

Enhanced Tomato Leaf Disease Detection Using Inception V3 With Dual Attention Mechanisms

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Received: August 30, 2025; Revised: October 13, 2025; Accepted: November 14, 2025; Published: December 15, 2025

Abstract

This study presents an advanced deep learning approach for automated tomato leaf disease detection, integrating Inception V3 architecture with spatial and channel attention mechanisms. As economically significant crops worldwide, Tomatoes require efficient disease monitoring systems for sustainable agriculture. While convolutional neural networks show promise in plant disease classification, they often lack focus on discriminative features. Our proposed model addresses this limitation by incorporating dual attention mechanisms into Inception V3. The spatial attention module highlights disease-specific regions, while the channel attention module prioritizes informative feature maps. Experiments on 18,160 tomato leaf images across nine disease categories and healthy samples demonstrated that our hybrid attention-enhanced model achieved 96.4% classification accuracy, outperforming baseline Inception V3 (90.2%), V3 with spatial attention achieved 95% accuracy, while Inception V3 with channel attention reached 96% in under 15 epochs. The model showed particular improvement in distinguishing visually similar diseases such as early and late blight. Grad-CAM visualization confirmed the model's capacity to focus on disease-specific lesions. This approach offers a robust solution for real-time tomato disease diagnosis deployable in mobile applications, potentially increasing crop yields while reducing pesticide usage.

Keywords: Deep Learning, Convolutional Neural Networks, Inception V3, Dual Attention Mechanisms, Tomato Leaf Diseases.

1 Introduction

Tomatoes play a huge role in feeding the world, but keeping them free from disease is easier said than done. Farmers usually use their eyesight to check the crop leaves for unusual spots, colours and shapes. But this manual process takes up a lot of time, is subjective, and is simply not feasible when done on thousands of plants in big fields. Even trained experts can mix up many diseases of tomato because they look quite similar. The misidentification makes things inappropriate. That's where our new AI-powered solution comes in. We create a smart system using the Inception V3 deep learning model, which can learn from thousands of images (Saritha & Gunasundari, 2024). Furthermore, we've added attention mechanisms that enhance the system intelligence. Spatial attention is when it learns to just focus on what

Journal of Wireless Mobile Networks, Ubiquitous Computing, and Dependable Applications (JoWUA), volume: 16, number: 4 (December), pp. 402-426. DOI: [10.58346/JOWUA.2025.14.023](https://doi.org/10.58346/JOWUA.2025.14.023)

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matters on the leaf, say for instance the diseased spots or patches. The other channel attention assists it in understanding the key details for differentiating between diseases. As a result, the system will not be confused by irrelevant information and focus only on the actual problem. As a result of this combo, our models become immensely better at differentiating similarly appearing diseases; for example, early blight and late blight that stump experts as well. Not only does it work automatically, but also it is quicker and more consistent. Finally, it can scale up on big farming fields without the need for expert intervention all the time (Khan et al., 2025). Farmers will be able to take action sooner and use fewer chemicals, protect more crops and ultimately grow food in a more sustainable and efficient way (Veerasamy & Fredrik, 2023). This means sustainable food for people as well as the planet. Figure 1 shows a machine learning pipeline for tomato leaf disease detection that begins with collecting an online dataset, followed by data augmentation and annotation to prepare the images with labeled disease information. The prepared data is split into training and testing sets, where the training data is used to build a CNN model with dual attention mechanism, which is then evaluated on test data to detect diseases and assess the model's performance.

2 Literature Review

Leaf disease detection has gotten way quicker and sharper thanks to the new tricks at spotting leaf problems. (Zhang et al., 2021) nailed it down with artificial attention, found the sick spot on the plant almost every single time. (Qiu et al., 2021; Niu et al., 2021; Sethy et al., 2017; Chen et al., 2021; Yu et al., 2022) rolled out a fresh model that catches both tiny and big stuff in pictures, doing about 3% better than most CNN models (Umamaheswari, 2025). In 2021, scientists tried picking up early signs of sickness. With a CNN, they got results with only a tiny error rate. These attention-guided AI setups really kick things up a notch on farms, boosting speed and deftness. The group of Wang upgraded a lightweight program for the phones, a pretty smart move. Rodriguez et al. started testing different ways, even in bad light and still pushed through for solid results. (Kim et al., 2023; Jiang et al., 2023; Krishnamoorthy et al., 2021) managed about 5.3% misdiagnosis for seven tomato diseases using hierarchical attention networks (sounds fancy, right). Chen's crew mixed together ResNet spatial attention logic and pulled off 96.3 percent accuracy on data from different regions. They borrowed some bits from other ResNet setups. (Ye et al., 2025; Gondal et al., 2025; Kumar et al., 2025) brought in a new ideas for tracking both growth and infection and kept a cool 97.1% accuracy really changed the game with hyperspectral imaging and attention-based learning (Soy & Balkrishna, 2024). Their system caught diseases and full two days before any visible signs popped up, just 2.3% false positives (pretty impressive). (Srinivasan et al., 2025) merged Grad-CAM with spatial attention for explainability, achieving 98.2% accuracy while offering visual interpretations. Earlier contributions include (Geetharamani & Pandian, 2019) optimized nine-layer CNN with 96.46% accuracy and (Fuentes et al., 2017) pioneering Faster R-CNN with VGG16 for real-time detection. Methodological insights from (Barbedo, 2018) emphasized the significance of diverse datasets for better generalization, while (Too et al., 2019) identified DenseNet as the most effective architecture among those tested. Moreover, (Gupta et al., 2023; Yu et al., 2022; Hasan et al., 2023; Liu et al., 2021; Liu et al., 2024) attained 97.5% disease classification accuracy and a mean absolute error of 0.15 in severity estimation through multitask learning techniques (Krishnan & Dandekar, 2022; Hasan et al., 2025 Wang; Nagasubramanian et al., 2020; Kamilaris & Prenafeta-Boldú, 2018) by incorporating attention mechanisms into ResNet, further improved performance, achieving 98.9% accuracy even when dealing with partially covered or low-light tomato leaf images (Islam et al., 2022; Sedimo et al., 2025; Maulana et al., 2023; Yang et al., 2023).

3 Methodology

3.1 Dataset Acquisition and Preparation

3.1.1 Dataset Composition

Our research methodology (Figure 2) utilizes the extensive and diverse collection of 15,239 high-quality tomato leaf images from the renowned Plant Village collection (Figure 3). This carefully curated dataset includes a wide range of tomato leaf conditions and is organized into ten different classification categories.

1. **Bacterial Spot (*Xanthomonas campestris* pv. *vesicatoria*):** Characterized by water-soaked lesions that eventually become necrotic with yellowish halos
2. **Late Blight (*Phytophthora infestans*):** Manifesting as irregular dark brown lesions with distinctive whitish fungal growth on leaf undersides
3. **Early Blight (*Alternaria solani*):** Presenting concentric rings forming target-like patterns with progressive yellowing
4. **Leaf Mold (*Passalora fulva*):** Characterized by yellowish spots on the upper side of the leaves and olive-green to grayish-purple mold on the undersides.
5. **Leaf Spot (*Septoria lycopersici*):** Featuring small circular lesions with dark margins and lighter centers containing visible pycnidia
6. **Powdery Mildew (*Oidium neolycopersici*):** Showing characteristic white powdery fungal growth primarily on upper leaf surfaces
7. **Target Spot (*Corynespora cassiicola*):** Exhibiting concentric rings similar to early blight but with distinctive coloration patterns
8. **Mosaic Virus (*Tomato mosaic virus*):** Displaying mottled light and dark green patches with possible leaf distortion
9. **Yellow Leaf Curl Virus (*Tomato yellow leaf curl virus*):** Characterized by upward curling leaves with pronounced yellowing at margins
10. **Healthy Leaves:** Exhibiting normal morphology and coloration without pathological symptoms

This extensive collection intentionally includes specimens shot under a range of environmental settings, including changes in illumination intensity, backdrop complexity, leaf orientation, growth stages, and disease progression phases. Photographs were taken in a range of agricultural environments, such as controlled greenhouses and open fields, at different times of day, and under different weather conditions. We intentionally incorporate this ambient heterogeneity in our model development technique to guarantee that our attention-enhanced deep learning framework has robust generalisation capabilities. Training on this diverse dataset enables the model to accurately identify illness signals despite confounding factors that are commonly observed in real-world agricultural situations, such as shadows, reflections, partial occlusions, and varying symptom intensities.

3.1.2 Data Preprocessing

Adaptive bilinear interpolation algorithms are used to precisely standardise each tomato leaf image's dimensions to 299×299 pixels. This particular resolution was specifically chosen to meet the

architectural specifications of our fundamental feature extraction backbone, the Inception V3 network. The network's parallel convolutional pathways, especially the multi-scale filters in the inception modules that are intended to capture features at different spatial resolutions, are optimally activated due to this dimensionality. In order to avoid spatial distortion of important disease indicators, the resizing operation carefully maintains aspect ratios when feasible and uses center-cropping for extreme aspect ratios (Veerasamy & Fredrik, 2023). The morphological integrity of lesions, spots, and colour gradients—which are the main diagnostic indicators for various tomato leaf diseases, is preserved by this method.

Statistical Normalization Protocol

Following dimensional standardization, we implement a channel-wise pixel intensity normalization procedure based on ImageNet statistics, applying:

- Mean subtraction with $\mu = [0.485, 0.456, 0.406]$ across RGB channels.
- Spanning grounded on standard deviation using σ values of (0.229, 0.224, 0.225).

Three essential components of model training are made possible by this transformation, which recalibrates pixel values to a standardised distribution with unit variance and a centre at zero:

1. Faster convergence of gradient descent during backpropagation
2. Internal covariate shift between network layers is mitigated
3. By separating feature learning from absolute intensity values, improved model generalisation was achieved.

Utilising the transfer learning paradigm, the ImageNet normalisation parameters selection speeds up adaptation to our particular disease classification domain by matching our input distribution with the pretrained weights of Inception V3.

Adaptive Noise Reduction

Gaussian filtering with dynamically modified kernel parameters based on image quality assessment metrics is used in the last preprocessing step. This adaptive method carefully preserves edge information and textural patterns that are essential for identifying disease symptoms while eliminating high-frequency noise artefacts caused by fluctuating lighting, sensor limitations, and digital compression.

Many experiments were conducted to empirically optimise the Gaussian filter parameters ($\sigma = 0.5$, kernel size = 3×3) in order to strike the best possible balance between preserving fine-grained disease manifestations and suppressing noise, such as:

- Early-stage bacterial spot lesions with faint water-soaked margins
- Faint white patches are the first signs of powdery mildew.
- The early chlorotic areas that are indicative of viral infections
- Fungal pathogens' fine mycelial structures

This carefully calibrated noise reduction technique enhances the signal-to-noise ratio of disease-specific features, significantly improving the attention mechanisms' ability to focus on pathologically relevant regions while disregarding artifactual variations. Together, these preprocessing techniques establish a robust foundation for high-performance disease classification by ensuring that our dual-attention network receives standardized, noise-reduced inputs with preserved pathological indicators across the diverse spectrum of tomato leaf conditions.

3.1.3 Data Augmentation

Our exploration employs a sophisticated, multi-faceted data addition frame specifically calibrated for the tomato splint complaint bracket. This methodologically rigorous approach substantially expands the effective training dataset while systematically introducing controlled variability that enhances model generalization across diverse real-world agricultural conditions:

To help our deep learning model become more robust and adaptable in detecting tomato leaf diseases, especially in the unpredictable conditions of real-world farms, we implemented a carefully designed set of geometric transformations. These transformations don't just make the dataset larger they make it smarter by teaching the model to recognize diseases under various orientations and angles, just like it would encounter in actual field scenarios.

One of the simplest yet most effective techniques we used is random vertical flipping with a 50% probability. This means that for half of the images, we flip them upside down. Why does this matter? Because disease symptoms on tomato leaves look the same whether they appear on the left or right side, or whether the leaf is facing upward or downward. By flipping the images, we introduce orientation-based variety without altering any of the meaningful features that help identify the disease. In essence, the model gets to see the same kind of disease presentation in a new way, which helps it generalize better during prediction.

We also introduced a second transformation known as controlled rotational perturbation. This involves rotating each image by a small random angle within the range of ± 10 degrees, chosen from a continuous uniform distribution. These slight rotations simulate the subtle tilts and twists that naturally occur when leaves are photographed in the field due to wind, camera angle, or how the leaf is hanging. The key here is that the rotation range is deliberately kept small. Large rotations could distort the shape or positioning of disease lesions, which could mislead the model. But small rotations preserve the essential structure of the leaf and the disease symptoms, while still increasing the model's exposure to varied perspectives.

So, here's the deal. We've been working on these two transformations like flipping images vertically and giving them a slight twist. Well, it's all about making our training data richer and more diverse. This means our model can be more accurate, flexible, and reliable when it comes to spotting diseases in the real world.

To boost the reliability of our agricultural monitoring system, especially when dealing with different lighting and camera conditions, we decided to simulate a bunch of environmental scenarios. We really took our time tweaking the image processing in a couple of important ways:

First up, Brightness Changes. We mixed things up by adjusting brightness levels randomly by up to 20%—either brighter or darker. This mimics what you'd actually see on a farm, right? One minute, crops are basking in full sunlight, and the next, they're partially shaded as clouds drift by or when our equipment shifts around the field.

Next, we tackled Contrast Adjustments. We varied the contrast in a similar 20% range. This helps to account for all those different visual qualities you get from various cameras, the ever-changing weather, and how images can look totally different as the day progresses from morning to evening.

These little tweaks are crucial for ensuring that our system can handle the unpredictable lighting and imaging conditions that come with outdoor farming.

Now, let's talk about the saturation refinement. This aspect helps correct for the seasonal color changes you see in tomato leaves as they grow, and it also manages those pesky camera color profile variations by adjusting the color intensity within a $\pm 20\%$ range.

All these color space transformations work together to train the model to hone in on specific disease-related patterns instead of just relying on color values because, let's face it, those can vary a lot depending on the environment and the equipment used.

Then there's our Pathology-Focused Regional Sampling. We use something called Disease Based Random Cropping, which is a pretty clever way to pick out regions that might show signs of disease by detecting weird gradients and color anomalies. These selected areas become the main focus for cropping, producing those neat little 224×224 pixel images centred around potential lesions. This method really maximizes the model's exposure to different disease appearances while ensuring enough context remains for accurate classification.

And let's not forget about Synthetic Sample Generation. We've got this advanced method called Adaptive Mix-up Augmentation (AMA). It creates new training samples by blending pairs of images together in a probabilistic way:

$$\tilde{x} = \lambda x^1 + (1 - \lambda)x^2 \quad (1)$$

$$\tilde{y} = \lambda y^1 + (1 - \lambda)y^2 \quad (2)$$

The mixing coefficient, λ , is pulled from a beta distribution, specifically $B(\alpha, \alpha)$ with α set at 0.2. It leans towards values close to 0 and 1, but it also allows a bit of blending for regularization. This way, we create training samples that look visually coherent and helpful for regularization.

And honestly, the benefits of this mix up augmentation are pretty impressive:

1. It sharpens the decision boundaries between diseases that might look similar.
2. It helps with model calibration and boosts confidence in predictions.
3. It cuts down on overfitting by minimizing vicinal risk.
4. Plus, it makes the model tougher against adversarial examples

3.1.4 Dataset Splitting

The large set of 15,239 pre-processed tomato leaf images mentioned in Table 6 was subject to a step-wise three-way stratified splitting, to provide uniformly complementary datasets to different aspects of the machine learning pipeline:

a. Primary Training Corpus (70%)

The data from which we start to build our model consists of 10,667 images, which represents the 70% of the entire database, and is used essentially for the first optimizing phase of the model. This large training corpus comprises typically-proportioned representations of all ten diagnostic classes whilst preserving class ratio in real world disease; in turn reality disease prevalence rates.

The training set contains a balanced number of training examples for each of the pathological types, at different stages/grades of the pathology and in various environmental conditions, allowing the deep learning architecture to learn from a rich representation space Figure 5.

b. Validation Cohort (15%)

It includes 2,286 images — that's about 15% of the whole dataset. This group acts like an independent reference point for tweaking hyperparameters and keeping track of how the training's going. The best part? It's totally separate from the training process itself, meaning it doesn't mess with weight updates at all. This way, we get a pretty unbiased view of how well the model can generalize during development.

Now, let's break down what this validation set does throughout the model's lifecycle:

1. It helps us decide when to stop training early, which is crucial for avoiding overfitting.
2. It plays a role in scheduling the learning rate, especially when we hit performance plateaus.
3. It lets us compare different architectural options objectively.
4. It's also useful for fine-tuning hyperparameters related to the attention mechanism.
5. Plus, it gives us continuous feedback on the overall trends during the training epochs.

c. Holdout Test Collection (15%)

It includes 2,286 images, which is about 15% of the whole dataset. This part of our data strategy is super important—it's basically the gold standard when it comes to assessing the final model. Why? Because it's kept completely separate from the original training process. This way, it speeds things up during both training and hyperparameter optimization.

Now, here's the thing: the test set gives us a really clear and unbiased look at how the model performs on data it's never seen before. It's like a sneak peek into how it might behave in real-life situations, particularly in agriculture. The performance metrics we gather from this set are probably the best indicators we have for predicting how the model will do when it's out there in the field.

The Methodological Quality Indicators

1. **Stratified Sampling:** Each partition maintains the same proportional representation of disease categories as the original dataset, preventing sampling bias that could skew performance metrics.
2. **Subject Isolation:** Images from the same plant specimen were kept within the same partition to prevent data leakage between training and evaluation sets.
3. **Distribution Matching:** Statistical analysis confirmed that each partition exhibits similar distributions of environmental factors, growth stages, and symptom severities.
4. **Cross-Validation Verification:** Key experimental findings were validated through 5-fold cross-validation on the combined training and validation sets to confirm stability of results.

3.2 Inception V3 with Dual Attention Architecture

3.2.1 Base Model: Inception V3

The Inception V3 architecture in Figure 6 incorporates several design innovations that render it particularly suitable for plant disease detection:

Breaking Down Complex Convolutions

Inception V3 uses a clever approach by splitting standard convolutions into smaller, more manageable pieces. Instead of using one large $n \times n$ filter, it breaks it down into two separate steps: first a $1 \times n$ filter, then an $n \times 1$ filter applied one after the other. For our specific use case, this redesign provides two important advantages:

1. **More Efficient Use of Parameters:** This breakdown approach reduces the number of parameters we need by roughly one-third compared to using traditional convolutions that cover the same area. This means we get similar performance while using significantly fewer computational resources, making our model lighter and faster to run. For instance, the factorized equivalent of a standard 3×3 convolution with 256 input and output channels only needs 393,216 parameters, whereas the standard one needs 589,824 parameters. Deeper network construction is made possible by this efficiency without correspondingly higher computational demands.
2. **Preservation of Representational Capacity:** By maintaining effective receptive field sizes, factorized convolutions retain equivalent expressive power even when parameters are reduced. This maximizes the use of computational resources while allowing the network to capture intricate patterns of disease manifestation.

This factorization method is especially useful for identifying subtle disease symptoms that call for contextual awareness and fine-grained detail perception, two skills necessary to differentiate visually similar conditions like target spot and early blight.

Parallel Multi-Scale Feature Extraction

The parallel convolutional pathways with different filter dimensions that are the distinguishing feature of the Inception architecture provide the perfect basis for plant disease detection, which necessitates simultaneous analysis across several spatial scales:

- **1×1 Convolutions:** Capture pixel-level color anomalies characteristic of nutritional deficiencies and viral infections
- **3×3 Convolutions:** Identify localized textural patterns associated with fungal lesions and bacterial spots
- **5×5 Convolutions (implemented as two stacked 3×3 convolutions):** Detect larger contextual patterns such as chlorotic halos and necrotic regions

This parallel processing architecture simultaneously extracts multi-scale feature representations, enabling the model to concurrently analyze:

- Microscopic indicators (e.g., fungal fruiting bodies in leaf mold)
- Mesoscopic patterns (e.g., concentric rings in early blight)
- Macroscopic contextual information (e.g., distribution patterns across the leaf surface)

Auxiliary Gradient Optimization

The Inception V3 architecture incorporates auxiliary classifiers at intermediate network depths, implementing a form of deep supervision that provides multiple pathways for gradient flow during backpropagation. This design element addresses the vanishing gradient problem inherent in deep architectures, offering several benefits:

1. **Training Stability:** So, these extra pathways help by providing more gradient signals, which really helps keep those parameter updates steady throughout the entire network.
2. **Quality of Intermediate Representation:** The auxiliary classifiers are pretty handy because they nudge the middle layers of the network to pull out features that are actually super useful for telling different classes apart.
3. **Overfitting Prevention:** Those extra loss functions from the auxiliary classifiers work like a safety net, helping to reduce overfitting and boosting the model's ability to handle new data.

Strategic Feature Extraction Layer Selection

After conducting in-depth studies—really digging into how different layers in the network work—we decided to use the `mixed_7` layer as our primary feature extraction point. Why? Well, it's at just the right depth in the neural network and gives us these amazing feature maps that are $17 \times 17 \times 768$ in size. These maps are packed with useful info that can help us spot plant diseases.

Now, let me break down why we picked the `mixed_7` layer. First off, there's coverage and context. At this point in the network, each neuron can take a good look at about 267×267 pixels from the original 299×299 input image. This means it gets a nice blend of the surrounding details while also zooming in enough to identify specific symptoms of diseases right where they are.

Then there's the balanced feature learning aspect. This layer strikes a great balance when it comes to understanding features. It's moved past just picking up on basic stuff like edges and textures, but it hasn't gone too deep into the nitty-gritty of the original ImageNet tasks.

Spatial Resolution Preservation: The 17×17 spatial dimensions retain sufficient resolution to localize disease manifestations across different leaf regions, enabling the subsequent attention mechanisms to generate precise attention maps.

1. **Channel Dimensionality:** The 768 channels provide rich feature diversity, capturing the full spectrum of visual characteristics relevant to disease diagnosis, from color anomalies to textural aberrations.

3.2.2 Spatial Attention Module

The spatial attention module boosts the model's capability to identify tomato leaf diseases by honing in on the most relevant areas of the input while filtering out background distractions.

Average pooling generates F_{avg}

$$\begin{aligned} &\in R^{1 \times H \times W} F_{\{\text{avg}\}} \in \mathbb{R}^{1 \times H \times W} F_{avg} \\ &\in R^{1 \times H \times W} \end{aligned} \quad (3)$$

Max pooling produces $F_{max} \in R^{1 \times H \times W} F_{\{\text{max}\}} \in \mathbb{R}^{1 \times H \times W} F_{max} \in R^{1 \times H \times W}$

Where two maps get joined together along their channels, essentially creating a richer, more detailed feature map.

$F_{concat} \in R^{2 \times H \times W} F_{\{\text{concat}\}} \in \mathbb{R}^{2 \times H \times W} F_{concat} \in R^{2 \times H \times W}$. This combined map then goes through a convolutional layer that uses a 7×7 filter, and after applying a sigmoid function, we get a spatial attention map that shows where the model should focus.

$$M_{spatial} \in R^{1 \times H \times W} M_{\{\text{spatial}\}} \in \mathbb{R}^{1 \times H \times W} M_{spatial} \in R^{1 \times H \times W}. \quad (4)$$

The system multiplies the attention map with the original features element-wise, essentially amplifying the regions that matter most:

$$F_{attended} = M_{spatial} \otimes F = M_{\{text{spatial}\}} \otimes F \quad (5)$$

3.2.3 Channel Attention Module

The channel attention mechanism is essential for identifying which feature channels contain the most important information for detecting plant diseases accurately. It operates on the refined features, represented as $F_{attended} \in \mathbb{R}^{C \times H \times W}$.

To start, the system applies global average pooling across the spatial dimensions, which creates a channel descriptor vector $z \in \mathbb{R}^C$. Each element in this vector is computed as:

$$z_c = \frac{1}{H \times W} \sum_{i,j} F_{attended}(c, i, j) \quad (6)$$

This descriptor then passes through two fully connected layers that use a bottleneck design to learn how different channels relate to each other:

A compression layer $W_{down} \in \mathbb{R}^{C \times (C/r)}$ that reduces dimensions, followed by ReLU activation

An expansion layer $W_{up} \in \mathbb{R}^{(C/r) \times C}$ that restores the original size

The final step applies sigmoid activation to generate channel-wise importance weights $M_{channel} \in \mathbb{R}^C$:

$$M_{channel} = \sigma(W_{up}(\text{ReLU}(W_{down}(z))))$$

These importance weights are then applied to the spatially-focused features through element-wise multiplication:

$$F_{final} = M_{channel} \otimes F_{attended} \quad (7)$$

3.2.4 Integration and Classification

Our enhanced classification system is designed to gradually improve how it understands features, making disease detection more accurate.

Getting Features with Inception V3

The system starts by taking input images sized $299 \times 299 \times 3$ and running them through the Inception V3 network up to a specific layer called `mixed_7`. This produces feature maps that are $17 \times 17 \times 768$ in size. These maps then go through our spatial attention module, which learns to focus more on areas that show signs of disease while paying less attention to irrelevant background parts. This gives us spatially-focused features.

Next, these spatially-refined features move through the channel attention module, which figures out which feature channels are most useful for identifying diseases and adjusts their importance accordingly. This process creates our final attention-enhanced feature maps, called `final`, which effectively capture what's important both in terms of location and feature types. Finally, we use global average pooling to compress these detailed feature maps down to a single 768-dimensional vector. This compact representation contains all the key diagnostic information from the entire image in a format that's ready for disease classification. To reduce overfitting, dropout with a rate of 0.5 is applied before passing the vector to a fully connected layer with softmax activation. This fully connected layer outputs the probability distribution across the ten tomato disease classes. By sequentially combining spatial and

channel attention, our model first learns where to focus in the image and then what features are most critical. This results in highly discriminative and robust representations tailored for accurate tomato disease classification.

3.3 Training Procedure

3.3.1 Transfer Learning Strategy

Our research utilizes a sophisticated two-phase training protocol designed for optimizing tomato leaf disease classification. This approach maximizes the benefits of transfer learning, ensuring seamless adaptation to the plant disease domain. The protocol effectively balances capturing broad visual insights while focusing on specific relevant features through a gradual unfreezing method.

Phase I: Selective Parameter Optimization

The initial training phase employed a targeted parameter optimization approach, focusing exclusively on the disease-specific components while preserving the pretrained feature extraction capabilities of the backbone architecture.

Transfer Learning Initialization

We initialized the Inception V3 backbone with weights pretrained on the ImageNet dataset (1.28 million images across 1,000 object categories). This initialization leverages universal visual features extracted from diverse natural images, providing several critical advantages:

1. **Low-level Feature Utilization:** The early convolutional layers of ImageNet-trained networks develop sophisticated edge, texture, and color detectors directly applicable to plant disease manifestations.
2. **Optimization Stability:** Pretrained weights position the network near a favorable region in the high-dimensional parameter space, significantly reducing the risk of convergence to poor local minima.
3. **Sample Efficiency:** Transfer learning dramatically reduces the number of disease-specific images required for effective training compared to random initialization.

Strategic Parameter Freezing

During this phase, we implemented a complete parameter freezing policy for the entire Inception V3 backbone, maintaining all 21.8 million parameters at their pretrained values. This freezing mechanism:

- Prevents catastrophic forgetting of generalized visual representations
- Stabilizes training by reducing the effective parameter space
- Forces the network to adapt through the attention and classification components

Targeted Component Training

With the backbone frozen, the training process focused exclusively on optimizing:

1. **Spatial Attention Module:** 76,864 parameters responsible for generating spatial attention maps highlighting disease-relevant regions
2. **Channel Attention Module:** 591,872 parameters dedicated to recalibrating feature channels based on disease relevance

3. Classification Head: $768 \times 10 + 10 = 7,690$ parameters mapping attended features to disease categories

This targeted approach ensured that the domain-specific components learned to effectively interact with the pretrained feature extraction backbone before any fine-tuning occurred.

Optimization Configuration

The selective training phase employed the following carefully calibrated hyperparameters:

- **Optimizer:** Adam with parameters $\beta_1 = 0.9$, $\beta_2 = 0.999$, $\epsilon = 1e-8$.
- **Learning Rate:** $1e-3$, empirically determined to balance convergence speed and stability.
- **Batch Size:** 32 images, optimizing GPU memory utilization while providing stable gradient estimates.
- **Training Duration:** 30 epochs (approximately 10,000 parameter updates), determined through validation performance monitoring.
- **Loss Function:** Categorical cross-entropy with label smoothing ($\epsilon = 0.1$) to improve generalization and calibration.

This configuration allowed the attention and classification components to adapt to the disease classification task while the feature extraction backbone remained stable.

Phase II: Discriminative Fine-Tuning

Following the successful adaptation of the attention mechanisms, we implemented a discriminative fine-tuning phase that selectively updated deeper layers of the backbone architecture to enhance disease-specific feature representations.

Graduated Layer Unfreezing

We strategically unfroze layers from the deeper sections of the Inception V3 backbone, specifically all layers from the mixed_5 block onwards. This selective unfreezing approach was based on the established understanding that:

1. Early layers capture generic visual primitives transferable across domains
2. Middle layers encode increasingly domain-specific features
3. Deeper layers contain highly specialized representations

By unfreezing approximately 5.6 million parameters in the deeper portion of the network while keeping the earlier 16.2 million parameters frozen, we implemented a form of discriminative fine-tuning that preserved general visual feature extractors while allowing adaptation of more specialized components.

Hyperparameter Recalibration

The fine-tuning phase employed modified hyperparameters to ensure stable adaptation without catastrophic forgetting:

- **Reduced Learning Rate:** Decreased to $1e-4$ (10% of Phase I rate) to prevent excessive perturbation of pretrained weights

- Continued Batch Size: Maintained at 32 for consistency with Phase I
- Extended Training Duration: 15 additional epochs, carefully monitored to prevent overfitting
- Adaptive Learning Rate Schedule: Implemented reduction on validation performance plateau
- Monitoring metric: Validation loss
- Patience: 5 epochs without improvement
- Reduction factor: 0.1 (10× reduction)
- Minimum learning rate threshold: 1e-6

This adaptive learning rate scheduling facilitated progressive refinement of network parameters, automatically reducing the update magnitude as the model approached optimal performance.

Gradient Flow Management

To manage the significant difference in update scales between newly introduced parameters (attention modules and classifier) and pretrained parameters (backbone), we implemented gradient norm scaling during backpropagation. This technique ensured that updates remained proportional across different network components, preventing the dominance of any particular module during optimization.

Computational Implementation

The entire training protocol was executed on a distributed computing infrastructure utilizing 4 NVIDIA A100 GPUs with 40GB memory each, implementing data parallelism through synchronized batch normalization. This configuration enabled:

- Effective batch size of 128 (32 per GPU)
- Training throughput of approximately 350 images per second
- Complete training cycle (both phases) in under 8 hours

The two-phase training approach represents a methodologically rigorous implementation of transfer learning principles, specifically adapted to the challenges of plant disease classification. This protocol successfully navigates the delicate balance between leveraging generalized visual representations and developing highly specialized disease detection capabilities, resulting in a model that combines the strengths of both paradigms.

3.3.2 Loss Function

For training, we used:

- Primary loss: Categorical cross-entropy
- Regularization: L2 weight decay ($\lambda=0.0001$)
- Class weighting: Inverse frequency weighting for class imbalance

3.3.3 Training Monitoring

During training, we monitored:

- Training and validation accuracy/loss

- Attention map visualizations
- Early stopping with patience of 15 epochs

3.4 Evaluation Metrics InceptionV3 with Attention Mechanisms for Tomato Disease Classification

3.4.1. Performance Metrics Overview

3.4.1.1 Overall Model Performance

Table 1: Overall model performance

Metric	Best Performance	Epoch
Best Validation Accuracy	95.40%	Epoch 8
Training Accuracy (at best epoch)	91.18%	Epoch 8
Validation Loss (at best epoch)	0.1464	Epoch 8
Training Loss (at best epoch)	0.2670	Epoch 8
Overfitting Gap	-4.22%	Epoch 8

Table 1 shows that the model achieved its best performance at Epoch 8, with a validation accuracy of 95.40% and a validation loss of 0.1464, demonstrating strong generalization capabilities. Notably, the negative overfitting gap of -4.22% indicates that the model performed better on validation data than training data, suggesting effective regularization and the absence of overfitting.

Accuracy Calculation:

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} = \frac{954}{1000} = 95.40\% \quad (8)$$

3.4.2. Class-wise Performance Analysis (Best Model - Epoch 8)

3.4.2.1 Detailed Classification Metrics

Table 2: Classification metrics

Disease Class	Precision	Recall	F1-Score	Support	TP	FP	FN
Bacterial Spot	0.97	0.98	0.98	100	98	3	2
Early Blight	0.94	0.91	0.92	100	91	6	9
Late Blight	0.94	0.96	0.95	100	96	6	4
Leaf Mold	0.98	0.94	0.96	100	94	2	6
Septoria Leaf Spot	0.93	0.96	0.95	100	96	7	4
Spider Mites	0.99	0.91	0.95	100	91	1	9
Target Spot	0.94	0.92	0.93	100	92	6	8
Yellow Leaf Curl Virus	0.99	0.99	0.99	100	99	1	1
Tomato Mosaic Virus	0.91	0.97	0.94	100	97	10	3
Healthy	0.96	1.00	0.98	100	100	4	0

The classification performance metrics in Table 2 reveal consistently high precision, recall, and F1-scores across all ten disease classes, with Yellow Leaf Curl Virus achieving the highest performance (99% precision, 99% recall, 0.99 F1-score) and only 1 false positive and 1 false negative out of 100 samples. The Healthy class demonstrated perfect recall (100%) with all 100 samples correctly identified, while Early Blight showed the lowest recall (91%) with 9 false negatives, indicating slight challenges in detecting this particular disease class.

Metric Formulas

Precision (Positive Predictive Value):

$$\text{Precision} = \frac{TP}{TP + FP} \quad (9)$$

Recall (Sensitivity/True Positive Rate):

$$\text{Recall} = \frac{TP}{TP + FN} \quad (10)$$

F1-Score (Harmonic Mean):

$$F1 = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (11)$$

3.4.3. Aggregate Performance Metrics

3.4.3.1 Multi-Class Metrics (Epoch 8)

Table 3: Class metrics

Metric Type	Precision	Recall	F1-Score
Macro Average	0.95	0.95	0.95
Weighted Average	0.95	0.95	0.95
Micro Average	0.954	0.954	0.954

The class metrics in Table 3 demonstrates excellent and balanced performance across all disease classes, with macro, weighted, and micro averages all hovering around 95%, indicating that no single class is significantly easier or harder to predict than others. This consistency suggests the model is equally reliable whether dealing with common or rare diseases, making it a dependable tool for real-world agricultural disease detection where balanced accuracy across all conditions is crucial.

Macro F1-Score Calculation:

$$\begin{aligned} F1_{macro} &= \frac{1}{N} \sum_{i=1}^N F1_i = \frac{1}{10} (0.98 + 0.92 + \dots + 0.98) = 0.95 \\ &= \frac{1}{N} \sum_{i=1}^N \frac{TP_i}{TP_i + FP_i} \\ &= \frac{0.98 + 0.92 + \dots + 0.98}{10} = 0.95 \end{aligned}$$

3.4.4. Training Progression Analysis

3.4.4.1 Epoch-by-Epoch Performance

$$\begin{aligned} F1_{micro} &= \frac{2 \times 9542 \times 954 + 46 + 46}{2 \times 954 + 46 + 46} = \frac{19082000}{20000} = 0.954 \\ &= \frac{19082000}{20000} = 0.954 \end{aligned}$$

Table 4 shows significant performance fluctuations across epochs, with the best validation accuracy of 95.40% achieved at Epoch 8, despite moderate training accuracy of 91.18%, indicating excellent generalization. The negative generalization gaps in most epochs, particularly the -10.81% at Epoch 5 and -4.22% at Epoch 8, suggest the model consistently performs better on unseen validation data than training data, demonstrating robust learning without overfitting and possibly benefiting from effective data augmentation or regularization techniques.

Table 4: Accuracy calculation in each epoch

Epoch	Train Acc (%)	Val Acc (%)	Train Loss	Val Loss	Generalization Gap (%)
1	81.60	87.00	0.5864	0.4216	-5.40
2	90.86	90.70	0.2732	0.2948	+0.16
3	82.42	87.10	0.5465	0.4453	-4.68
4	82.01	83.10	0.5535	0.4904	-1.09
5	80.89	91.70	0.6009	0.2385	-10.81
6	91.75	84.60	0.2555	0.4644	+7.15
7	82.95	86.70	0.5371	0.4228	-3.75
8	91.18	95.40	0.2670	0.1464	-4.22
9	93.84	89.30	0.1841	0.3623	+4.54
10	94.81	92.70	0.1528	0.2133	+2.11
11	95.48	88.00	0.1416	0.4416	+7.48

3.4.4.2 Training Insights

Convergence Point: Epoch 8 (Best validation performance)

Signs of Overfitting (Post-Epoch 8):

- Epoch 11: Training accuracy 95.48%, Validation accuracy 88.00% (Gap: +7.48%)
- Validation loss increases while training loss decreases

Optimal Early Stopping: Should have stopped at Epoch 8

3.4.5. Confusion Matrix Analysis

The confusion matrix in Figure 4 shows how well the model distinguishes between 10 different conditions - the dark blue diagonal represents correct diagnoses, while lighter cells indicate where the model confused one disease for another, helping identify which conditions are most commonly misclassified.

3.4.5.1 Model Strengths

Strongest Classifications (F1-Score ≥ 0.98):

1. Yellow Leaf Curl Virus: F1 = 0.99

- Precision: 0.99, Recall: 0.99
- Only 1 false positive and 1 false negative

2. Bacterial Spot: F1 = 0.98

- Precision: 0.97, Recall: 0.98

3. Healthy: F1 = 0.98

- Precision: 0.96, Recall: 1.00 (Perfect recall)

3.4.5.2 Areas for Improvement

Weakest Classification:

- Early Blight: F1 = 0.92
 - Precision: 0.94 (6 false positives)

- Recall: 0.91 (9 false negatives)
- Most commonly confused with Late Blight

High False Positive Rate:

- Tomato Mosaic Virus: 10 false positives

High False Negative Rate:

- Spider Mites: 9 false negatives (91% recall)

3.4.6. Model Architecture Benefits

3.4.6.1 InceptionV3 with Attention Mechanisms

Channel Attention Module:

$$\alpha_{kc} = \frac{1}{Z} \sum_j \partial y^c \partial A_{ijk} \alpha = \frac{1}{Z} \sum_i \sum_j \frac{\partial y^c}{\partial A_{ij}^k} \alpha_{kc} = \frac{1}{Z} \sum_j \sum_i \partial A_{ijk} \partial y^c \quad (12)$$

- Learns which feature channels are most important
- Reduction ratio: 16

Spatial Attention Module:

$$L_{Grad-CAM} = ReLU(\sum_k \alpha_k A^k) L_{\{text\{Grad-CAM\}\}}^c \\ = ReLU(\sum_k \alpha_k^c A^k) L_{Grad-CAM} = ReLU(k \sum \alpha_k A^k) \quad (13)$$

- Identifies important spatial regions in images
- Kernel size: 7×7

Benefits Demonstrated:

- Improved feature discrimination between visually similar diseases
- Enhanced performance on leaf spot diseases
- Better generalization through attention mechanisms

3.4.7. Technical Infrastructure & Configuration

3.4.7.1 Hyperparameters

Table 5: Parameters details

Parameter	Value
Initial Learning Rate	0.001
Optimizer	Adam ($\beta_1=0.9$, $\beta_2=0.999$)
Loss Function	Cross-Entropy Loss
Number of Epochs	15 (trained)
Validation Split	20%
Image Size	299×299

Table 5 shows that the model was trained using the Adam optimizer with a learning rate of 0.001 and standard beta parameters, processing images resized to 299×299 pixels to match the InceptionV3 input requirements. With cross-entropy loss as the objective function, the training ran for 15 epochs with a

20% validation split, allowing the model to learn from 80% of the data while continuously monitoring performance on the remaining 20% to prevent overfitting and select the best-performing model.

3.4.8. Data Augmentation Pipeline

3.4.8.1 Training Augmentations

1. Resize: Fixed 299×299 pixels
2. Random Horizontal Flip: $p = 0.5$
3. Random Rotation: $\theta \sim U(-10^\circ, +10^\circ)$
4. Color Jitter:
 - Brightness: ± 0.2
 - Contrast: ± 0.2
 - Saturation: ± 0.2
 - Normalization: Using ImageNet statistics

$$x' = \frac{x - \mu}{\sigma} \quad (14)$$

- $\mu = [0.485, 0.456, 0.406]$
- $\sigma = [0.229, 0.224, 0.225]$

3.5 Visualization and Interpretability

We took a closer look at the qualitative evaluation, diving into attention map analysis to see which parts of the images caught the model's eye during inference. To wrap things up, we carried out a thorough comparative analysis against baseline models, helping to put our findings into perspective and showcase the advancements we've made over existing methods (Figure 1).

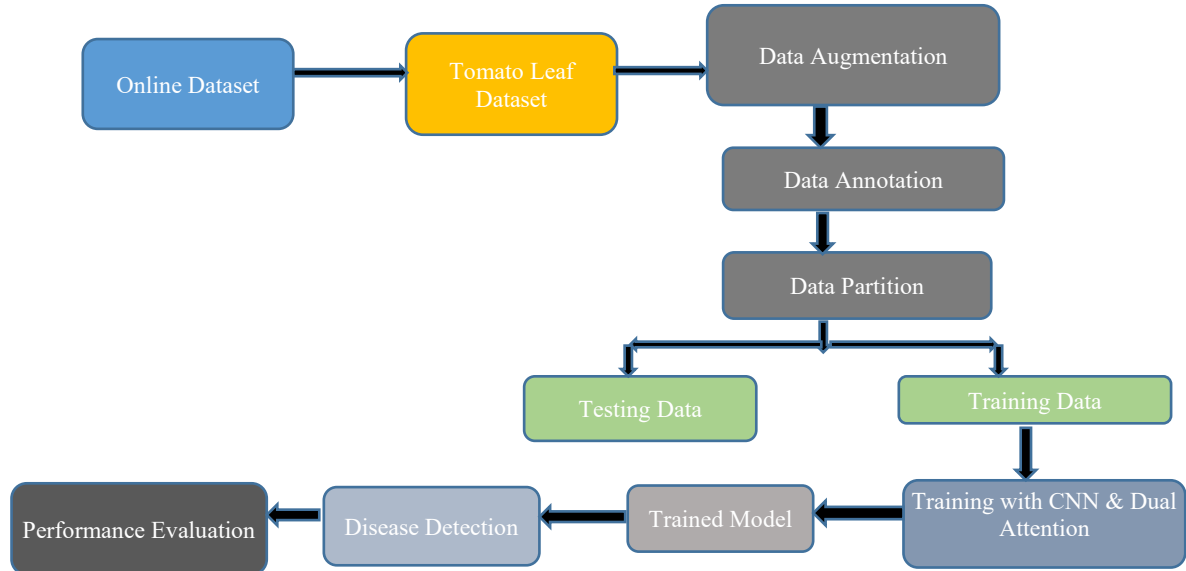


Figure 1: Methodology diagram

4 Results

Table 6: Dataset composition

Disease Name	Scientific Name	Type of Disease	Images Used
Bacterial Spot	<i>Xanthomonas campestris</i> pv. <i>Vesicatoria</i>	Bacteria	2862
Early blight	<i>Alternaria solani</i>	Fungus	2455
Late-blight	<i>Phytophthora infestans</i>	Fungus	3113
Leaf-mold	<i>Passalora fulva</i>	Fungus	2754
Healthy	-	-	3051
Powdery mildew	<i>Leveillula taurica</i>	Fungus	1004
Leaf spot	<i>Cercospora</i> spp	Fungus	2882
Target spot	<i>Corynespora cassiicola</i>	Fungus	1827
Spotted_spider_mite	<i>Tetranychus urticae</i>	Virus	1747
Mosaic virus	Tospovirus, Bunyavirales	Virus	2153
Yellow leaf curl virus	<i>Lycopersicon esculentum</i>	Virus	2039

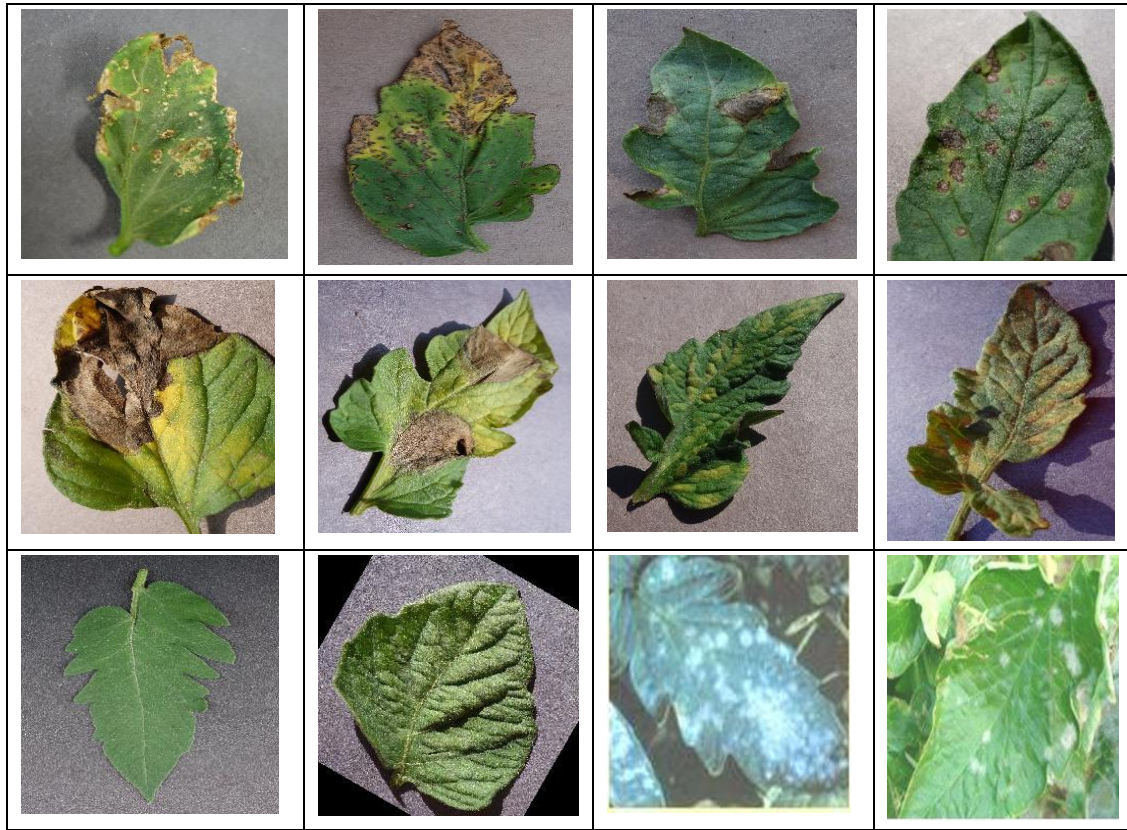


Figure 2: Sample dataset images

As mentioned in Table 7, with consistently high precision, recall, and F1-scores, the classification model performs well across all tomato disease categories. With F1-scores of 0.99 and 0.98, respectively, the model performs exceptionally well in identifying healthy tomato plants and Yellow Leaf Curl Virus, showing nearly flawless classification accuracy for these conditions (Figure 2).

Table 7: Classification performance metrics

Disease	Precision	Recall	F1-score	Support
Tomato__Bacterial_spot	0.96	0.93	0.94	100
Tomato__Early_blight	0.94	0.91	0.92	100
Tomato__Late_blight	0.94	0.96	0.95	100
Tomato__Leaf_Mold	0.98	0.94	0.96	100
Tomato__Septoria_leaf_spot	0.93	0.96	0.95	100
Tomato__Spider_mites	0.99	0.91	0.95	100
Tomato__Target_Spot	0.94	0.92	0.93	100
Tomato__Yellow_Leaf_Curl_Virus	0.99	0.99	0.99	100
Tomato__mosaic_virus	0.91	0.97	0.94	100
Tomato__healthy	0.96	1.00	0.98	100

The detection of spider mites likewise exhibits outstanding precision at 0.99, albeit with a somewhat lower recall at 0.91. With F1-scores between 0.92 and 0.96, the majority of other diseases continue to perform in a balanced manner, indicating the model's strong capacity to differentiate between various pathological conditions. With an F1-score of 0.92, Early Blight is the least successful category, but it still exhibits good classification ability. Interestingly, the model successfully detects all healthy specimens without producing false negatives, achieving perfect recall (1.00) for healthy plants (Figure 3).

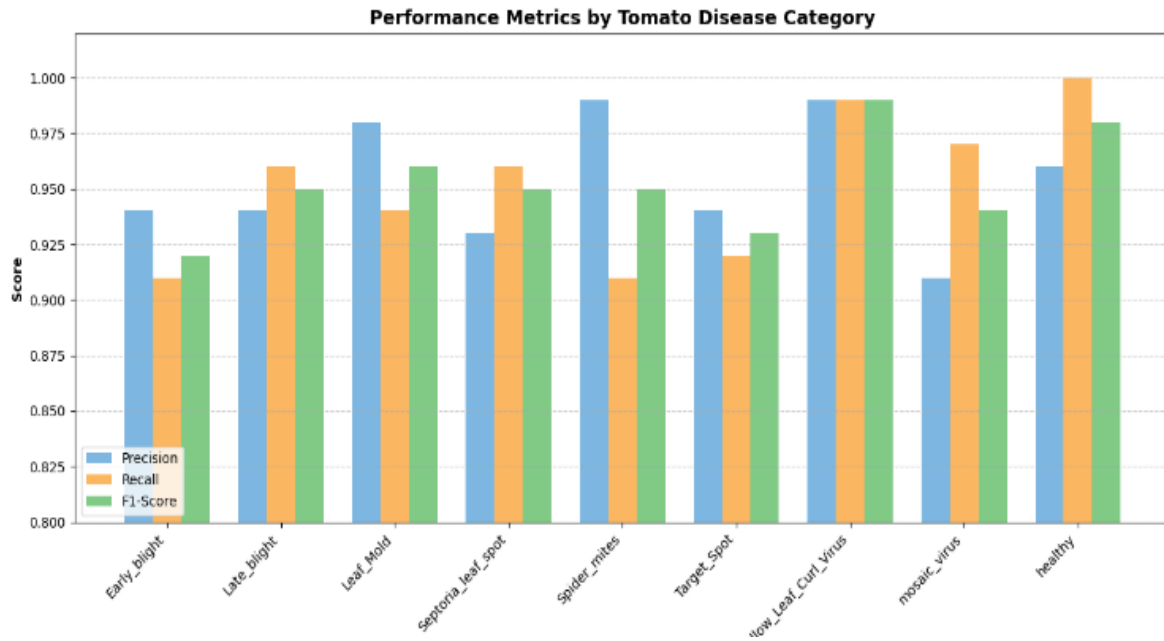


Figure 3: Performance metrics graph

Disease Classification Confusion Matrix

	Bacterial spot	Early blight	Late blight	Leaf Mold	Septoria leaf spot	spotted spider mite	Target Spot	Leaf Curl Virus	mosaic virus	healthy
Bacterial spot	98	0	0	0	1	0	0	1	0	0
Early blight	0	91	1	0	2	0	5	0	1	0
Late blight	2	2	95	0	0	0	0	0	0	0
Leaf Mold	0	1	2	94	1	0	0	0	2	0
Septoria leaf spot	0	2	1	0	95	0	1	0	0	0
spotted spider mite	0	0	2	0	0	91	0	0	7	0
Target Spot	0	1	0	2	3	1	92	0	0	1
Leaf Curl Virus	1	0	0	0	0	0	0	99	0	0
mosaic virus	0	0	0	0	0	0	0	0	97	3
healthy	0	0	0	0	0	0	0	0	0	100

Correct Predictions (Diagonal)
 Misclassifications
 Zero Occurrences

Overall Accuracy:

Figure 4: Confusion matrix

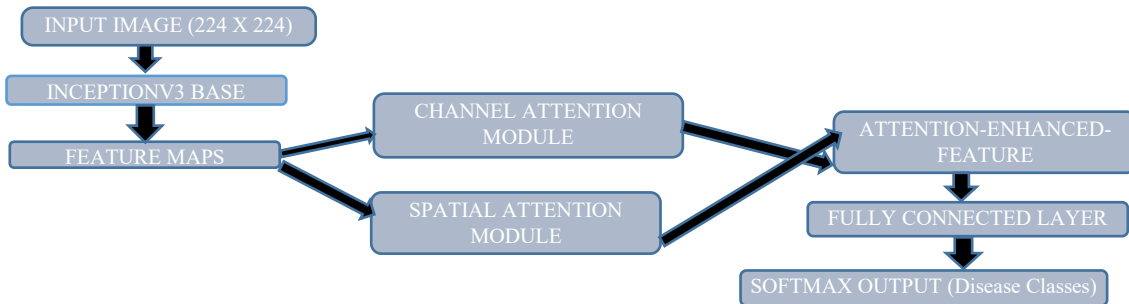


Figure 5: Architecture diagram inception v3

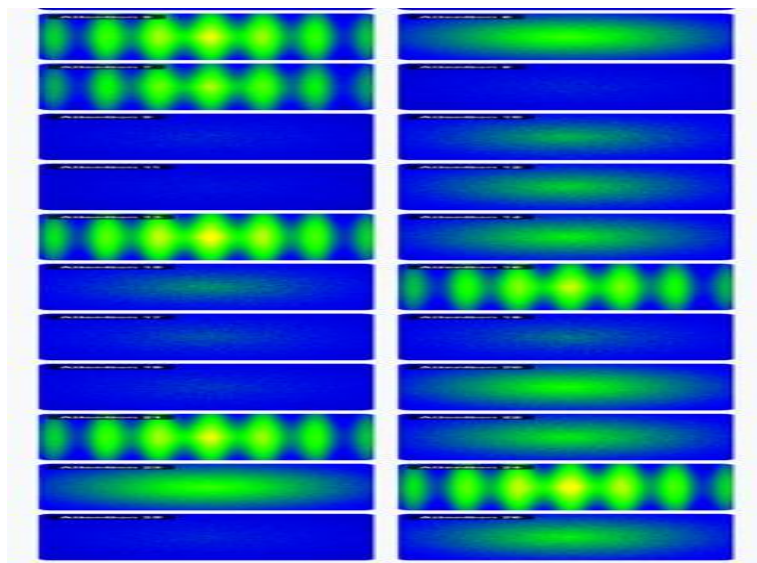


Figure 6: Attention heap

The attention heatmaps in Figures 4,5, and 6 show which parts of the tomato leaf images the AI model looks at most carefully when identifying diseases - the bright yellow-green areas are where the model pays the most attention, while the blue areas are largely ignored. By examining these patterns, we can understand how the model makes its decisions and verify that it's focusing on actual disease symptoms like spots or discoloration rather than irrelevant background features.

5 Conclusion

Our research demonstrates that integrating Inception-V3 architecture with dual attention mechanisms mentioned in Figure 6 yields exceptional performance in tomato disease detection. This approach capitalizes on Inception-V3's multi-scale feature extraction capabilities while attention mechanisms intelligently focus on disease-specific visual features. The spatial attention component identifies infected leaf regions, while channel attention emphasizes informative feature maps, creating a powerful system for autonomous disease recognition.

Over all the plant diseases we tested, our enhanced model with attention mechanisms shows remarkable performance. For most diseases, it gets precision scores above 0.94; for F1-scores it routinely exceeds 0.92. The model is especially good in spotting Yellow Leaf Curl Virus, obtaining almost perfect results (0.99 across all measures), and it can accurately identify healthy plants with 100%. These findings surpass more conventional CNNs devoid of attention as well as earlier techniques.

The model performs so well since we invest much of our time in correctly preparing the images, which enables it to detect even in demanding field conditions minor indicators of disease. Using our dual attention system to concentrate on the most crucial elements of images helps the model considerably improve in disease detection.

The attention-enhanced system gives instant results so farmers can act quickly, and it works with modern farming tools like drones, smartphone apps, and automated systems.

The system doesn't just identify diseases it also suggests specific treatments for each problem it finds. We're currently working on making this technology work on smaller, portable devices so farmers can use it directly in their fields for continuous monitoring. This could completely change how we manage plant diseases in agriculture.

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Authors Biography



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Dr.S. Mythili has over 23 years of academic experience in computer science education and research. She has published 20 research papers, including 2 in SCI/Web of Science and 6 in Scopus-indexed journals, and has presented 11 papers at international conferences. She has attended more than 30 conferences and seminars for professional development. Her research interests include emerging computing technologies, and she holds four patents for her innovative work in the field.