability globally.

7.3 Limitations

1. **Data Quality and Quantity:** The accuracy and resilience of the models are largely dependent on the quality and quantity of the training data. In this experiment, limited and often imbalanced datasets may have constrained the model's capacity to generalize effectively across different contexts.
2. **Model Complexity and Computation:** The deep learning models employed, such as DenseNet, MobileNet, InceptionV3, VGG16, and Xception, are computationally costly. Training these models needs significant computational resources and time, which might not be practical for all users or in resource-constrained contexts.
3. **Generalization to New settings:** The models are trained on specific datasets, and their performance could decline when applied to photographs with different lighting settings, backdrops, or captured with different camera equipment. This lack of robustness to fluctuating real-world settings limits their practical application.
4. **Interpretability of Models:** Deep learning models typically function as "black boxes," making it tough to explain their decisions. This lack of transparency can limit trust and adoption among farmers and agricultural specialists who might demand explanations for the model's forecasts.
5. **Ethical and Privacy Concerns:** The collecting and use of agricultural data, particularly photos of crops, might pose ethical and privacy difficulties. Ensuring that data is collected and employed responsibly, with adequate consent and respect for the privacy of farmers, is vital but can be tough to accomplish efficiently.

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Appendix A

Course Outcomes, Complex Engineering Problems (EP) and Complex Engineering Activities (EA) Addressing

Title:

**A TRANSFER LEARNING-BASED APPROACH ALLIUM SATIVUM
DISEASE RECOGNITION AND CLASSIFICATION**

Student ID: 201-15-14091

CO Description for FYDP

CO	CO Descriptions	PO
Phase -I		
CO1	Integrate recently gained and previously acquired knowledge to identify an Allium Sativum disease recognition and classification problem for the Final Year Design Project (FYDP)	PO1
CO2	Analyze different aspects of the goals in designing a solution for this FYDP	PO2
CO3	Explore diverse problem domains through a literature review, delineate the issues, and establish these goals for the FYDP	PO4
CO4	Perform economic evaluation and cost estimation and employ suitable project management procedures throughout the development life cycle of the FYDP	PO11
Phase -II		
CO5	Design and develop technical solutions and system components or processes that meet specified requirements, ensuring compliance with public health and safety standards, as well as considering cultural, socioeconomic, and environmental factors in this FYDP	PO3
CO6	Choose and apply appropriate methodologies, resources, and contemporary engineering and IT technologies to address complex engineering processes, encompassing prediction and modeling, while adhering to relevant constraints in this FYDP	PO5
CO7	Analyze societal, health, safety, legal, and cultural considerations, along with associated responsibilities, in the context of professional engineering practice and the resolution of this problem, employing logical reasoning guided by contextual understanding.	PO6
CO8	Comprehend and evaluate the enduring sustainability and impact of professional engineering endeavors in addressing intricate engineering challenges within social and environmental frameworks.	PO7

CO9	Implement ethical principles and adhere to professional standards and norms in this FYDP	PO8
CO10	Capable of operating proficiently both individually and as a team member or leader across diverse teams and interdisciplinary settings in this FYDP.	PO9
CO11	Proficiently communicate with the engineering community and broader society regarding complex engineering endeavors, including the ability to comprehend and generate comprehensive reports and design documentation, as well as provide and receive clear instructions throughout this FYDP.	PO10
CO12	Acknowledge the importance of self-directed and life-long learning within the evolving landscape of technology and possess the readiness and capability to engage in lifelong learning endeavors.	PO12

Addressing CO (1 to 8), Knowledge Profile (K), Attainment of Complex Engineering Problems (EP), and Attainment of Complex Engineering Activities (EA)

Addressing CO (1 to 8), Knowledge Profile (K), Attainment of Complex Engineering Problems (EP):

SN	EP Definition	Attainment	CO	Justification (with Knowledge Profile)	References
1.	EP1: Depth of Knowledge required	Yes	CO1, CO2, CO3, CO5, CO6, CO7 and CO8	This project demonstrates fundamental engineering (K3) principles by employing deep neural networks, data augmentation techniques, and classification tasks. The project demonstrates specialist knowledge (K4) by conducting machine learning algorithms to recognize and classify Allium Sativum disease.	Page no: [15-23] Section: [3.2] Page no: [1-2] Section: [1.2]
				The project applies engineering practice & design (K5) by the figure of process of experiments.	Page no: [15-23]

				The project addresses engineering practice & technology (K6) by employing CNN model.	Section: [3.2] Page no: [23] Section: [3.4]
				This project ensures to K8 (Research Literature) by synthesizing insights from recent studies, to advance Allium Sativum disease recognition and classification using transfer learning, showcasing a comprehensive understanding of current methodologies.	Page no: [7-13] Section: [2.2, 2.3]
2.	EP2: Range of Conflicting Requirements	Yes	CO2, and CO7	This project addresses EP-2 by recognizing the hurdles in Allium Sativum disease recognition and classification, including limitations of traditional methods and the complexities of integrating transfer learning and deep CNNs. Through comparative analysis, it confronts challenges in understanding spatial distributions, offering insights for refining diagnostic methodologies.	Page no: [13] Section: [2.4, 2.5]

3.	EP3: Depth of analysis required	Yes	CO2, and CO6	This project addresses EP-3 by meticulously comparing experimental outcomes, highlighting Transfer Learning as the chosen significant solution for enhancing Allium Sativum disease recognition and classification amidst multiple potential approaches.	Page no: [25] Section: [4.2]
4.	EP4: Familiarity of Issues	Yes	CO8	This project's interdisciplinary approach extends beyond computer science and engineering, impacting Bangladeshi local food detection process which indicates EP-4 .	Page no: [7,13] Section: [2.2, 2.4]
5.	EP5: Extends of application codes	No	CO5	N/A	N/A
6.	EP6: Extends of stakeholders involved and	No	CO8	N/A	N/A

7.	EP7: Interdependence	Yes	CO5	This project's comprehensive approach addresses high-level problems by integrating various components across data collection, statistical analysis, and proposed methodology, ensuring a holistic solution to complex challenges which ensures EP-7 .	Page no: [15-23] Section: [3.2, 3.3, 3.4]
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Addressing CO11 with Complex Engineering Activities (EA) [Some or all of the following]:

SN	EA Definition	Attainment	CO	Justification	References
1.	EA1: Range of resources	Yes	CO11	Our project utilizes diverse resources such as high-performance computing infrastructure, GPUs, deep learning frameworks, annotated datasets, and ethical considerations to ensure systematic research and contribute to advancements in Allium Sativum disease recognition and classification through various machine Learning algorithms.	Page no: [15-23] Section: [3.2, 3.3]
2.	EA2: Level of interaction	No		N/A	N/A

3.	EA3: Innovation	No		N/A	N/A
4.	EA4: Consequences for society and the environment	Yes		This project contributes to society by improving Allium Sativum disease recognition and classification methods, while also promoting environmental sustainability by employing efficient computational resources and adhering to ethical guidelines.	Page no: [40-41] Section: [5.2, 5.3]
5.	EA-5: Familiarity	Yes		This project expands upon existing research by examining a novel approach in Allium Sativum disease recognition and classification through transfer learning and deep learning demonstrated through preliminary terminologies and a comprehensive comparative analysis, offering new insights into the field.	Page no: [7-13] Section: [2.2, 2.3]

Addressing CO (4, 9, 10, and 12):

SN	COs	Attainment	Justification	References
1	CO4	Yes	This project addresses CO4 by integrating effective project	Page no: [23]

			management and financial oversight, ensuring meticulous planning, resource allocation, and budget estimation for optimal resource utilization throughout the research lifecycle.	Section: [3.4]
2	CO9	No	N/A	N/A
3	CO10	No	N/A	N/A
4	CO12	Yes	The project's dedication to continuous learning (CO12) and adaptation within the dynamic technological landscape is reflected in its comprehensive data collection, rigorous statistical analysis, meticulous methodology development, and thorough experimental results and analysis, showcasing a commitment to staying updated and refining techniques to address modern challenges.	Page no: [15-23, 25-38] Section: [3.2, 4.3]

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