



Adaptive Pixel Integration in Joint Segmentation (APIJS) for Plant Disease Detection

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Abstract

Plant diseases pose a significant threat to agriculture worldwide, impacting both productivity and food security. Effective disease management relies on early detection and accurate diagnosis. Traditional methods, which depend on visual inspection, are often slow and subjective. However, recent advancements in computer vision and machine learning offer promising alternatives. This paper introduces the improved framework for segmentation, which integrates preprocessing and segmentation. Initial preprocessing employs median filtering for data refinement. Segmentation, utilizing the Adaptive Pixel Integration in Joint Segmentation (APIJS) approach, isolates disease-affected regions in plant images through a variant of DJS. This framework has the potential to enhance the effectiveness and accuracy of plant disease segmentation stages, hence aiding in promoting sustainable agriculture and global food security.

Keywords: plant disease detection, Median filter, APIJS.

I. Introduction

In recent years, automated plant disease detection has emerged as a significant challenge in precision agriculture. Advances in disease detection technology have revolutionized early diagnosis and accurate prediction of plant diseases [12]. These technologies enable farmers to consistently monitor plant health and growth, even amidst varying environmental conditions. Despite these advancements, the high degree of similarity among different disease groups and the variability within the same disease class continue to present challenges. Early identification and prediction of plant diseases are crucial for effective disease management and control [13]. Plants are susceptible to a range of factors, including weeds, insects, bacteria, and fluctuating climate conditions. Timely detection is essential to mitigate damage and ensure optimal crop yields, particularly for common issues such as green leaf spots, scabs, and mosaic viruses. Therefore, a more reliable diagnostic method is necessary. To tackle this challenge, contemporary technologies have been implemented to automatically detect plant diseases, providing a more precise and effective method.

In recent years, automated plant disease detection has become a major difficulty in precision agriculture. Plant disease early diagnosis and accurate prediction have been changed by advances in disease detection technology [12]. Farmers can reliably keep an eye on the health and growth of their plants even in the face of changing environmental conditions thanks to these automated technologies. The great degree of similarities across many illness groups and the heterogeneity within the same disease class, however, make the process still difficult.

For efficient disease management and control, early identification and prediction of plant diseases are essential [13]. Numerous elements, including weeds, insects, bacteria, and different climate conditions, can affect plants. To minimize plant damage and preserve optimal crop yield, early detection is crucial for common plant diseases such as green leaf spots, scabs, and mosaic viruses.

With the use of ML and DL approaches, plant disease detection has advanced quickly and is showing promising results. DL [20] [21] is one of these techniques that has shown to be especially successful at picture identification since it automatically extracts features rather than depending on features that are chosen by humans.

This makes DL a powerful tool for automating the identification of disease-related features in plants [14]. However, this technology faces several challenges. Firstly, acquiring real field datasets suitable for training DL models is a significant hurdle [15]. Plant diseases are randomly distributed across leaves, stems, and roots, exhibiting diverse textures, sizes, and shapes, which adds complexity to detection tasks. The procedure is further complicated by environmental elements like wind-blown haze, overlapping leaves, complicated backgrounds, and different angles of view.

Training a classification model on a dataset encompassing all crop kinds and diseases is necessary to develop a universal method for plant disease classification [17]. Unfortunately, it is not yet possible to create such a comprehensive dataset; in fact, it would be extremely difficult, if not prohibitive. Since there are millions of plant species in the world and a plethora of illnesses that can impact them, compiling enough data takes time.

The performance of DL [18] systems is directly impacted by this lack of data. These systems find it difficult to generalize the patterns required for accurate plant disease identification when they lack access to large datasets. As a result, this research suggests a unique method for dataset image segmentation.

This work contributes the following:

- Contributing Median filtering technique that filters the input image and preprocesses the image for further analysis.
- Proposing the APIJS approach in the segmentation step that avoids excessive noise or over-segmentation within the preprocessed image.

The remainder of the document is structured as follows: Section 2 contains an overview of the literature on the works currently in publication. Section 3 explains the suggested methodology. Section 4 presents the results and discussion and Section 5 provides a summary of the suggested model.

II. Literature review

In 2024, SasikalaVallabhajosyula *et al.* [1] proposed a model designed to aid in the early detection of leaf diseases. They introduced an innovative hierarchical residual vision transformer that combined enhanced features from ResNet9 and Vision Transformer models. The model aimed to retrieve more discriminative and meaningful details while lowering the computational requirements and number of trainable parameters. The method was assessed on three datasets: “the Local Crop dataset, Plant Village dataset, and Extended Plant Village Dataset”. The model was trained using optimized parameters from the Improved Vision Transformer as well as utilized ResNet9 for feature classification.

In 2024, Imane Bouacida *et al.* [2] introduced a novel deep learning-based system designed to recognize diseased and healthy leaves across various crops, regardless of whether the system had been specifically trained on them. Rather than simply classifying a leaf as diseased or healthy, this method identifies specific areas where the disease is affecting the leaf. It also quantifies the percentage of the leaf that is diseased. This approach was built specifically for analyzing small areas effectively, without any slowdown. For validation, the researchers trained and tested their model on the respected PlantVillage dataset, known for its comprehensiveness and the wide range of plant diseases it encompasses.

In 2024, K. Mahadevan *et al.* [3] introduced a novel approach for detecting rice plant leaf diseases using the DSGAN combined with Improved Artificial Plant Optimization. The method began with inputting healthy and diseased leaf images from a collected dataset. Subsequently, ITNN technique was employed to enhance image quality. Following this, a Segmentation using SMNS algorithm identified regions of interest based on enhanced color saturation in the images. Finally, disease detection utilized the proposed SMLAF in conjunction with the DSGAN algorithm, leveraging the selected features for accurate classification.

In 2023, Mitali V. Shewale and Rohin D. Daruwala, [4] investigated automated intelligent approaches using deep learning CNNs, which had become increasingly popular due to their ability to provide precise diagnoses efficiently. By analyzing image sequences with image processing, these methods were able to detect patterns of change in leaves, ultimately revealing the presence of plant diseases. The high accuracy of this disease classification method comes from its ability to automatically identify key characteristics within the images. This removes the need for manual effort in feature extraction and setting specific image thresholds. Their network was adapted and expanded to handle spatial images taken in challenging environmental conditions.

Table I: Features and Challenges of extant works

Authors [Citation]	Methodology	Features	Challenges
SasikalaVallabhajosyula, <i>et al.</i> [1]	Improved Vision Transformer and ResNet9 models	Consistent results were observed with the Adam optimizer, while the SGD optimizer achieved the highest accuracy.	In future endeavors, the authors aim to create a compact DNN to address the challenges associated with real-time data processing.
ImaneBouacida, <i>et al.</i> [2]	DL	It demonstrates enhanced versatility and resilience in addressing a broad spectrum of crops and diseases.	Future studies should focus on improving the model's efficiency and effectiveness when applied to practical situations.
K. Mahadevan, <i>et al.</i> [3]	DSGAN ²	In simulated testing, the proposed model exhibited faster processing times than the majority of existing models, achieving a processing time of 98 milliseconds.	To make the models even better in the future, researchers could expand the training data by including more datasets with a wider variety of rice plant species and diseases.
Mitali V. Shewale and Rohin D. Daruwala, [4]	CNN	It accurately identifies the type of disease based on visual representations.	Future research should focus on developing applications that extend the current solution to encompass all types of plant leaf species, thereby making a significant impact on sustainable development through advancements in agricultural production for future generations.

III. Problem statement

The fast and accurate plant disease identification is essential for food security and sustainable agriculture. Automated systems capable of analyzing images of plant parts, particularly leaves, to identify and classify diseases play a pivotal role in modern agriculture. There are numerous challenges associated with accurately identifying and classifying plant diseases using image-based methods. K. Mahadevan *et al.* [3] have proposed an innovative approach, the DSGAN method, specifically designed for the detection of diseases in rice plant leaves. This method incorporates an Improved Artificial Plant Optimization technique and leverages SMNS algorithm for precise image segmentation. The SMNS algorithm focuses on identifying regions of intense color saturation in enhanced images, which are indicative of potential disease symptoms. However, one critical factor influencing the accuracy of the segmentation process is the choice of grid size used for averaging. Larger grid sizes may oversimplify the image, potentially missing subtle disease symptoms, while smaller grids could introduce excessive noise or overly detailed segmentation. SasikalaVallabhajosyula, *et al.* [1] proposed a model designed to facilitate early detection of leaf diseases using an innovative hierarchical residual vision transformer, which integrates advanced Vision Transformer and ResNet9 models.

An overview on Transfer Learning-based Plant disease detection

Ensuring global food security is of utmost importance amid the expanding global population. Plant diseases present a formidable threat to essential crops like wheat, rice, maize, and various fruits and vegetables, causing significant yield reductions and impairing the availability and nutritional value of food resources. Timely detection and intervention are essential to mitigate these losses by swiftly implementing effective treatment and management strategies. This paper introduces an innovative approach known as the Transfer Learning-based Plant Disease Detection (TL-PDD) framework.

The framework is structured into two stages: “preprocessing, and segmentation”, as shown in Figure 1. At first, preprocessing prepares raw data for subsequent analysis. In this work, it utilizes median filtering for ensuring data quality and consistency. Segmentation process then conducted that isolates regions of interest by using APIJS approach within plant images, focusing specifically on areas potentially affected by diseases. The APIJS approach is the variant of DJS that modifies the pixel values in the Joining phase. Following segmentation, feature extraction identifies and quantifies key characteristics from these segmented regions, which is crucial for subsequent disease classification. This work specifically extracts several important features like Multi-texton, PHOG, and NMA-LGIP because there are many features to extract.

Moreover, this predictive capability provides actionable insights for agricultural decision-making, enabling farmers to apply targeted treatments and interventions promptly. As agricultural challenges escalate alongside global demand, innovative frameworks like APIJS represent significant advancements in the segmentation process safeguarding crop health and ensuring food security for future generations.

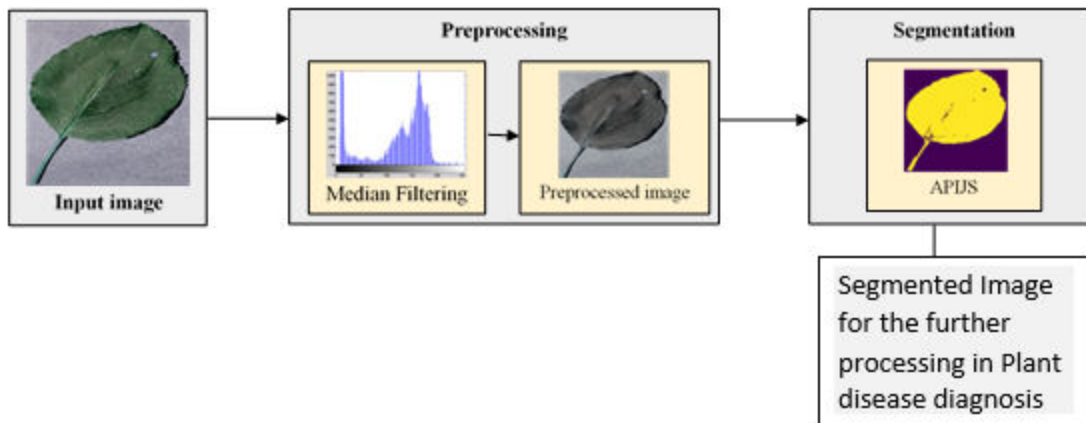


Figure 1: Architecture of proposed model

Let I^{inp} be the input plant leaf image for predicting the plant disease. Plant leaf images captured under varying conditions may contain noise such as background clutter, lighting variations, or artifacts from the imaging process. Preprocessing techniques like noise reduction filters (e.g., median filtering) help to clean up these images, ensuring that the features relevant to disease detection are clear and distinct. The description of median filtering is as follows:

IV. Median filtering

Median filtering [25] is a widely used nonlinear technique in image processing that effectively reduces image noise while maintaining edge clarity. This technique is highly effective for tasks like detecting diseases in plant leaves, where maintaining precise image features is crucial. It excels in handling input noise with large magnitudes without distorting or blurring edges.

It is a method in image processing that reduces noise while keeping the edges of objects sharp. It works by evaluating each pixel individually within a specified window size where both dimensions are odd. Instead of replacing a pixel's value with the average of its neighbors' values (which can blur edges), median filtering assigns it the median value from the surrounding pixels. This approach ensures that noise is minimized without sacrificing the clarity of image details. The median value is calculated by averaging the two central values when the window size contains an even number of pixels. Eq. (1) expresses the median filter in this way.

$$z[p, q] = \text{median}\{I^{inp}[i, j], (i, j) \in M\} \quad (1)$$

where, $[p, q]$ is the centered round location in the image and M is the neighborhood represented by the user. Thus, the preprocessed image can be denoted as I_{pre} .

V. Segmentation

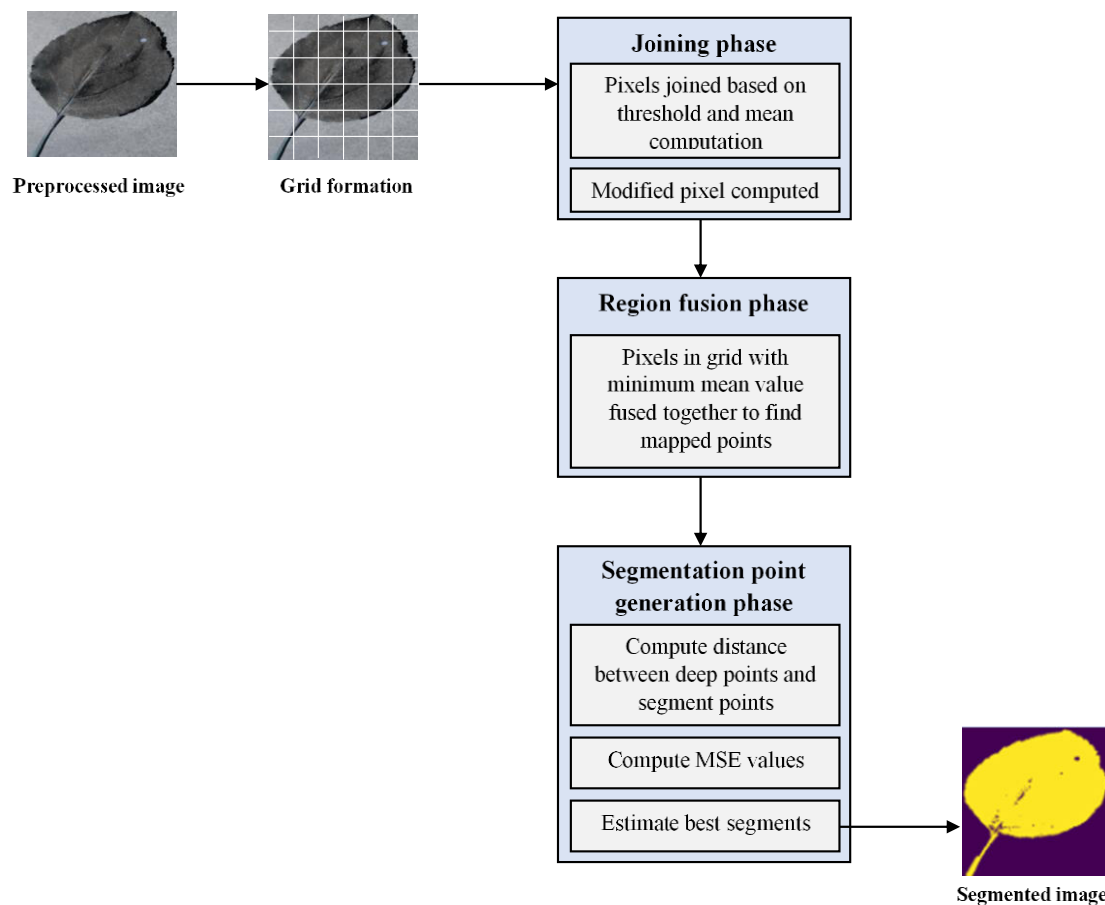
In image processing, segmentation is the process of dividing image I_{pre} up into discrete areas or segments according to standards such as motion, texture, color, intensity, or other factors. This process aims to simplify the image representation and make it more manageable for analysis. In this work, an adapted version of DJS method known as APIJS is employed and the process of APIJS approach is discussed in the following.

APIJS approach for image segmentation

In this step, the pre-processed image, I_{pre} undergoes the proposed APIJS method, which is the extension of DJS approach [26]. This method finds the best segments by considering the distance between segmentation points and deep spots in the image, as well as area similarity. The DJS algorithm comprises three primary stages: joining, region fusion, and segmentation point generation.

As depicted in Figure 2, the input image is initially split into grids for the joining phase, where pixels are joined using a threshold and mean computation. This step aims to establish initial segments within the image. Following this, the region fusion phase merges regions based on their certain bi-constraints and similarity, determining new mean values. Pixels within grids exhibiting the lowest mean values are fused together to identify mapped points, thereby refining the segmentation. During the segmentation point creation phase, optimal segments are identified by calculating the distance between deep points and segmentation points. Estimating mean square error (MSE) values guides this assessment, ensuring that the final segmentation appropriately captures the underlying features and structure of the image. The steps to be followed in the DJS approach are given in the following.

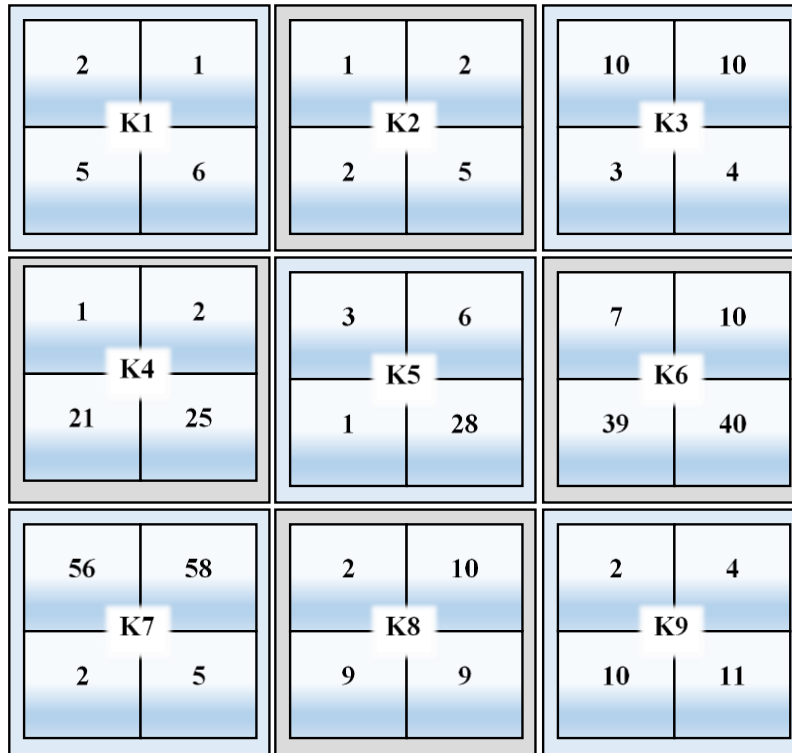
Figure 2: Architecture of proposed model used for segmentation



Initially, the input image is divided into multiple 2x2 grids as part of the preprocessing Stage of These grids, derived from the pre-processed image I_{pre} , serve as the foundational units for subsequent processing steps. Then, the partitioned grids are defined as in Eq. (2).The grid structure for an sample image is illustrated in Figure 3.

$$K = \{K_1, K_2, \dots, K_j, \dots, K_y\} \tag{2}$$

where, y indicates total grid count and K_j indicates j^{th} grid in the image



After partitioning the image into grids, pixels within each grid are consolidated based on their predefined threshold of 1 and mean values. The mean value is derived from averaging the pixel values within the grid, and this average is used to determine which pixels should be joined together, as defined in Eq. (3). This method ensures effective grouping of pixels with similar attributes while maintaining the integrity of the image's details and structure.

$$K_j = \frac{\sum_{i=1}^N g_i}{N} \tag{3}$$

where, N indicates pixels count in the K_j grid; and g_i indicates pixel value according to K_j grid. Then, the pixel joining is defined as in Eq. (4). Here, Th represents threshold.

$$K_j = \frac{\sum_{i=1}^N g_i}{N} \pm Th \quad (4)$$

For instance, the average value is estimated as in Eq. (5) for the second grid as illustrated in Figure 3.

$$K_j = \frac{1+2+2+5}{4} = 2.5 \pm 1 \quad (5)$$

Which means $K_2 = 2.5+1=3.5$ and $K_2 = 2.5-1=1.5$. This indicates that the pixel for K_1 value ranges among 1.5 and 3.5. Likewise, the average values are estimated as well as the pixels are joined together for the remaining pixels.

A significant drawback of this method is the potential for excessive noise or over-segmentation. The choice of grid size used for averaging has a considerable influence on the outcome of the segmentation process. Larger grid sizes can overly simplify the image, while smaller grids may introduce too much noise or result in excessive segmentation.

To avoid this, APIJS approach is proposed. The proposed APIJS approach modifies the pixel value in this phase that can be estimated according to Eq. (6). This approach is repeated for every 3x3 matrix of 256x256 pixel image.

$$g_i^{New} = \frac{C*(T+B)+C*(R-L)}{N} \quad (6)$$

where, C is the center pixel; T is the top pixel; B is the bottom pixel; R is the right pixel; L is the left pixel and N indicates the number of pixels. Thus, the large grids can over simplify the outcomes.

Step 3: Region fusion stage

This stage follows the pixel joining stage and involves evaluating pixel intensity similarities and creating a region fusion matrix using the provided grids. This matrix guides the merging of regions, adhering to constraints that ensure both pixel intensity similarity and bi-constraints are met. This process effectively integrates criteria to combine regions based on their similarities.

(1) The mean value R_j must be below 3.

(2) Each grid selects only one grid point.

Region similarity is evaluated based on these two criteria, and the merged regions are utilized to estimate the mapped points. The similarity of the region is then expressed using Eq (7). Here, J represents joined pixels' count in K_j ; and g_a^y indicates joined pixels in specified grid K_j . The combined grids, known as mapped points, are represented by Eq. (8).

$$R_j = \frac{\sum_{a=1}^Z g_a^y}{J} \quad (7)$$

$$G = \{G_1, G_2, \dots, G_c, \dots, G_x\} \quad (8)$$

where, x refers to mapped points count; and G indicates mapped points for the image.

Step 4: Identification of deep points

Deep points are identified by examining pixels missed during the joining phase, along with mapped points. These are pixels remaining in the image post-joining or outside the

specified threshold boundary, termed as missed pixel, g . Moreover, the missed pixel is expressed as in Eq. (9).

$$(E) = \{g_H\}; 1 < G \leq H \tag{9}$$

Here, H indicates missed pixels count; and g_H indicates pixel, which is missed to create the joined one in the image. Subsequently, deep points are calculated by summing the mapped and missed pixels, as shown in Eq. (10).

$$H_{pts} = E + G_c \tag{10}$$

Step 5: Evaluate optimal segments

Iteratively, optimal segments are determined from deep locations. The points with the shortest distances are chosen as the new segmented points. The distances between the segmented points, S points, and the deep points are then established.








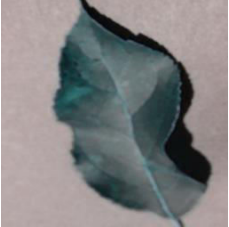
Healthy		
Black Rot		
CedarAppleRust		
Scab		
	(a)	(b)

Figure 4: Images for plant disease detection using Apple Class a) Original Images and b) Median Filtering using Pre-processed image

This selection process relies on computing a minimum distance function to refine the segmentation as in Eq. (11).

$$D = \sqrt{\sum_{s=1}^{20} (S_s - H_{pts})^2} \tag{11}$$

Therefore, the segmented image is signified as I_{seg} .

Table II: Distribution of Classes and Total Number of Images in the Dataset

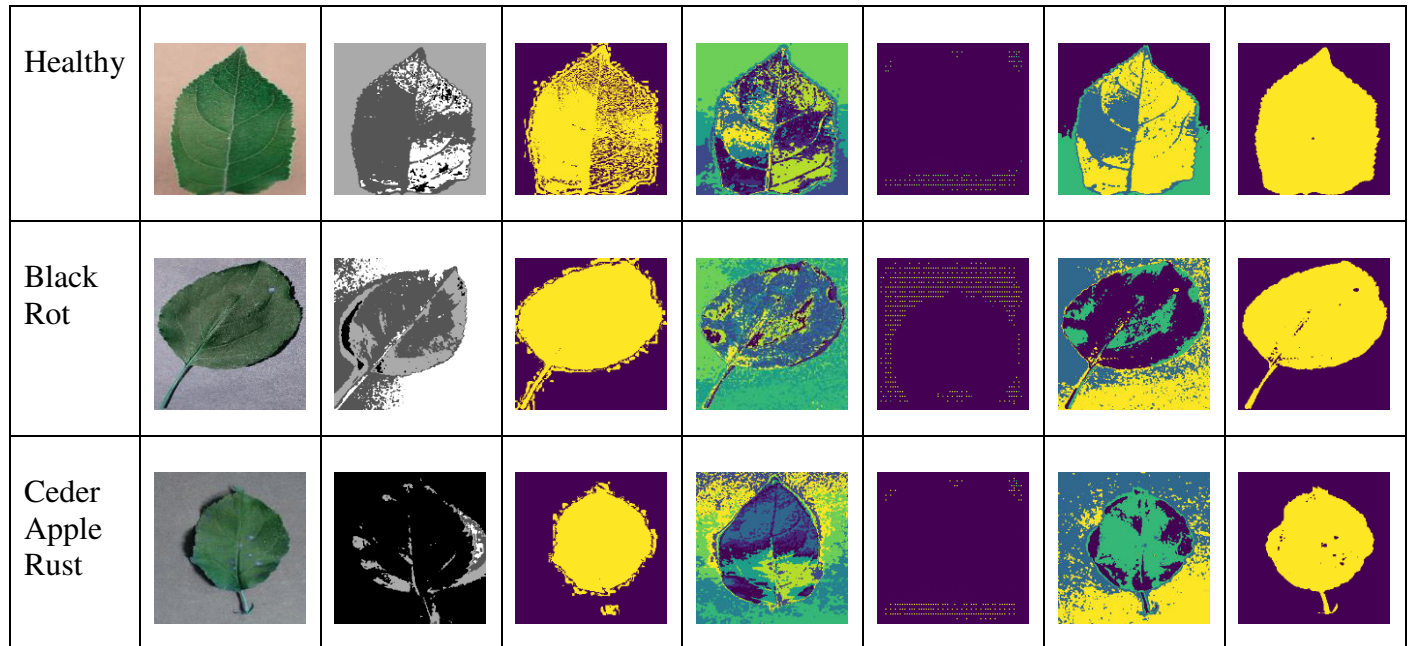
Classes	Total Number of Images
Apple_Blackrot	621
Apple_Healthy	1645
Apple_Ceder Apple Rust	275
Apple-Scab	630

Performance Analysis

Sample and pre-processed images that underwent median filtering as part of the plant disease detection system are shown in Figures. These images pertain to Apple crops (Healthy, Black Rot, Cedar Apple Rust, and Scab).

Segmentation Analysis on Apple Class

The figure 5 shows the original images alongside segmented images generated by various segmentation models used in plant disease prediction, including BIRCH, Conventional DJS, FCM, U-Net, K-means, and APIJS. These figures showcase how each segmentation method processes and identifies diseased regions within the plant images. Notably, APIJS stands out by producing superior outcomes contrasted to existing segmentation models, demonstrating its enhanced ability in precisely delineating and highlighting diseased areas.



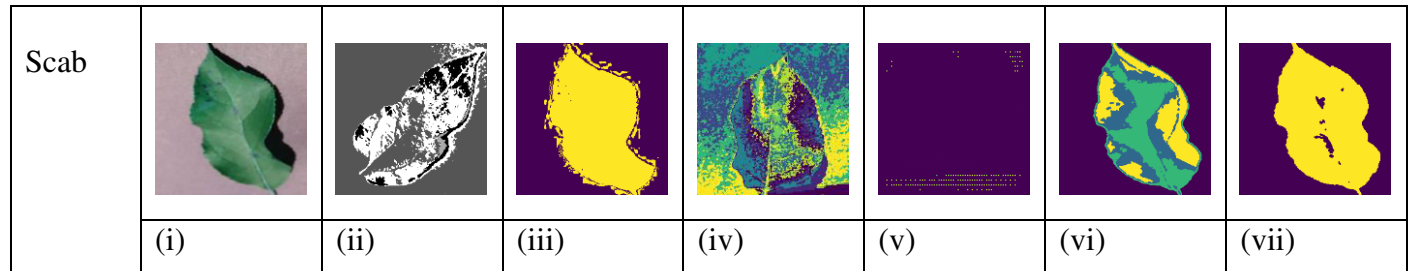


Figure 5: Images for plant disease prediction using Apple Class i) Original Image ii) BIRCH iii) Conventional DJS iv) FCM v) U-Net vi) K-means and vii) APIJS

Table III present a segmentation analysis comparing the performance of APIJS with Conventional DJS, K-Means, FCM, U-Net, and BIRCH in predicting plant diseases for both Apple classes. These tables provide a comprehensive evaluation of segmentation methods crucial for accurately delineating diseased areas in plant images. In the segmentation evaluation for Apple Class using the Dice coefficient, Conventional DJS achieved a moderate score of 5.685, indicating some accuracy in identifying diseased areas. K-means showed improvement with a score of 6.541, suggesting better segmentation alignment with ground truth. FCM scored 5.766, demonstrating variable performance in accurately delineating diseased regions. BIRCH performed well with a score of 6.566, indicating higher accuracy in segmenting diseased areas. APIJS stood out with a high score of 9.657, highlighting its exceptional precision and effectiveness in accurately identifying and delineating diseased regions in plant images.

Table III: Evaluation of segmentation using APIJS for the Apple class

Methods	Dice	Jaccard
Conventional DJS	5.685	6.222
K-means	6.541	5.257
APIJS	9.657	9.457
FCM	5.766	6.466
BIRCH	6.566	6.135
U-Net	5.257	5.157

VI. Conclusion

This paper introduced the Transfer Learning-based Plant Disease Detection (TL-PDD) framework. Initially, raw data was prepared and preprocessed using median filtering to ensure consistency and quality. Segmentation isolated regions of interest using the APIJS approach, a variant of DJS that modified pixel values during the Joining phase within plant images to focus on potentially diseased areas. The efficiency and precision of plant disease detection systems were greatly improved by this approach, supporting efforts for global food security and sustainable agriculture.

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Nomenclature

Abbreviation	Description
ANN	Artificial Neural Network
Bi-GRU	Bidirectional Gated Recurrent Unit
CAE	Convolutional Autoencoder
CNN	Convolutional Neural Network
CNN-TL	Convolutional Neural Network-Transfer Learning
DJS	Deep Joint Segmentation
DL	Deep Learning
DMO	Deep Maxout
DNN	Deep Neural Network
DSGAN	Deep Spectral Generative Adversarial Neural Network
FAO	Food And Agriculture Organization
ITNN	Improved Threshold Neural Network
LSTM	Long Short Term Memory
ML	Machine Learning
OTV	Overall Trend Vector

SVM	Support Vector Machine
TV	Trend Vectors
WGAN	Wasserstein generative adversarial network