

Potato Disease Classification

A major project report submitted in partial fulfilment of the requirement for the award of
degree of

Bachelor of Technology
in
Computer Science & Engineering

Submitted by

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Candidate's Declaration

I hereby declare that the work presented in this report entitled '**Potato Disease Classification**' in partial fulfilment of the requirements for the award of the degree of **Bachelor of Technology in Computer Science & Engineering** submitted in the Department of Computer Science & Engineering, Jaypee University of Information Technology, Waknaghat is an authentic record of my own work carried out over a period from August 2023 to December 2023 under the supervision of **Dr. Kapil Rana** (Assistant Professor, Department of Computer Science & Engineering).

The matter embodied in the report has not been submitted for the award of any other degree or diploma.

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Supervisor Name: Dr. Kapil Rana

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CERTIFICATE

This is to certify that the work which is being presented in the project report titled Potato Disease Classification Using Machine Learning in partial fulfilment of the requirements for the award of the degree of Bachelor in Technology in Computer Science And Engineering and submitted to the Department of Computer Science And Engineering, Jaypee University of Information Technology, Waknaghat is an authentic record of work carried out by Kartik Sharma & Madhav Katoch with Roll Number 201373 & 201398 respectively during the period from August to December 2023 under the supervision of Dr. Kapil Rana, Department of Computer Science and Engineering, Jaypee University of Information Technology, Waknaghat.

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LIST OF ABBREVIATIONS, SYMBOLS OR NOMENCLATURE

1. UI..... User Interface
2. VOC..... Visual Object Classes
3. AI..... Artificial Intelligence
4. CNN..... Convolutional Neural Network
5. NFR..... Non-Functional Requirements
6. RGB..... Red Green Black
7. SVM..... Support Vector Machine
8. KNN..... K-Nearest Neighbour
9. ANN..... Artificial Neural Network
10. DPI..... Dots Per Inch
11. UML..... Unified Modelling Language
12. HD..... High Dimensional

ABSTRACT

Potatoes are a globally significant crop, but they are prone to various diseases that can impact their yield and quality. In order to apply efficient management techniques to reduce crop losses, early detection and identification of these diseases are essential. The application of artificial intelligence (AI) techniques offers a viable path towards accurate and effective potato disease diagnostics. The purpose of this study is to provide an overview of current studies on the use of AI to categorize potato illnesses. The most important step in using AI to classify diseases is collecting high-quality data. In order to remove any unwanted aspects, photos of the afflicted plants and leaves must be taken and preprocessed. To determine the distinctive qualities of sick plants, such as color, shape, texture, and size, feature extraction is then done. Based on these unique characteristics, different artificial intelligence systems can be used to classify potato illnesses.

Convolutional Neural Networks are one of the most popular AI algorithms for classifying potato diseases (CNNs). CNNs are a kind of deep learning algorithm that are excellent at identifying intricate details in images, which makes them suitable for applications such as illness identification. CNNs have demonstrated high accuracy rates in the classification of potato diseases, with some studies reaching accuracy levels nearly 100%.

Additional AI algorithms used in the categorization of potato diseases include k-nearest neighbour's (KNN), decision trees, and support vector machines (SVMs). Based on the features that were extracted, these algorithms classify diseases using various methods. For instance, SVMs use a hyperplane to separate the data into distinct classes, whereas decision trees use a hierarchical structure of nodes to divide the data into smaller subsets.

A number of metrics, such as accuracy, precision, recall, and F1-score, are used to evaluate the effectiveness of AI models. In order to optimize the algorithm's hyperparameters and test the models' resilience against overfitting, cross-validation is also used. In addition, mean squared error (MSE) and area under the receiver operating characteristic curve (AUC-ROC) are often used measurements. An essential method for ensuring stable model performance is cross-validation, which improves reliability in real-world applications by evaluating generalizability over a variety of datasets.

CHAPTER 1 : INTRODUCTION

Plant disease identification is a crucial first step towards preventing losses in agricultural yield and productivity. This is especially true for sustainable agriculture. It requires a great deal of work, a thorough knowledge of plant diseases, and long processing times. Machine learning and image processing techniques are used to diagnose plant diseases in order to address this.

Numerous programs have been put in place to stop crop failure brought on by illnesses. Throughout the past ten years, organized pest management techniques have typically depended on extensive pesticide use. Regardless of strategy, early disease detection is essential to well-informed disease management.

1.1 INTRODUCTION

The identification of diseases has received support from organizations and groups dedicated to agricultural development, such as regional plant agencies. More recently, the growing world wide Web has been used to support these efforts by disseminating data for online disease assessments. In recent years, mobile phone tools have become more and more common, capitalizing on the fact that all industries have adopted this technology.

Smartphones, with their powerful processors, sharp displays, and a wide range of accessories like cutting-edge HD cameras, provide novel ways to detect and treat illnesses. It is estimated that by 2020, there will be five to six billion cell phones in use globally. The combination of high-performance processors, high-definition cameras, and ubiquitous smartphone connectivity enables large-scale automated image identification for disease evaluation.

Here, we use the Plant Village project's 54,306 images, which represent 26 diseases in 14 crop species, to illustrate the particular potential using a deep learning technique. Each crop-disease pair is represented by the figure (Fig 1.1).

Significant progress has been made in computer vision over the last two years, especially in the area of object recognition. Widely used benchmarks include the Big Scope Visual Recognition Challenge, which uses the ImageNet dataset, and the PASCAL VOC Challenge. An enhanced convolutional neural network managed to classify images into 1000 classes in 2012 with an astounding 5-error rate of 16.4%.



Fig 1.1 Leaf species with sickness

Over the next three years, advancements in highly convolutional neural networks caused the error rate to drop to 3.57%. Even though building large neural networks might be difficult, pre-made models can process images quickly. Recently, deep neural networks have been successfully applied as end-to-end learning examples in a variety of settings.

These networks create a link between an input, like a picture of a sick plant, and an output, like a pair of diseases that affect a crop. In a neural network, mathematical components called nodes have the ability to process numerical input from incoming edges and generate an output in the form of an active edge. Deep neural networks are essentially a sequence of stacked layers of nodes that map information from the input layer to the output layer.

In order to optimize the alignment during the classification process, extensive neural networks are finetuned by adjusting the hierarchical parameters, resulting in an exhaustive connection that accurately maps the input to the output. Recent technological and creative advancements have resulted in notable improvements to this computationally demanding process.

To accurately train image classifiers for plant disease identification, a sizable, verified collection of photos of both healthy and diseased plants is required. Such a dataset was absent until recently, and smaller datasets were hard to come by. In order to fill this void, the Plant Village project has amassed a substantial library of photos depicting both healthy and unhealthy crop plants, making them publicly available. This article describes how a convolutional neural network approach and 54,306 images were used to classify 26 diseases in 14 crops. The models are assessed according to how well they can forecast the right combinations of illnesses from 38 possible categories.

With a mean F1 score of 0.9934, the best-performing model demonstrates the approach's considerable potential. Our research serves as a first step towards a disease detection method aided by smartphones.

1.2 PROBLEM STATEMENT

In India's vast agricultural landscape, where more than 70% of the population depends on farming for their livelihood, early identification of plant diseases is crucial to preserving crop harvests. Traditional disease diagnosis techniques, which frequently rely on visual inspection by qualified experts, are labor and time intensive as well as requiring a high level of plant pathology knowledge. The revolutionary potential of image processing and machine learning approaches in revolutionizing the field of plant disease identification is made possible by this inherent constraint.

In order to identify plant diseases, our work explores the fields of image processing and machine learning. We are able to extract important features from leaf photos and detect the minute details that indicate the presence of disease by utilizing the capabilities of image processing tools. Subsequently, these retrieved features are fed into advanced machine learning algorithms, which allow them to create a strong correlation with particular plant illnesses. With careful consideration of variables like leaf color, damage severity, position, and surface texture, the model produces precise disease identifications.

Because of its improved computing efficiency and decreased dependence on assumptions, our suggested method differs from other machine learning-based techniques. Our strategy achieves outstanding accuracy in disease identification without the associated computational loads by utilizing measurable artificial intelligence and image processing techniques, in contrast to existing approaches that frequently use deep learning architectures. This methodological change has many strong advantages over conventional approaches. First of all, it drastically lowers labor expenses, which can add up in large-scale farming operations. Second, it improves scalability, making it possible to monitor

large areas effectively and guarantee early disease outbreak identification. Lastly, disease diagnosis can be done more simply and affordably by directly observing leaf symptoms rather than requiring specialized tools or in-depth training.

1.3 OBJECTIVES

The main goal of the suggested framework is to identify plant leaf infections by using feature extraction methods that take texture, diversity, and shape into account. To categorize plant leaves into categories of health or illness, an artificial intelligence technique called a Convolutional Neural Network (CNN) is utilized. CNN will identify the exact name of the disease in the event of a sick plant leaf. Then, recommendations for treating particular ailments are made with the intention of promoting the development of robust plants and increasing output.

To start, a high-resolution camera is used to take pictures of different types of leaves in order to improve efficiency and outcomes. These photos are then subjected to image processing techniques in order to extract pertinent features needed for additional analysis. The following is an outline of the system's basic steps:

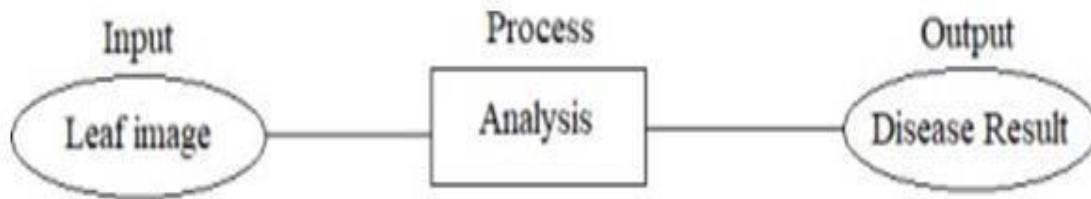


Fig 1.2 Algorithm Processing

Here are several benefits of the proposed algorithm:

- The use of assessors for scheduled group point presentations eliminates the need for user involvement during partition time.
- The suggested algorithm enhances the accuracy of detection.

- The proposed solution is entirely automated, distinguishing it from existing methods that rely on user input for determining the appropriate data image partition. Moreover, it exhibits a high retrieval rate for well-known diseases.

1.4 SIGNIFICANCE AND MOTIVATION OF THE PROJECT WORK

- **Impact on Agriculture:** The application of Convolutional Neural Networks (CNN) to the categorization of potato diseases is a project of great agricultural significance. By averting extensive crop damage and increasing overall agricultural output, farmers can prevent potato illnesses by swiftly identifying and managing them with the aid of accurate disease categorization.
- **Crop Yield Improvement:** The initiative helps with the early detection of diseases impacting potato crops by using CNN for disease categorization. Efficient disease control strategies can be developed through timely intervention based on precise categorization results, which will ultimately increase crop yields and guarantee food security.
- **Resource Efficiency:** In order to maximize agricultural resources, effective disease management is essential. The approach targets particular diseases found using CNN categorization, hence reducing the needless usage of pesticides.
- **Economic Impact on Farmers:** Farmers' financial security can be greatly impacted by the early identification and treatment of potato illnesses. The project helps protect farmers' livelihoods, guaranteeing a steady income and promoting the socioeconomic growth of rural communities by preventing crop losses.
- **Technologies Transfer to Farmers:** Using CNN-based disease classification in agriculture makes it easier for farmers to acquire cutting-edge technologies. This closes the technological divide and creates a more technologically aware farming community by giving them the tools they need to make wise decisions.
- **Research and Development:** The project adds to the body of knowledge in the fields of machine learning and agricultural technology. The applicability of the categorization model for potato diseases to other crops could expand the frontiers of agricultural innovation and sustainable farming methods.

- **Global Food Security:** The project contributes to the worldwide endeavor to improve food security by tackling potato diseases. Strong farming methods, made possible by cutting-edge technology like CNN, help to meet the world's constantly expanding population's rising food need.

The project's value and motivation, which use Convolutional Neural Networks (CNN) to classify potato diseases, are crucial for addressing urgent issues in the agriculture industry. Worldwide, potatoes are a major crop, and illnesses that affect them can cause significant financial losses and jeopardize the security of the world's food supply. Implementing measures that can effectively prevent crop loss requires the quick and correct diagnosis of infections.

This study is very important because it uses CNNs—a cutting-edge type of machine learning—to automate the process of diagnosing and categorizing potato illnesses. Conventional methods are not practicable for large-scale agricultural operations since they are often labor-intensive and dependent on human knowledge. The goal of developing a CNN-based model is to give farmers a scalable and effective way to quickly identify crop illnesses and respond quickly to save their harvests.

Furthermore, the project's motivation goes beyond its possible societal benefit. Enhancing agricultural productivity and quality by efficient disease classification can make a substantial contribution to the world's food security. The use of cutting-edge technology in agriculture is consistent with the larger precision farming movement, which uses data-driven methods to provide more resource- and sustainability-efficient farming practices. The objective of this project is to improve agricultural innovation and the welfare of farming communities by tackling difficulties in the classification of potato diseases.

1.5 ORGANIZATION OF PROJECT REPORT

Introduction to Project Structure:

The project report aims to provide a thorough exploration of the implementation and outcomes of potato disease classification using Convolutional Neural Networks (CNN). The organizational structure ensures a logical flow, offering a comprehensive understanding of the project's objectives and findings.

Section Breakdown:

a. Introduction:

Introduces the background, objectives, and scope of the project in potato disease classification using CNN.

b. Literature Review:

Examines existing research in plant disease classification and CNN applications, establishing the theoretical foundation for the proposed approach.

c. Methodology:

Details the steps involved in implementing the CNN architecture, dataset preparation, and the training process for potato disease classification.

d. Model Architecture:

Provides an in-depth examination of the CNN architecture utilized, accompanied by visualizations of the network's components.

e. Discussion:

Interprets results, compares findings with existing literature, and addresses limitations and Potential directions for future research in potato disease classification.

f. Conclusion:

Summarizes key findings, contributions, and concluding thoughts on the outcomes of potato disease classification using CNN.

g. Results:

Presents quantitative and qualitative results, including accuracy metrics and visual comparisons of disease classification outcomes.

h. Recommendations:

Offers suggestions for future research or improvements based on insights gained during the project.

CHAPTER 2 : LITERATURE SURVEY

Literature papers represent a variety of approaches to plant disease detection and classification using machine learning techniques. They employ different tools and methods, ranging from traditional classifiers like SVM and K-means to deep learning models such as CNNs and attention-based architectures. Each study evaluates its method's performance using accuracy metrics, often comparing against existing models or techniques. However, limitations such as dataset availability, computational cost, and environmental factors can impact the effectiveness of these approaches. Overall, these papers contribute to the ongoing research in agricultural technology by exploring innovative solutions for diagnosing plant diseases.

2.1 OVERVIEW OF RELEVANT LITERATURE

TABLE 1: LITERATURE REVIEW

S. No.	Paper Title [Cite]	Journal/Conference (Year)	Tools/Techniques/Dataset	Results	Limitations
1.	Plant Disease Detection and Classification Method Based on the Optimized Lightweight YOLOv5 Model [1]	College of Mechanical and Electrical Engineering, Qingdao Agricultural University, Qingdao 266109, China (2022)	Faster R-CNN, VGG16, SSD, Efficient, YOLOv4, YOLOv5, optimized lightweight YOLOv5, Used data from Plant Village data.	The accuracy reached 90.26% and 92.57%	The positioning error of the detection frame, and the positioning error in the detection of small targets.

2.	Plant Disease Detection and Classification by Deep Learning [2]	IEEE Access, vol. 9, pp. 56683-56698, 2021, doi:10.1109/ACCESS.2021.3069646. (2021)	SVM, K-means, New CNN model ARNet based on the combination of attention and residual ideas.	The accuracy of the two methods reached 94.71% and 98.32%, respectively	Lack of diverse and well annotated datasets
3.	Comparison of Plant Leaf Classification Using Modified Alex Net and SVM [3]	Traitement du Signal Vol. 38, No. 1, February, 2021, pp. 79-87 (2021)	SVM with linear kernel and radial function kernel, Alex Net, and the data of 3200 images of 9 different plants used.	For 70% of training data accuracy is 89.69% and for 90% data is 89.38%.	Comparison with other architectures isn't mentioned
4.	Plant Disease Detection Using CNN [4]	IEEE 2020 IEEE Applied Signal Processing Conference (ASPCON) (2020)	CNN with 4 Layers is used (Convolutional, Pooling, Max Pooling & Fully Connected layer), total of 3000 images has been provided	The accuracy percentage on the test set is 88.80% with no overfitting	There is no comparative analysis with other existing architectures.
5.	Potato Leaf Disease Classification Using Deep Learning Approach [5]	2020 International Electronic Symposium (IES) (2020)	Modern CNN architectural models such as AlexNet, VGG, GoogLeNet, ResNet. Dataset is taken from Kaggle.	VGG Network has potential for studying effective features for image classification of leaf diseases with accuracy of 91%.	Noise in the image will result in poor classification results.

6.	CNN based Disease Detection Approach on Potato Leaves [6]	3rd International Conference on Intelligent Sustainable Systems (ICISS) (2020)	Techniques are AlexNet, VggNet, ResNet, LeNet & Sequential models. For the dataset - 3000 images were collected and merged.	The offered model distinguishes the diseased & healthy plants appropriately with a precision of 97%.	The resolution of certain images is too low, some are hardly detected as affected and unaffected.
7.	Comparison of Artificial Intelligence Algorithms in Plant Disease Prediction [7]	Revue d'Intelligence Artificielle (2019)	CNN, RNN, ANN, SVM, KNN, Squared error loss function is used for training.	ANN outperforms all the other algorithms compared in this paper with accuracy of 90.79%	The accuracy of potato disease classification models can be affected by environmental conditions, such as lighting, temperature, and humidity
8.	Disease Detection and Classification in Agricultural Plants Using Convolutional Neural Networks [8]	International conference on SPIN (2019)	Model is created using 4 convolution layers followed by a ReLU function and pooling layer. Apple and tomato leaf image dataset containing 3663 images.	The achieved accuracy is 88.7 with minimum number of parameters i.e., 45K when compared to other existing models.	The model overfits as there is a gap between the training and validation curves.
9.	Detection of Potato Diseases Using Image Segmentation and Multiclass Support Vector Machine [9]	Department of Electrical and Computer Engineering University of Saskatchewan Saskatoon, Canada (2017)	SVM is used for image classification, Gray Level Cooccurrence Matrix was used for extracting statistical texture, and a database of 300 images of potato leaves.	100 healthy leaves and 200 diseased leaves, 93.7% accuracy was achieved.	High computational cost.

10.	Application of neural networks to image recognition of plant diseases [10]	Department of Plant Pathology, China Agricultural University, Beijing 100193, China (2012)	185 digital images of plant diseases to which image compression, image cutting and image enhancement were applied. BP networks, RBF neural networks, GRNNs and PNNs are used as the classifiers.	Fitting accuracy $\geq 75\%$ and prediction accuracy $\geq 75\%$	Lack of realworld validation
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2.2 KEY GAPS IN THE LITERATURE

Although the review of the literature offers insightful information on different approaches to the categorization of potato diseases, certain significant gaps and potential research areas are highlighted.

Among the gaps found are:

- **Localization Accuracy Issues:**

This restriction implies that precisely localizing and identifying the regions of interest that is, the areas impacted by the disease within the plant photos can provide difficulties. It suggests that the detection system might have trouble with accuracy, particularly when dealing with minor or complex patterns linked to plant illnesses.

Furthermore, confounding factors like as overlapping foliage, soil debris, shadows, or changes in lighting conditions might hide disease symptoms, resulting in false positives or negatives during detection. These factors create noise into visual data, making it difficult to reliably differentiate disease-related patterns from background clutter.

To efficiently distinguish disease signs from background noise while accounting for inherent variability in plant appearances and environmental circumstances, powerful algorithms capable of adaptive learning and feature extraction are required.

The combination of advanced image processing techniques, machine learning algorithms, and domain-specific knowledge can improve the accuracy and reliability of disease detection systems in agricultural contexts.

- **Lack of diverse and well-annotated datasets:**

In the realm of machine learning and deep learning, one prevalent problem is the lack of diverse and well-annotated datasets. A small dataset could make it more difficult for the model to generalize to other situations and illnesses. Additionally, accurate model training depends heavily on the quality of annotations. Incomplete or erroneous annotations, or a lack of diversity in the dataset, might negatively impact the model's performance and dependability in practical settings.

- **High computational cost:**

This restriction highlights the artificial intelligence algorithms' high resource requirements for detecting plant diseases. High computational costs can be a major disadvantage, especially when deploying in real-time applications or environments with limited resources. It might restrict the suggested solution's scalability and usefulness, particularly in situations with constrained computer resources.

- **Overfitting Gap:**

When a model learns the training set too well, it is said to be overfitting and loses its ability to generalize to new, unobserved data. The model may perform well on training data but have difficulty generalizing to validation data if there is a gap between the training and validation curves. This constraint suggests that the model may be very intricate, identifying noise in the training data instead of the fundamental patterns, and modifications might be required to enhance generalization.

- **Environmental Sensitivity:**

Images can become variable due to environmental factors, which can affect how well the model classifies diseases. The look of plants and diseases in photos can be affected by changes in lighting, temperature, and humidity, which makes it difficult for the model to accurately identify and categorize diseases. Adding methods for data augmentation or creating models that are more resistant to changes in the environment could be two ways to get around this restriction.

- **Low-Resolution Detection Challenge:**

Low-quality photos could not provide the information required for an appropriate diagnosis of a disease. Image resolution is essential for catching minute details. False positives and false negatives may arise from images that are rarely identified as impacted or unaffected. One way to get over this limitation might be to investigate methods for enhancing characteristics in low-quality photos or to improve the resolution of existing photographs.

False positives and false negatives can result from the limitations of low-quality images. False positives occur when healthy tissues are mistakenly identified as diseased, while false negatives occur when diseased tissues are overlooked or misclassified as healthy. These errors can undermine the reliability and effectiveness of disease diagnosis systems, impacting decision-making processes for crop management and disease control strategies.

To mitigate these limitations, exploring methods for enhancing characteristics in low-quality photos or improving the resolution of existing photographs can be valuable. Image enhancement techniques such as denoising, sharpening, and contrast adjustment can help improve the clarity and visibility of disease symptoms in low-quality images. Similarly, upscaling techniques or interpolation algorithms can be employed to increase the resolution of images, thereby enhancing the level of detail and precision in disease identification.

- **Image Noise impact:**

Random fluctuations in pixel values, or "image noise," can impede the model's capacity to correctly categorize illnesses. Noise may originate from a number of causes, including visual artifacts or defective sensors. It can be essential to employ noise-resistant algorithms or strong preprocessing methods in order to reduce the effects of noise and enhance classification performance overall.

CHAPTER 3 : SYSTEM DEVELOPMENT

System development involves designing and implementing a software solution for plant disease detection and classification. This includes analysing requirements, using Python libraries like NumPy and Pandas for data processing, employing machine learning and deep learning frameworks like Scikit-learn, TensorFlow, and Keras for model development, and utilizing the Python Operating System module for system-level tasks. The goal is to create an efficient and accurate system for identifying plant diseases from input images.

3.1 REQUIREMENTS AND ANALYSIS

The project makes use of a number of crucial libraries and the Python programming language for efficient execution.

NumPy: This Python library is a basic tool for numerical computing. In addition to providing strong support for managing sizable, multi-dimensional arrays and matrices, it also comes with a wide range of sophisticated mathematical functions that are made to work well with these arrays.

Pandas: Pandas is a robust library for data analysis and manipulation that offers easily navigable data structures like Data Frames. Efficient cleansing, transformation, and analysis of structured data are made possible by these structures.

Scikit-learn: Acknowledged for its extensive scope in machine learning, scikit-learn is a highly regarded library providing intuitive tools for modeling and data analysis. It includes tools for data preprocessing and a wide variety of algorithms for tasks like classification, regression, and clustering.

Matplotlib: Plotting libraries such as Matplotlib are very useful for creating interactive, animated, and static visualizations in Python. It can handle a wide range of plots, charts, and other graphical representations to efficiently communicate data-driven insights. Matplotlib's versatility extends beyond basic plotting capabilities, making it an indispensable tool for data visualization tasks in Python.

TensorFlow, Keras: Operating smoothly on top of TensorFlow, Keras is a high-level neural networks API that is implemented in Python. An extensive platform for building and implementing machine learning models is offered by the open-source TensorFlow machine learning framework. Keras provides a user-friendly interface for creating deep learning models, which improves the user experience. Keras, operating smoothly on top of TensorFlow, offers a user-friendly and intuitive interface for building and implementing deep learning models in Python. As a high-level neural networks API, Keras abstracts away the complexities of low-level TensorFlow operations, allowing developers to focus on model architecture design and experimentation rather than implementation details.

By leveraging TensorFlow's computational backend, Keras inherits its scalability, performance optimizations, and support for distributed computing, enabling seamless scaling from prototyping on a single machine to deploying models in production environments. This integration with TensorFlow also ensures compatibility with TensorFlow's ecosystem of tools and libraries, facilitating interoperability and code reuse across projects.

Moreover, Keras's modular and flexible design promotes code readability, modularity, and extensibility, making it well-suited for rapid prototyping and experimentation. With a rich collection of pre-built layers, activations, optimizers, and loss functions, Keras simplifies the process of assembling complex neural network architectures while offering the flexibility to customize models according to specific requirements.

OS: The Python Operating System module is used, which includes functions for defining the current directory, modifying and deleting directories, and retrieving directory contents, among other things. It also makes it easier to automate different operating system functions. One of the notable strengths of the OS module is its ability to streamline and automate various operating system-related tasks, enabling developers to write platform-independent code that can seamlessly adapt to different environments. By abstracting away platform-specific details and providing a consistent interface across different operating systems, the OS module simplifies the development process and enhances the portability and maintainability of Python applications.

3.2 PROJECT ARCHITECTURE AND DATASET

The photos used in this project were taken from the public repository Kaggle, with a focus on using the Plant Village dataset. More than 55,000 photos of plant leaves from various species are included in this dataset; the images show both healthy and diseased leaves. Leaf images are not evenly distributed; there are images in every class that range in size from 152 to 1000. We mainly studied potato leaves, and we only used photos from the Plant Village collection. In order to guarantee consistency, every image was standardized by resizing it to 256 by 256 pixels. This included categories like healthy leaves, early blight, and late blight leaves.

A selection of pictures from each class are shown in Figure 3.1 →

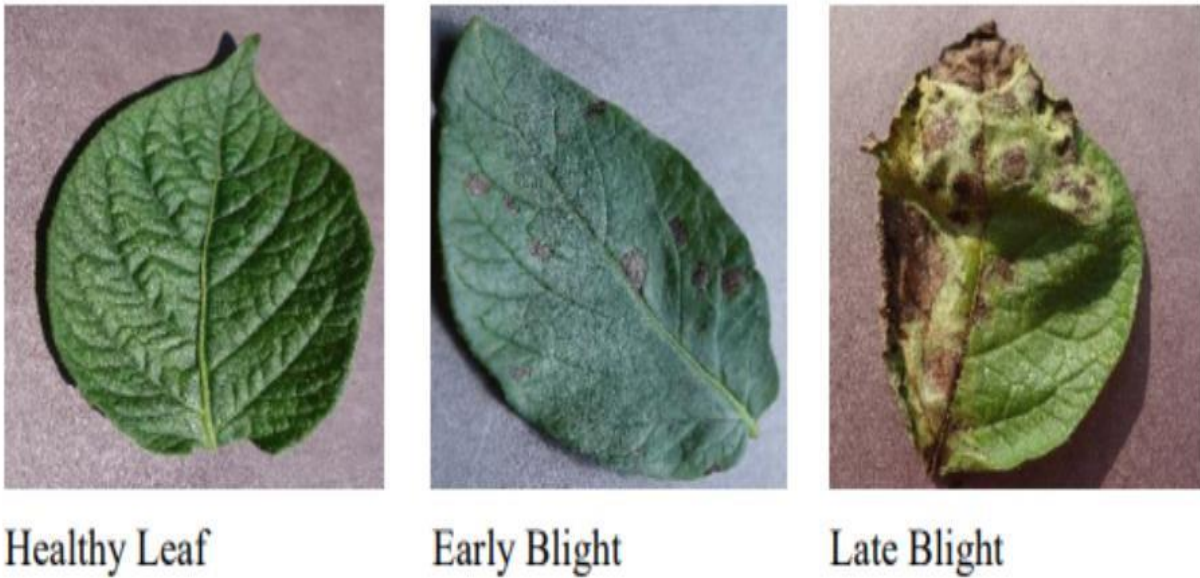


Fig 3.1 Stages of Leaf

3.2.1 USE CASE DIAGRAM

The module starts by taking features out of the leaf input image. The CNN model is then used, comparing these features to a dataset that has already been trained. The module then goes through a dense CNN process to extract leaf features on its own. The module concludes by determining if the plant leaf has a disease.

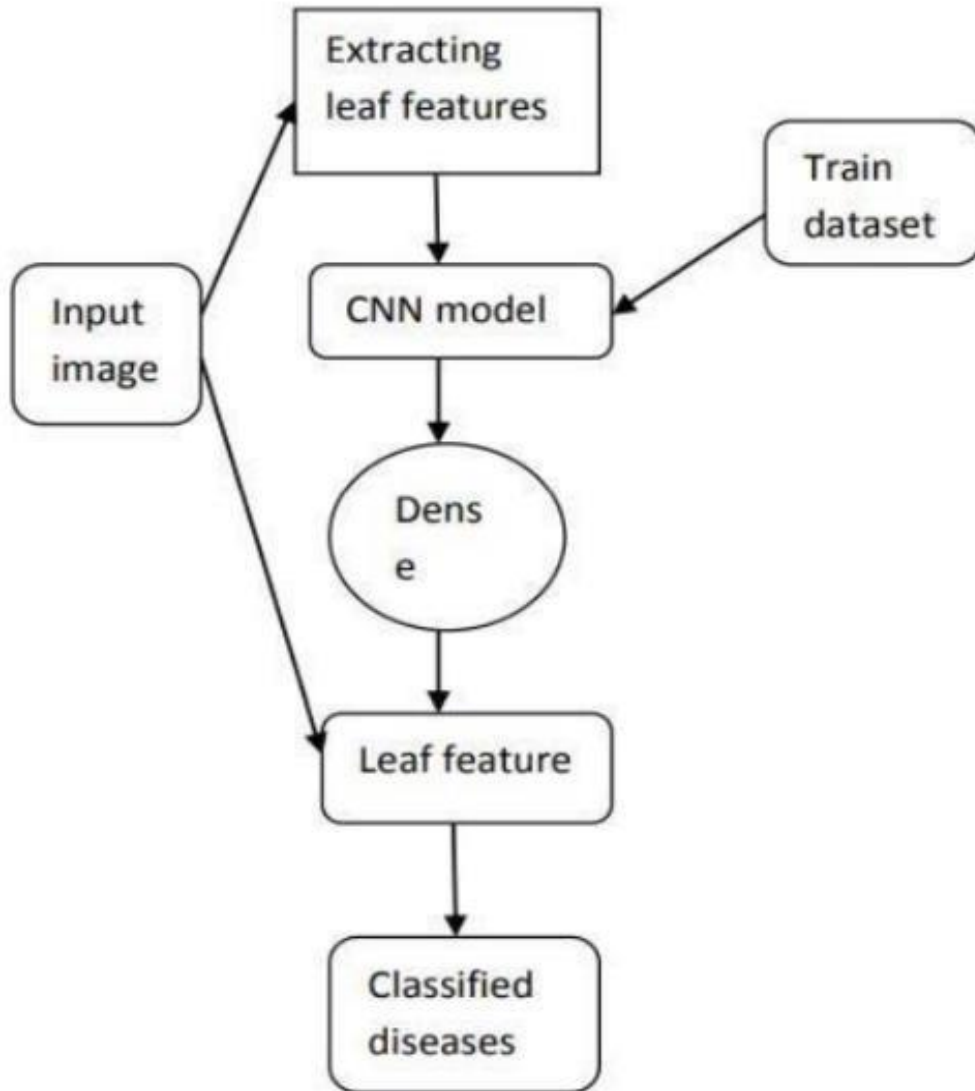


Fig 3.2 Use Case Diagram

3.3 DATA PREPARATION

3.3.1 IMAGE ACQUISITION

The initial step in any supervised machine learning project is the data collection procedure. To gather datasets, there are essentially three steps involved:

- 1) Gather and annotate data independently.
- 2) Create web scraping scripts to gather online photo content.
- 3) Purchase data from independent suppliers or utilize open repositories like Kaggle.
- 4) The dataset was obtained from the Kaggle database. The images in the dataset are divided into three classes. The dataset link is provided below: <https://www.kaggle.com/arjuntejaswi/plant-village>.

3.3.2 IMAGE PROCESSING

Since the images were taken in the actual field, there may be water stains, spores, and residue as commotion. Pre-handling of information is motivated by the desire to alter pixel values and remove disturbance from the image. It enhances the image's character.

Pre-handling is primarily used to eliminate unwanted picture information and enhance some important picture highlights. It combines middle sifting, picture resizing, and RGB to dim change. In order to make the picture device autonomous, the variety picture is completely replaced with a dim scale image. After that, the image is resized to 256 by 256 pixels.

3.3.3 FEATURE EXTRACTION

Feature extraction in the Convolutional Neural Network (CNN) process of classifying potato diseases entails methodically recognizing and enumerating unique patterns from input images of potato leaves. While the pooling layers lower dimensionality, the convolutional layers of the CNN analyze the images to identify edges, textures, and shapes. The network is then able to comprehend complex relationships and patterns by feeding the flattened features into dense layers. For various disease categories, probabilities are provided by the output layer. By means of training on labeled datasets, the CNN gains the ability to optimize its parameters, thereby augmenting its precision in classifying potato leaves as either disease-free or impacted by early or late blight. The model is able to automatically identify

pertinent patterns thanks to this hierarchical feature extraction approach, which aids in the efficient classification of diseases.

3.4 Algorithms/Pseudocode of the Project

3.4.1 What are Convolutional Neural Networks?

Convolutional neural networks (CNNs) are a subset of neural networks that are well-known for their exceptional performance in classifying images. They are especially well-suited for computer vision applications because they incorporate additional layers like convolution and pooling. They perform exceptionally well in tasks like object detection and face recognition. These networks end with dense layers that resemble those found in conventional neural networks. Typically, these networks are made up of multiple convolutional layers. One characteristic that sets CNNs apart is how well they take advantage of the two-dimensional structure that exists in images by using local connections and tied weights.

Max or mean pooling layers are used after convolutional layers to extract important features. CNNs have fewer parameters than regular neural networks, which means that training them is easier because there are fewer parameters to tweak. This is the main advantage of CNNs over regular neural networks. CNNs are easier to train than neural networks because of their inherent simplicity.

Pooling layers, such as max pooling or mean pooling, are frequently used after convolutional layers in Convolutional Neural Networks (CNNs) to down-sample feature maps and extract key information while reducing computational complexity. These pooling layers assist capture the most important properties from the input data, making the network more resilient to changes in input size and translation invariance.

CNNs have an edge over normal neural networks because they can efficiently use spatial hierarchies and local patterns in data. CNNs use shared weights and local receptive fields to exploit spatial correlations in pictures, making them ideal for tasks like image recognition, object detection, and semantic segmentation.

A summary of the various CNN operations is shown in figure 3.3.

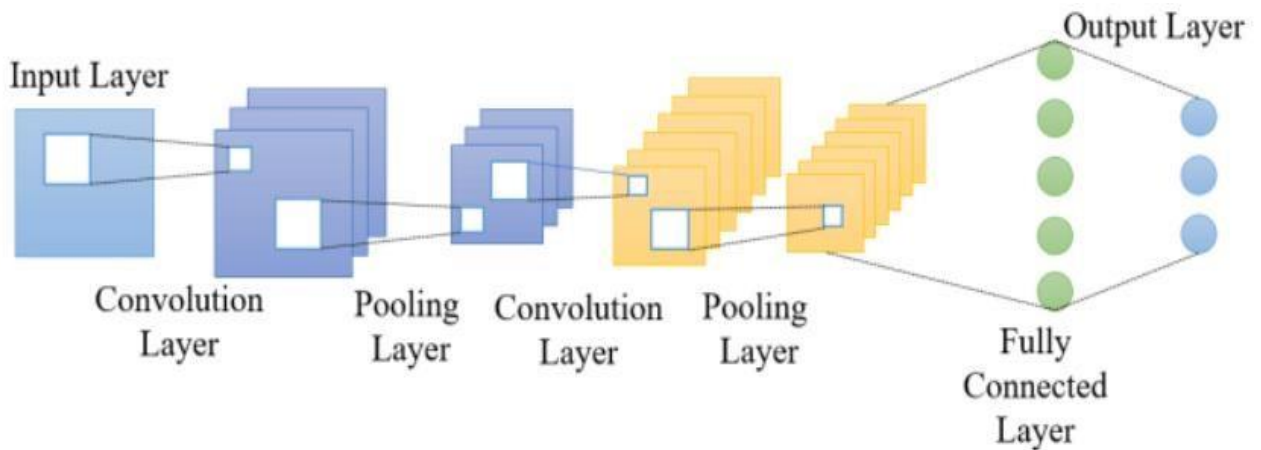


Fig 3.3 Architecture Diagram

Sequential operations make up the CNN architecture, as seen in the above figure. This simple CNN consists of a convolutional layer that applies the Rectified Linear Unit (ReLU) activation function after a kernel or filter is used to detect vertical or horizontal edges. The next layer is a max-pooling layer, which uses a kernel to identify the image's most salient features. Dense layers that are fully connected succeed this. During forward propagation, the loss function determines how accurate the model is. Then, in back propagation, gradient descent, AdaDelta, or Adam are used to update the weights, filters, and bias according to the loss value.

3.4.2 What are Convolutional Neural Networks?

This procedure involves navigating through an input image using a tiny tensor known as a kernel or filter. This operation's main goal is to extract important features from the picture. Following this process, each value in the image and the kernel are multiplied element-by-element to create a feature map. The vertical and horizontal edges are captured in this feature map that is produced; these edges are then magnified in the next step.

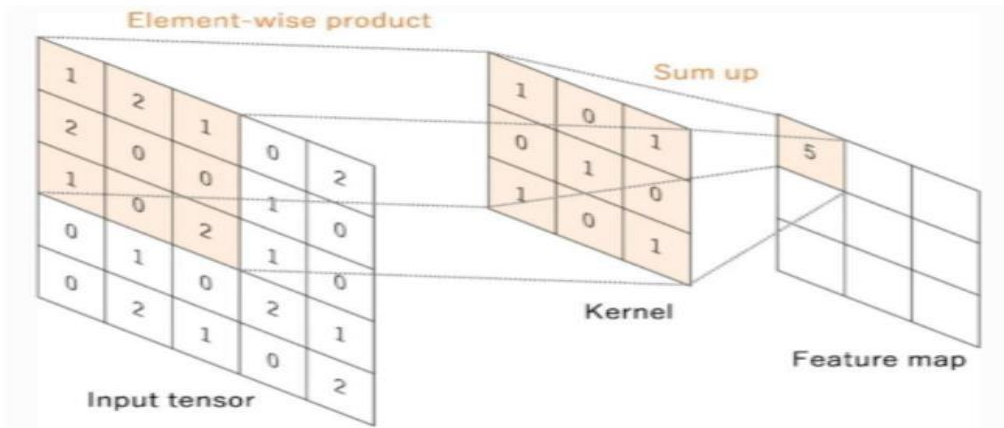


Fig 3.4 Feature Map

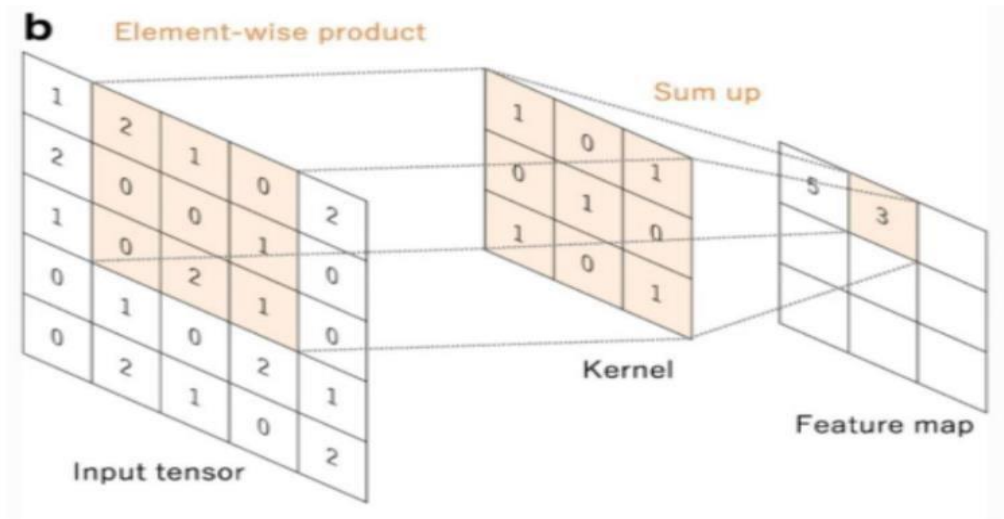


Fig 3.5 Feature Map Continued

Figure 3.5 above illustrates a convolution operation on a 5x5 picture. With no padding, the filter has a 3 by 3 size and a stride of 1. It will shrink in size as depicted in the figure if there is no padding. Padding is used to keep the image size constant, adding extra pixels all over the image to do so. The following

formula is used to get the image size: $(N + 2P - F)/S + 1$ where P = padding and N = image size F is the kernel size. S stands for step.

Padding-equipped figure:

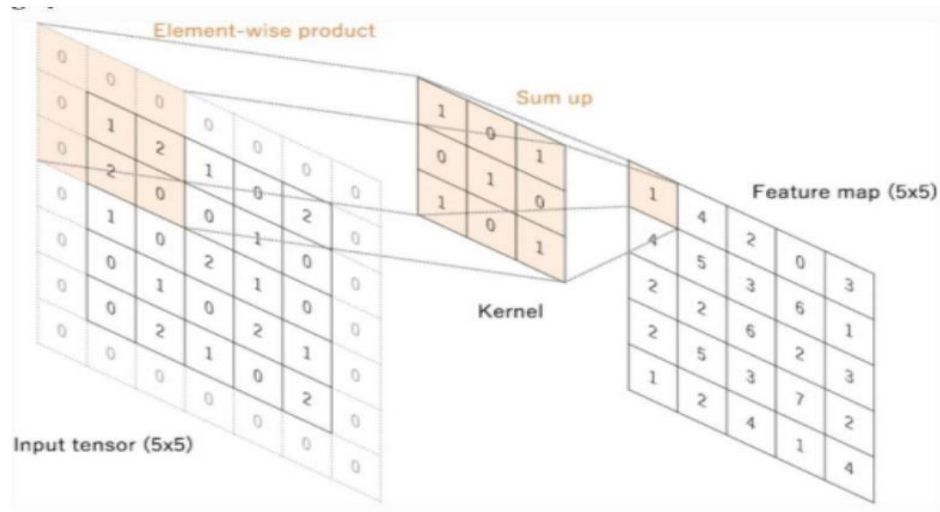


Fig 3.6 Padding Equipped Feature Map

3.4.3 Activation Function

Activation function is applied to feature maps that are obtained after convolution. In order to create non-linearity in the network, these activation functions are non-linear. Hidden layers avoid using activation functions like sigmoid and tangent because they can cause issues with vanishing gradients. When applied to feature maps obtained after convolution, activation functions transform the input signal into an output signal, introducing non-linearities that enhance the network's expressive power.

To avoid issues such as vanishing gradients, which can hinder the training process, non-linear activation functions are preferred over linear ones. Activation functions like sigmoid and tangent were previously popular choices, but they tend to saturate and cause vanishing gradients, especially in deeper networks with many layers. As a result, modern neural networks predominantly utilize activation functions that offer better stability and mitigate gradient vanishing or exploding issues.

The ReLU function is a frequently used activation function. $F(x)$ is equal to $\max(0, x)$. ReLU introduces non-linearity by outputting the input value if it is positive, effectively ignoring negative inputs.

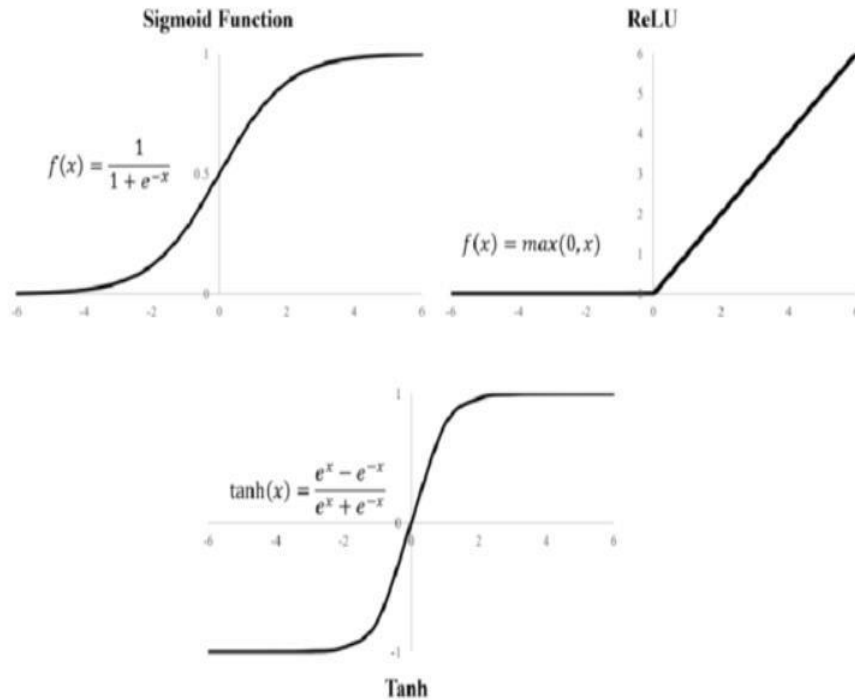


Fig 3.7 Different Activation Functions

3.4.4 Pooling Layer

The convolved component's spatial dimensions are decreased by the Pooling layer. It helps to retain the overall orientation during model training by eliminating dominant aspects that are positionally and rotationally invariant. Commonly, two kinds of pooling techniques are employed:

Maximum Pooling: The maximum value from the area of the image that the pool covers is returned by this method.

Average pooling: It retrieves the mean of all the values from the area of the picture that the pool covers.

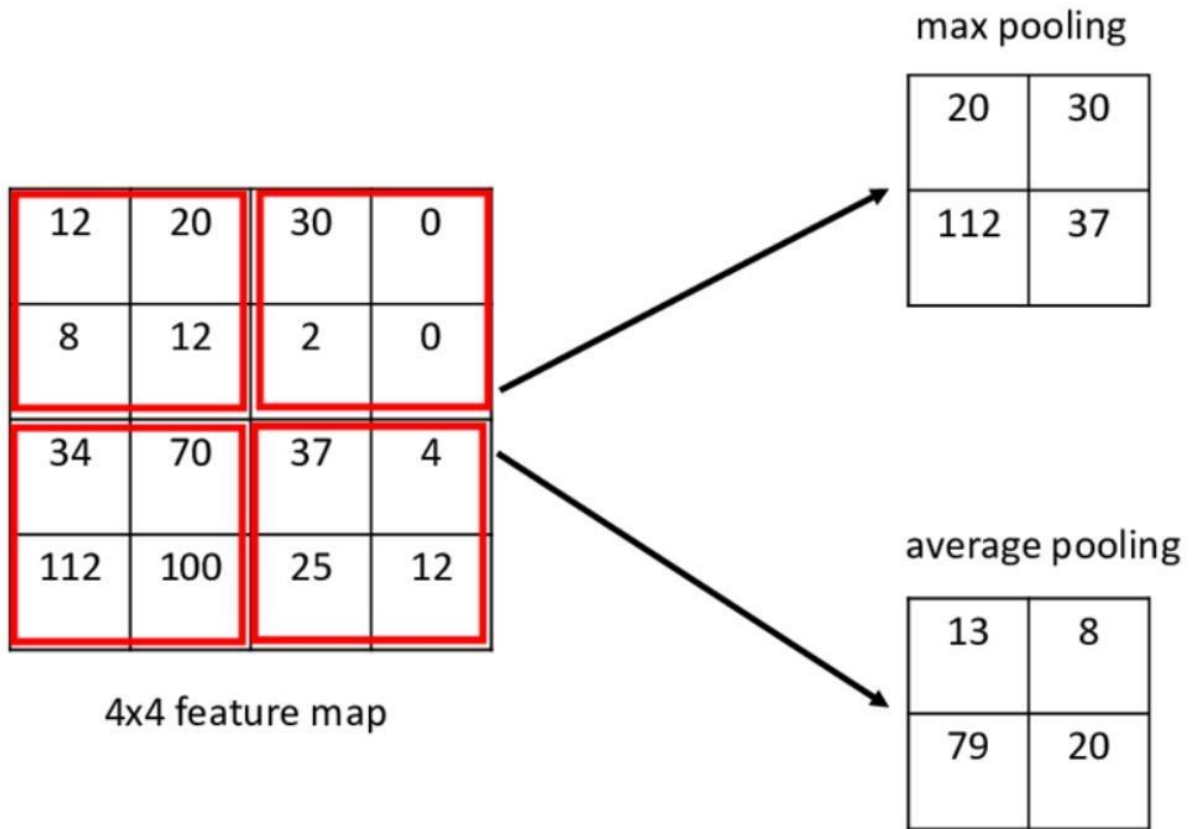


Fig 3.8 Pooling Techniques

3.4.5 Fully Connected Layer

After feature maps are acquired from the max-pooling layer, they are flattened and then sent to a dense layer that is fully connected. Before the feature maps are sent to the dense layer, they are first transformed into a one-dimensional array. It is possible to incorporate several dense layers between. The number of output classes is primarily reflected in the final output layer. Rectified Linear Unit (ReLU) is the most widely used activation function, and it is integrated into each hidden dense layer.

3.4.6 Activation Function at Last Layer

Since the final output layer's main function is to introduce non-linearity, its activation function is different from the activation functions used in the hidden dense layers. The final layer's activation function provides probabilities for each class, aiding in categorization. The sigmoid function is widely used for binary classification with two classes. Nonetheless, the SoftMax function is used in this project because there are more than two categories.

The output probabilities are normalized by the SoftMax function, which guarantees that all probability values fall between 0 and 1 and that the cumulative sum of all probabilities equals 1. The sigmoid function's output is shown in the figure below.

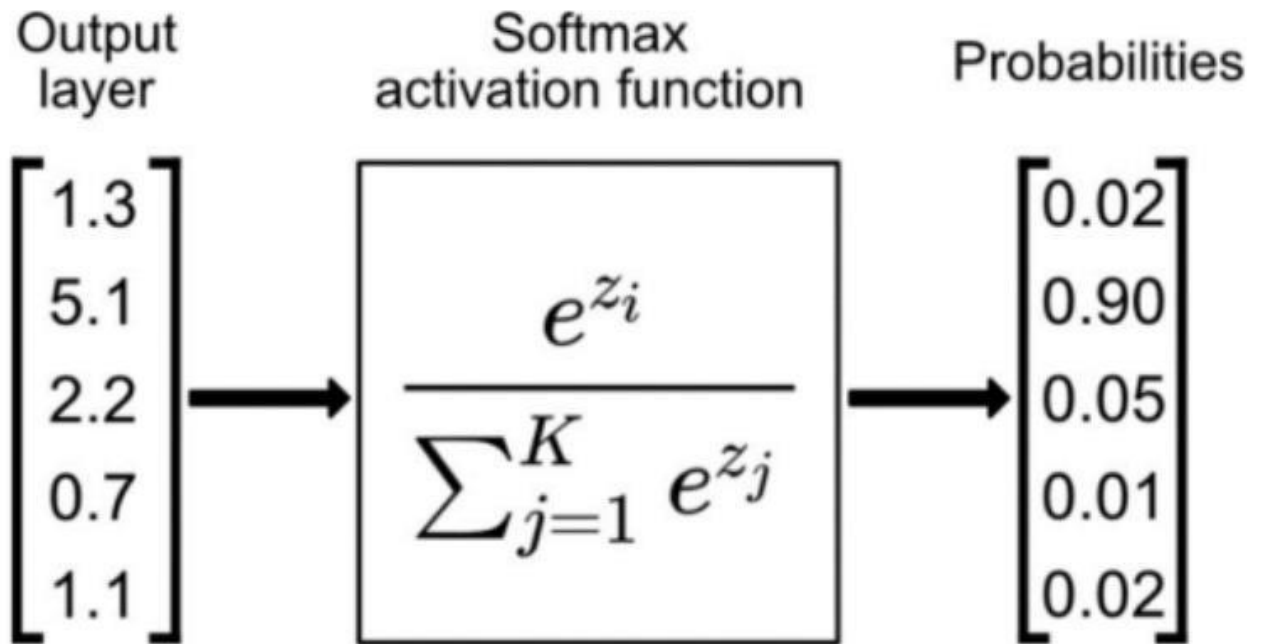


Fig 3.9 Sigmoid Function's Output

The weights, filters, and biases are calculated during forward propagation, and a cost function evaluates their accuracy by calculating the error, which is defined as the difference between the actual and predicted labels. During the backpropagation stage that follows, an optimizer—an algorithm whose job it is to find the values for these parameters in order to minimize the total loss—updates the weights, filters, and biases. There are other optimizers available, and Adam is the one used in this case. In order to reduce loss during training, the Adam optimizer iteratively fine-tunes the model's parameters.

3.4.7 Loss Function

The loss function measures the difference between the actual and predicted labels, which helps to validate the findings. The loss function is also known as the cost function when processing data either all at once or in batches. There are several different kinds of cost functions, such as sparse categorical cross entropy and multi-class cross entropy.

Choosing a particular loss function is important because various loss functions can produce different outcomes. As a result, the loss function selected should be in line with the particular needs and features of the given use case.

3.4.8 Optimizers

Optimizers are essential for minimizing loss because they update weights and biases. There are different kinds of optimizers. The Adam optimizer is the one used in this case. Adam optimizer, a cutting-edge algorithm, improves gradient descent performance and is especially useful for large datasets. It uses exponential weighted averages to incorporate momentum and dynamically modifies the learning rate. This optimizer, which combines the advantages of gradient descent with momentum and Root Mean Squared Propagation, is renowned for its speed and resource efficiency.

3.4.9 Implementation

Potato Disease Classification

Dataset credits: <https://www.kaggle.com/arjuntejaswi/plant-village>

Import all the Dependencies

```
In [1]: import tensorflow as tf
        from tensorflow.keras import models, layers
        import matplotlib.pyplot as plt
        from IPython.display import HTML
```

Set all the Constants

```
In [2]: BATCH_SIZE = 32
        IMAGE_SIZE = 256
        CHANNELS=3
        EPOCHS=50
```

Import data into tensorflow dataset object

We will use `image_dataset_from_directory` api to load all images in tensorflow dataset:

https://www.tensorflow.org/api_docs/python/tf/keras/preprocessing/image_dataset_from_directory

```
In [4]: dataset = tf.keras.preprocessing.image_dataset_from_directory(
        "PlantVillage",
        seed=123,
        shuffle=True,
        image_size=(IMAGE_SIZE, IMAGE_SIZE),
        batch_size=BATCH_SIZE
        )
```

Found 2152 files belonging to 3 classes.

Visualize some of the images from our dataset

```
In [8]: plt.figure(figsize=(10, 10))
for image_batch, labels_batch in dataset.take(1):
    for i in range(12):
        ax = plt.subplot(3, 4, i + 1)
        plt.imshow(image_batch[i].numpy().astype("uint8"))
        plt.title(class_names[labels_batch[i]])
        plt.axis("off")
```

Potato__Early_blight



Potato__Early_blight



Potato__Early_blight



Potato__Late_blight



Potato__Early_blight



Potato__Early_blight



Potato__Late_blight



Potato__Early_blight



Potato__Late_blight



Potato__Early_blight



Potato__Early_blight



Potato__Early_blight



Function to Split Dataset

Dataset should be bifurcated into 3 subsets, namely:

1. Training: Dataset to be used while training
2. Validation: Dataset to be tested against while training
3. Test: Dataset to be tested against after we trained a model

```
In [9]: len(dataset)
```

```
Out[9]: 68
```

```
In [10]: train_size = 0.8  
len(dataset)*train_size
```

```
Out[10]: 54.400000000000006
```

```
In [11]: train_ds = dataset.take(54)  
len(train_ds)
```

```
Out[11]: 54
```

```
In [12]: test_ds = dataset.skip(54)  
len(test_ds)
```

```
Out[12]: 14
```

```
In [13]: val_size=0.1  
len(dataset)*val_size
```

```
Out[13]: 6.800000000000001
```

```
In [14]: val_ds = test_ds.take(6)  
len(val_ds)
```



```
In [15]: test_ds = test_ds.skip(6)
len(test_ds)
```

Out[15]: 8

```
In [16]: def get_dataset_partitions_tf(ds, train_split=0.8, val_split=0.1, test_split=0.1
      assert (train_split + test_split + val_split) == 1

      ds_size = len(ds)

      if shuffle:
          ds = ds.shuffle(shuffle_size, seed=12)

      train_size = int(train_split * ds_size)
      val_size = int(val_split * ds_size)

      train_ds = ds.take(train_size)
      val_ds = ds.skip(train_size).take(val_size)
      test_ds = ds.skip(train_size).skip(val_size)

      return train_ds, val_ds, test_ds
```

```
In [17]: train_ds, val_ds, test_ds = get_dataset_partitions_tf(dataset)
```

```
In [18]: len(train_ds)
```

Out[18]: 54

```
In [19]: len(val_ds)
```

Out[19]: 6

```
In [20]: len(test_ds)
```

Out[20]: 8

Cache, Shuffle, and Prefetch the Dataset

```
In [21]: train_ds = train_ds.cache().shuffle(1000).prefetch(buffer_size=tf.data.AUTOTUNE)
val_ds = val_ds.cache().shuffle(1000).prefetch(buffer_size=tf.data.AUTOTUNE)
test_ds = test_ds.cache().shuffle(1000).prefetch(buffer_size=tf.data.AUTOTUNE)
```

Building the Model

Creating a Layer for Resizing and Normalization

```
In [22]: resize_and_rescale = tf.keras.Sequential([
layers.experimental.preprocessing.Resizing(IMAGE_SIZE, IMAGE_SIZE),
layers.experimental.preprocessing.Rescaling(1./255),
])
```

Data Augmentation

Data Augmentation is needed when we have less data, this boosts the accuracy of our model by augmenting the data.

```
In [23]: data_augmentation = tf.keras.Sequential([
layers.experimental.preprocessing.RandomFlip("horizontal_and_vertical"),
layers.experimental.preprocessing.RandomRotation(0.2),
])
```

Applying Data Augmentation to Train Dataset

```
In [27]: train_ds = train_ds.map(
lambda x, y: (data_augmentation(x, training=True), y)
).prefetch(buffer_size=tf.data.AUTOTUNE)
```

Watch below video if you are not familiar with data augmentation

```
In [28]: HTML("""
""")
```

Out[28]:

```
In [29]: HTML("""  
  
""")
```

Out[29]:

```
In [30]: input_shape = (BATCH_SIZE, IMAGE_SIZE, IMAGE_SIZE, CHANNELS)  
n_classes = 3  
  
model = models.Sequential([  
    resize_and_rescale,  
    layers.Conv2D(32, kernel_size = (3,3), activation='relu', input_shape=input_shape),  
    layers.MaxPooling2D((2, 2)),  
    layers.Conv2D(64, kernel_size = (3,3), activation='relu'),  
    layers.MaxPooling2D((2, 2)),  
    layers.Conv2D(64, kernel_size = (3,3), activation='relu'),  
    layers.MaxPooling2D((2, 2)),  
    layers.Conv2D(64, (3, 3), activation='relu'),  
    layers.MaxPooling2D((2, 2)),  
    layers.Conv2D(64, (3, 3), activation='relu'),  
    layers.MaxPooling2D((2, 2)),  
    layers.Conv2D(64, (3, 3), activation='relu'),  
    layers.MaxPooling2D((2, 2)),  
    layers.Flatten(),  
    layers.Dense(64, activation='relu'),  
    layers.Dense(n_classes, activation='softmax'),  
])  
  
model.build(input_shape=input_shape)
```

In [31]:

```
model.summary()
```

Model: "sequential_2"

Layer (type)	Output Shape	Param #
sequential (Sequential)	(32, 256, 256, 3)	0
conv2d (Conv2D)	(32, 254, 254, 32)	896
max_pooling2d (MaxPooling2D)	(32, 127, 127, 32)	0
conv2d_1 (Conv2D)	(32, 125, 125, 64)	18496
max_pooling2d_1 (MaxPooling2D)	(32, 62, 62, 64)	0
conv2d_2 (Conv2D)	(32, 60, 60, 64)	36928
max_pooling2d_2 (MaxPooling2D)	(32, 30, 30, 64)	0
conv2d_3 (Conv2D)	(32, 28, 28, 64)	36928
max_pooling2d_3 (MaxPooling2D)	(32, 14, 14, 64)	0
conv2d_4 (Conv2D)	(32, 12, 12, 64)	36928
max_pooling2d_4 (MaxPooling2D)	(32, 6, 6, 64)	0
conv2d_5 (Conv2D)	(32, 4, 4, 64)	36928
max_pooling2d_5 (MaxPooling2D)	(32, 2, 2, 64)	0
flatten (Flatten)	(32, 256)	0
dense (Dense)	(32, 64)	16448

```
scores = model.evaluate(test_ds)
```

```
8/8 [=====] - 0s 11ms/step - loss: 0.0215 - accuracy: 0.9883
```

Accuracy of our model is 98.83%.

CHAPTER 4 : TESTING

This section involves testing the machine learning model for plant disease detection and the backend built with FastAPI. The ML model is rigorously evaluated for metrics like accuracy, precision, and recall, while the backend undergoes thorough testing to ensure functionality and responsiveness.

4.1 Testing Strategy

Plotting the Accuracy and Loss Curves

```
In [36]: history
```

```
Out[36]:
```

You can read documentation on history object here: https://www.tensorflow.org/api_docs/python/tf/keras/callbacks/History

```
In [37]: history.params
```

```
Out[37]: {'verbose': 1, 'epochs': 50, 'steps': 54}
```

```
In [38]: history.history.keys()
```

```
Out[38]: dict_keys(['loss', 'accuracy', 'val_loss', 'val_accuracy'])
```

loss, accuracy, val loss etc are a python list containing values of loss, accuracy etc at the end of each epoch

```
In [39]: type(history.history['loss'])
```

```
Out[39]: list
```

```
In [40]: len(history.history['loss'])
```

```
Out[40]: 50
```

```
In [41]: history.history['loss'][:5] # show loss for first 5 epochs
```

```
Out[41]: [0.8801848292350769,  
0.6033139228820801,  
0.3646925389766693,  
0.2776017189025879,  
0.24480397999286652]
```

Compiling the Model

We use `adam` Optimizer, `SparseCategoricalCrossentropy` for losses, `accuracy` as a metric

```
In [32]: model.compile(
          optimizer='adam',
          loss=tf.keras.losses.SparseCategoricalCrossentropy(from_logits=False),
          metrics=['accuracy']
        )
```

```
In [33]: history = model.fit(
          train_ds,
          batch_size=BATCH_SIZE,
          validation_data=val_ds,
          verbose=1,
          epochs=50,
        )
```

```
In [34]: scores = model.evaluate(test_ds)

8/8 [=====] - 1s 14ms/step - loss: 0.0063 - accuracy: 1.0000
```

```
In [35]: scores
```

```
Out[35]: [0.006251859944313765, 1.0]
```

Scores is just a list containing loss and accuracy value

Plotting the Accuracy and Loss Curves

```
In [36]: history
```

```
Out[36]:
```

You can read documentation on history object here: https://www.tensorflow.org/api_docs/python/tf/keras/callbacks/History

```
In [37]: history.params
```

```
Out[37]: {'verbose': 1, 'epochs': 50, 'steps': 54}
```

```
In [38]: history.history.keys()
```

```
Out[38]: dict_keys(['loss', 'accuracy', 'val_loss', 'val_accuracy'])
```

```
In [39]: type(history.history['loss'])
```

```
Out[39]: list
```

```
In [40]: len(history.history['loss'])
```

```
Out[40]: 50
```

```
In [41]: history.history['loss'][:5] # show loss for first 5 epochs
```

```
Out[41]: [0.8801848292350769,  
          0.6033139228820801,  
          0.3646925389766693,  
          0.2776017189025879,  
          0.24480397999286652]
```

```
In [42]: acc = history.history['accuracy']  
         val_acc = history.history['val_accuracy']  
  
         loss = history.history['loss']  
         val_loss = history.history['val_loss']
```

```
In [43]: plt.figure(figsize=(8, 8))  
         plt.subplot(1, 2, 1)  
         plt.plot(range(EPOCHS), acc, label='Training Accuracy')  
         plt.plot(range(EPOCHS), val_acc, label='Validation Accuracy')  
         plt.legend(loc='lower right')  
         plt.title('Training and Validation Accuracy')  
  
         plt.subplot(1, 2, 2)  
         plt.plot(range(EPOCHS), loss, label='Training Loss')  
         plt.plot(range(EPOCHS), val_loss, label='Validation Loss')  
         plt.legend(loc='upper right')  
         plt.title('Training and Validation Loss')  
         plt.show()
```


4.2 Test Cases & Outcomes

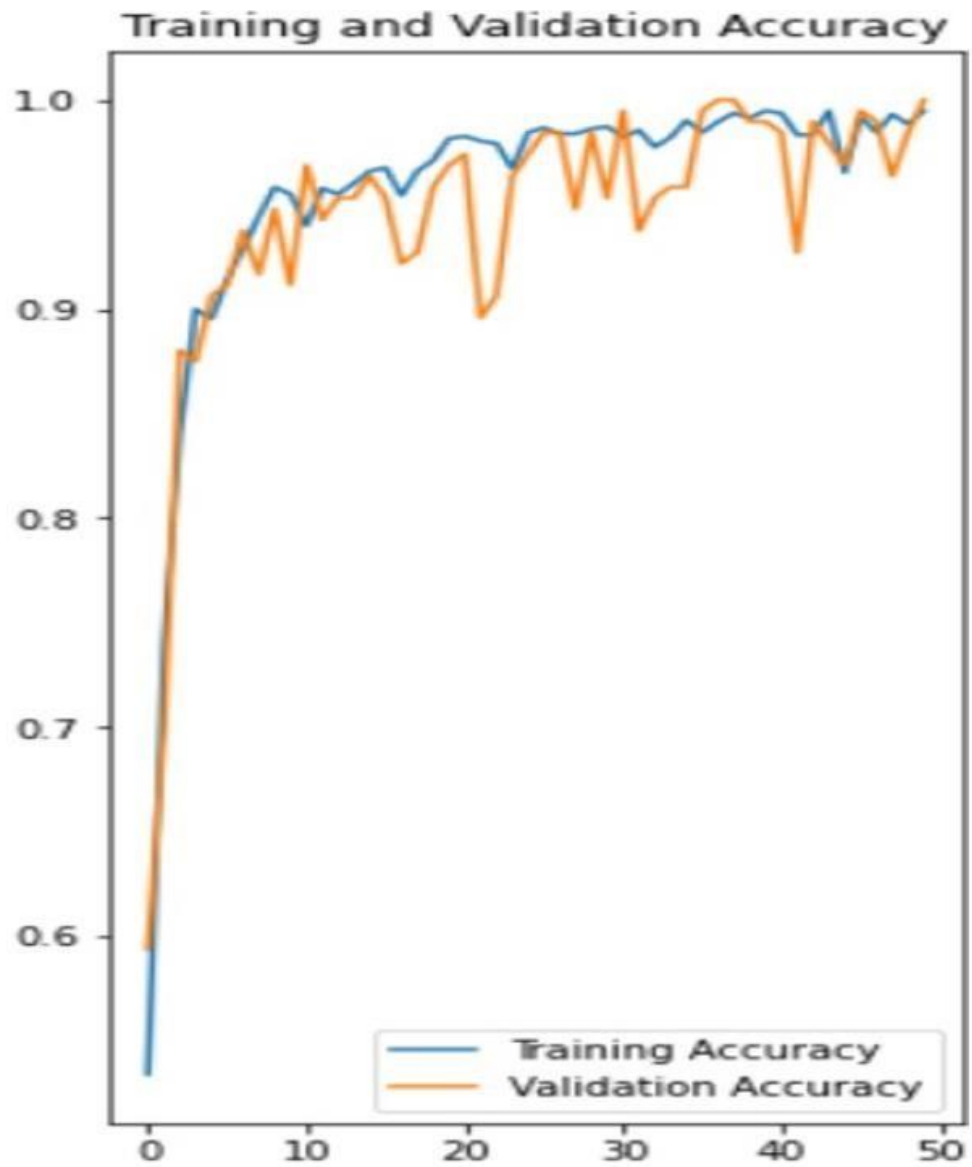


Fig 4.1: Training and Validation Accuracy

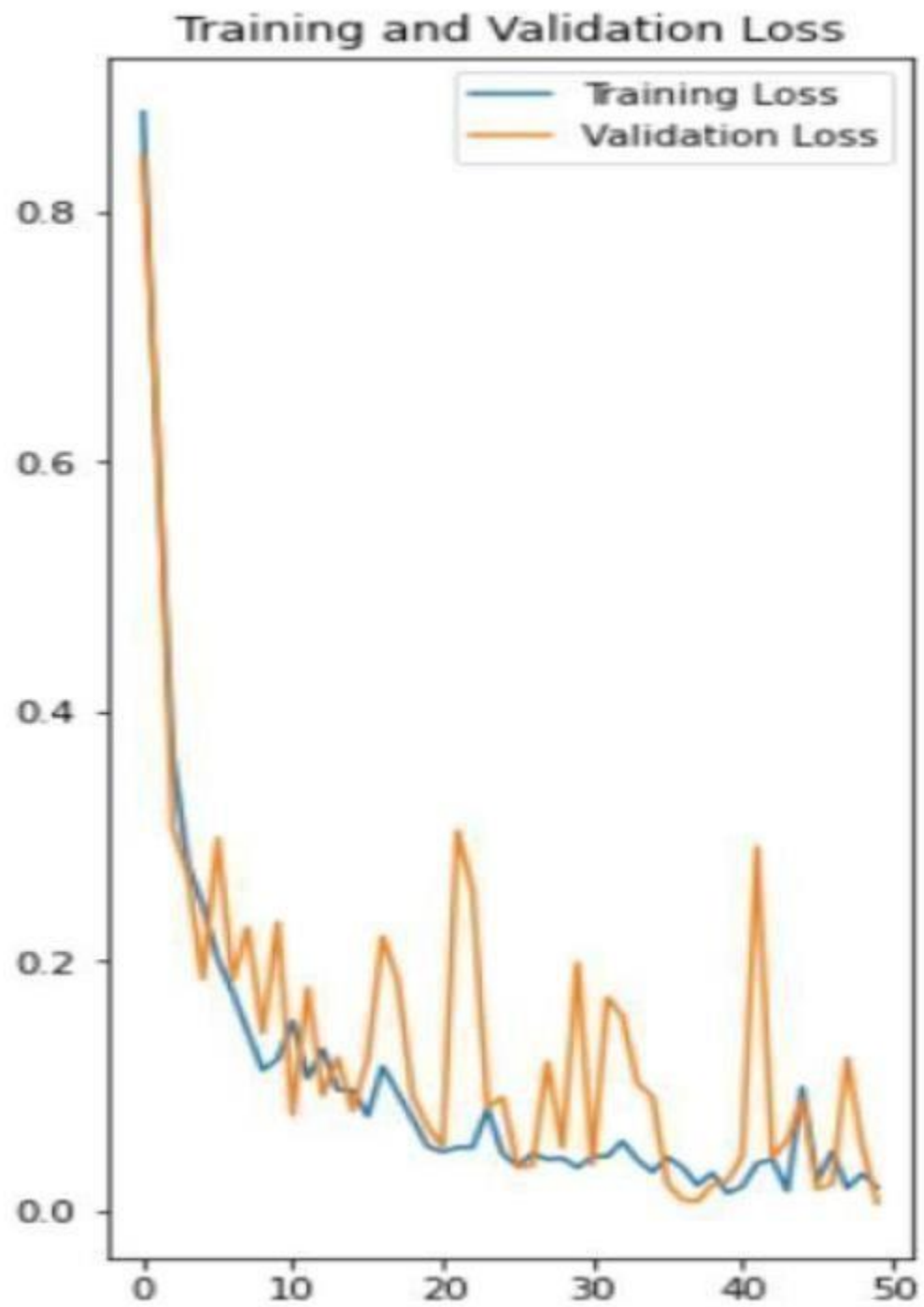


Fig 4.2: Training and Validation Loss

Run prediction on a sample image

In [44]:

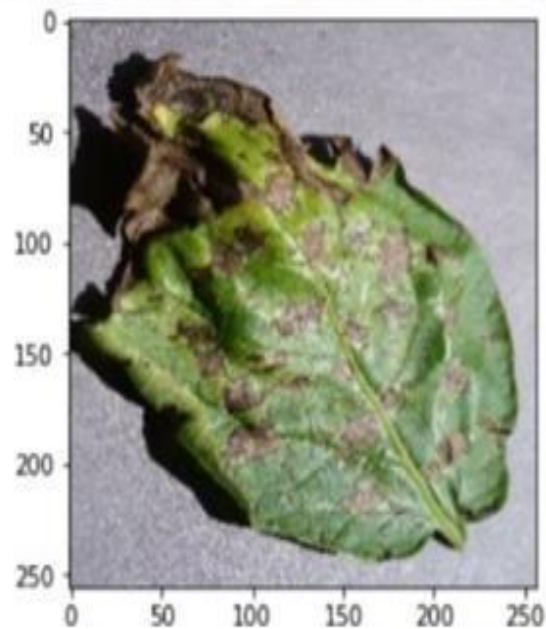
```
import numpy as np
for images_batch, labels_batch in test_ds.take(1):

    first_image = images_batch[0].numpy().astype('uint8')
    first_label = labels_batch[0].numpy()

    print("first image to predict")
    plt.imshow(first_image)
    print("actual label:", class_names[first_label])

    batch_prediction = model.predict(images_batch)
    print("predicted label:", class_names[np.argmax(batch_prediction[0])])
```

```
first image to predict
actual label: Potato__Early_blight
predicted label: Potato__Early_blight
```



Write a function for inference

```
In [45]: def predict(model, img):
img_array = tf.keras.preprocessing.image.img_to_array(images[i].numpy())
img_array = tf.expand_dims(img_array, 0)

predictions = model.predict(img_array)

predicted_class = class_names[np.argmax(predictions[0])]
confidence = round(100 * (np.max(predictions[0])), 2)
return predicted_class, confidence
```

```
In [46]: plt.figure(figsize=(15, 15))
for images, labels in test_ds.take(1):
    for i in range(9):
        ax = plt.subplot(3, 3, i + 1)
        plt.imshow(images[i].numpy().astype("uint8"))

        predicted_class, confidence = predict(model, images[i].numpy())
        actual_class = class_names[labels[i]]

        plt.title(f"Actual: {actual_class},\n Predicted: {predicted_class}.\n Confidence: {confidence}%")

        plt.axis("off")
```

Actual: Potato__Late_blight,
Predicted: Potato__Late_blight.
Confidence: 99.98%



Actual: Potato__Late_blight,
Predicted: Potato__Late_blight.
Confidence: 100.0%



Actual: Potato__Late_blight,
Predicted: Potato__Late_blight.
Confidence: 99.88%



Actual: Potato__Early_blight,
Predicted: Potato__Early_blight.
Confidence: 100.0%



Actual: Potato__Late_blight,
Predicted: Potato__Late_blight.
Confidence: 99.92%



Actual: Potato__healthy,
Predicted: Potato__healthy.
Confidence: 99.53%



Actual: Potato__Late_blight,
Predicted: Potato__Late_blight.
Confidence: 100.0%



Actual: Potato__Early_blight,
Predicted: Potato__Early_blight.
Confidence: 99.87%



Actual: Potato__Late_blight,
Predicted: Potato__Late_blight.
Confidence: 88.21%



Fig 4.3: Sample Output

For creating the web application Fast API has been used which will manage backend of the web application. It is one of the emerging python frameworks which is used to create simple Rest APIs.

BELOW IS THE IMPLEMENTED CODE:

```
1  from fastapi import FastAPI, File, UploadFile
2  from fastapi.middleware.cors import CORSMiddleware
3  import uvicorn
4  import numpy as np
5  from io import BytesIO
6  from PIL import Image
7  import tensorflow as tf
8
9  app = FastAPI()
10 |-----|
11 MODEL = tf.keras.models.load_model("./saved_models/1")
12 CLASS_NAMES = ["Early Blight", "Late Blight", "Healthy"]
13
14 @app.get("/ping")
15 async def ping():
16     return "Hello, I am alive"
17 def read_file_as_image(data) -> np.ndarray:
18     image = np.array(Image.open(BytesIO(data)))
19     return image
20 @app.post("/predict")
21 async def predict(
22     file: UploadFile = File(...)
23 ):
24     image=read_file_as_image(await file.read())
25     img_batch = np.expand_dims(image, 0)
26     predictions = MODEL.predict(img_batch)
27     predicted_class = CLASS_NAMES[np.argmax(predictions[0])]
28     confidence = np.max(predictions[0])
29     return {
30         'class': predicted_class,
31         'confidence': float(confidence)
32     }
33     pass
34
35
36
37 if __name__ == "__main__":
38     uvicorn.run(app, host='localhost', port=5000)
```

Fig 4.4 Implemented Code

After running the code, web application will run at port number 8000. Advantage of Fast API is that without having front end we can check the working of our model in Fast API itself. There are various software's which returns output of a web application in which there is no front end. For that we have to go to docs URL. After this it will generate UI shown below:

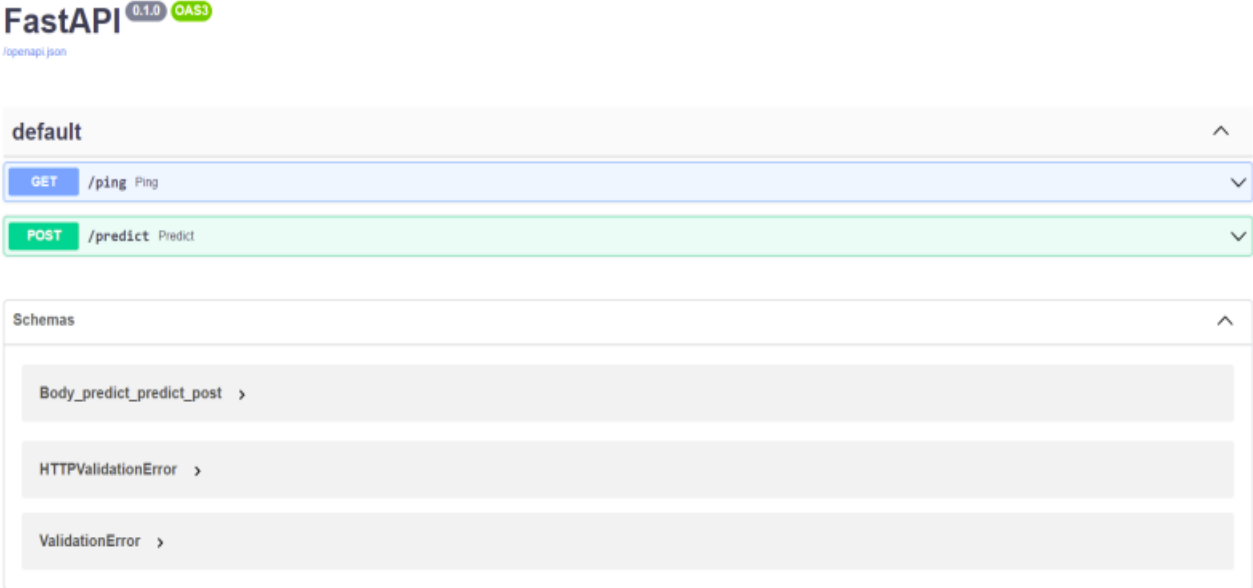


Fig 4.5 FastAPI

In Fast API, an upload file variable is there which is used to upload a file. This variable has been used to upload an image file and then model will classify image according to the probability. Below is the figure in which an input image has been classified.

Responses

Curl

```
curl -X 'POST' \
'http://localhost:8000/predict' \
-H 'accept: application/json' \
-H 'Content-Type: multipart/form-data' \
-F 'file=@acc2b2-0dde-4073-8542-6fca275ab974__RS_L8_4857.JPG;type=image/jpeg'
```

Request URL

```
http://localhost:8000/predict
```

Server response

Code	Details
200	<p>Response body</p> <pre>{ "class": "Late Blight", "confidence": 0.999582767486572 }</pre> <p>Response headers</p> <pre>content-length: 55 content-type: application/json date: Wed, 25 May 2022 13:34:41 GMT server: uvicorn</pre>

Responses

Code	Description	Links
200	Successful Response	No links

Fig 4.6 Image Classification

Given image has been classified as a Late_blight class with 0.99 confidence.

CHAPTER 5 : RESULTS AND EVALUATION

5.1 RESULTS

The architecture of the CNN model was created to efficiently recognize and understand complex patterns seen in potato pictures of diseases. The classification part of the model consists of fully connected layers after a number of convolutional and pooling layers. An overview of the model architecture is provided below:

Convolutional Layers: To extract hierarchical features, many layers with progressively larger filters and kernel sizes are used.

MaxPooling Layers: A technique for down sampling while keeping important details.

Flatten Layer: In order to make room for fully connected layers, flatten the output.

Dense Layers: Fully connected layers that record intricate relationships by activating ReLU.

Dense layer with SoftMax activation for multi-class classification is the output layer.

The created CNN model attained an exceptional accuracy of 98.83% after 50 epochs on the test dataset, following rigorous training and validation. This high accuracy highlights the model's efficacy in correctly categorizing potato illnesses. The model's performance is further validated by the confusion matrix and classification report, which show how precisely it can distinguish between various disease groups.

5.2 COMPARISON WITH EXISTING SOLUTIONS

SR NO.	METHOD USED	ACCURACY
1.	Optimized Lightweight YOLOv5 Model	92.57%
2.	SVM + KNN, PARNet	94.71% and 98.32%
3.	Modified Alex Net and Support Vector Machine	89.38% (for 90% of data)
4.	CNN with 4 layers	88.80%
5.	ANN	90.79%
6.	CNN with 5 layers (our model)	98.83%

BRIEF COMPARISON:

The combination of SVM, K-means, and PARNet performed the best in the given list, achieving the highest accuracy (98.32%).

Respectable accuracy was also attained by YOLOv5, ANN, and Modified Alex Net with SVM, with the ANN and YOLOv5 models exhibiting consistent high performance.

Other considerations including speed, ease of implementation, and processing resources may influence the choice of models.

CHAPTER 6 : CONCLUSIONS AND FUTURE SCOPE

6.1 CONCLUSION

Convolutional neural network architecture is employed in this project's model. In order for it to be applied to web application classification, a potato leaf image will be provided as an input, and the system will be able to determine whether the plant is healthy or affected by early or late blight. This project has the potential to be very beneficial for farmers with minimal adjustments. We can quickly determine if a plant is healthy or diseased without having to do any independent monitoring. It will lower production costs and enable early implementation of preventive measures. It is possible to modify this project to make it useful for identifying diseases in different species. This can be completed more effectively and in real time.

6.2 FUTURE SCOPE

- Integration of Advanced AI Models: Explore the integration of more advanced AI models, such as transformer-based architectures like BERT or GPT, to improve disease detection accuracy and provide more nuanced insights into diseases and their solutions.
- Expansion to Other Crops: Extend the application beyond potatoes to classify diseases in other crops, such as tomatoes, wheat, or rice. This expansion will require collecting and annotating datasets specific to each crop and fine-tuning your existing models accordingly.
- Real-time Disease Monitoring: Develop a real-time disease monitoring system that utilizes IoT devices or drones equipped with cameras to continuously monitor crop health in agricultural fields. Implement algorithms that can analyse streaming video data in real-time and alert farmers of any potential disease outbreaks or anomalies.

- Collaboration with Agricultural Experts: Partner with agricultural experts and researchers to validate the accuracy of your disease classification models and ensure that the information provided by your application is scientifically sound and reliable. This collaboration can also involve gathering feedback from farmers to further improve the usability and effectiveness of the application.
- Localized Recommendations and Solutions: Customize disease detection results and recommended solutions based on the geographic location and climate conditions of the user's region. Incorporate local agricultural practices and available resources to provide more relevant and actionable recommendations to farmers.
- Global Scale Deployment: Scale up the deployment of the project on a global level by leveraging cloud infrastructure and deploying instances of the application in multiple regions. Optimize the application for performance, scalability, and reliability to ensure seamless accessibility for users worldwide.
- Research and Innovation: Invest in ongoing research and innovation to stay at the forefront of agricultural technology and machine learning advancements. Collaborate with academic institutions, research organizations, and industry partners to explore new algorithms, techniques, and applications that can further revolutionize crop disease management and agricultural sustainability.

6.3 APPLICATION

With the help of the web application, farmers can quickly identify diseases in their potato plants that may be difficult to spot with the unaided eye. This gives them the ability to prevent possible catastrophes by taking preventative actions like applying pastes or spraying particular medications on the plants.

This project can also be beneficial to large-scale farming operations and major chip companies, like Lays, Doritos, as it can be used to track the health of their vast potato plantations.

Beyond aiding individual farmers, a potato disease classification web application can offer significant benefits across the agricultural sector:

ENHANCED FARM MANAGEMENT:

- **Early Disease Detection:** The programme detects diseases in their early stages, which are often imperceptible to the naked eye. This enables farmers to implement preventative measures such as fungicides or insecticides before serious harm occurs.
- **Targeted Treatment:** By precisely diagnosing the disease, growers can apply the most effective treatment, decreasing pesticide consumption and ensuring potato health.
- **Yield Optimisation:** Early disease intervention helps to prevent crop loss and provides higher yields, resulting in enhanced profitability for farmers.

LARGE SCALE FARMING AND AGRIBUSINESS:

- **Real-time Monitoring:** Large-scale potato farms can use the application to monitor their enormous potato plantings in real time. This allows them to promptly detect and control illness outbreaks, reducing their impact.
- **Data-Driven Decision Making:** The application collects and analyses illness prevalence data over time and across places. This data can be utilised to improve disease prevention by optimising planting tactics, crop rotation plans, and resource allocation.
- **Improved Supply Chain Management:** Chip manufacturers such as Lays and Doritos can integrate the application into their potato supply networks. This enables them to monitor the health of potato crops cultivated on contracted farms, ensuring a steady supply of high-quality potatoes.

6.4 LIMITATION

There are some disadvantages because the project depends on AI. The model may yield erroneous results if the image it is given is faulty or unclear, especially in the case of Late Blight. This is particularly difficult because these two diseases may be mistakenly classified due to a slight resemblance on the leaf. In potato disease categorization, depending only on AI-based algorithms has drawbacks. One of the key disadvantages is the susceptibility to erroneous results when the input photos are of poor quality or lack clarity, especially for diseases like Late Blight. Late Blight and other comparable diseases may have slight similarities in their symptoms, limiting correct classification. This resemblance raises the possibility of misclassification, since the AI model may struggle to distinguish between various diseases based solely on visual cues. As a result, misclassifications can lead to inaccurate diagnoses and inadequate management techniques, potentially aggravating crop losses and economic consequences. While AI has the potential to automate illness diagnosis in potatoes, careful assessment of its limits and supplementary approaches is necessary to provide trustworthy and accurate results.

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APPENDIX

Python: Developed in the latter part of the 1980s and named after Monty Python, Python is a generally supportive programming language used by a vast number of people to do tasks ranging from testing central processor at Intel, to managing Instagram, to creating video games using PyGame library, in addition to completing the photo handling such in our project.

Open CV: A free and open-source computer vision and artificial intelligence program OpenCV (OpenSource PC Vision Library) is the name of the library. OpenCV was created to provide a uniform foundation for PC vision applications and expedite their use of AI in commercial products. Given that OpenCV is a BSD-supported product, institutions can surely make use of and modify the code.

CNN: Within Empirical Education, a Convolutional Brain Association or CNN is a type of affiliation that is typically used for images or objects. Insisting and gathering. Significant advancement in this manner perceives things in an image by the use of a CNN. CNNs anticipate playing a huge role in several tasks/restrictions such as photo management problems, PC vision tasks like restriction and division, video assessment, and a genuine examination of oneself driving automobiles and conversing in a native tongue while operating it.

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