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ROBL-TSA AND SNAPSHOT ENSEMBLE CLASSIFIER FOR PAPAYA FRUIT DISEASE CLASSIFICATION

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ABSTRACT

Papaya fruit is a healthy tropical fruit that is grown in many countries. But its growth and quality are affected by various diseases. Early and accurate disease detection is crucial to minimizing crop loss and the diseases appear in different shapes, sizes, and colours. In this study, developed a Snapshot Ensemble method to classify papaya fruit diseases more accurately. It integrates Histogram of Oriented Gradients (HOG) for feature extraction and Random Opposition-Based Learning with Tuna Swarm Algorithm (ROBL-TSA) to choose the best features for classification. The snapshot ensemble is utilized to improve generalization when reducing overfitting by using cyclic cosine annealing for adjusting learning rate in training. Our approach achieved 89.83% accuracy and 93.27% AUC on the papaya fruit disease dataset and performed better than traditional models like the Feed-forward Artificial Neural Network (FANN). This method offers a low-cost, effective solution for detecting papaya diseases.

Keywords: *Papaya Fruit Disease, Random Opposition-Based Learning, Snapshot Ensemble, Tuna Swarm Algorithm.*

1. INTRODUCTION

Assessing and classifying fruit quality through visual inspection is prone to errors due to external factors such as bias, fatigue and inconsistency [1]. In the fruit industry, manual classification often leads to variability due to several papaya diseases processing individual visual perception [2-5]. An automatic system is essential for accurately examining fruits and providing precise data [6]. Analysis of the maturity of fruits is essential for determining optimal eating quality and estimating suitable storage time before consumption [7]. Conducting this analysis manually is both time-consuming and potentially damaging to the fruit. An automatic system is essential for accurately examining fruits and providing precise data [6, 7]. Relying on human inspection for this process can be time-consuming and often involves methods that may damage the fruit.

So, intelligent, rapid and non-destructive methods are needed in this domain of application [8]. This article presents a grading system for papaya fruits, categorising them into 5 classes based on disease severity and wide research has been conducted on disease prediction across numerous types of fruits. The papaya fruits are graded into five classes as per their diseased level fruits [9]. Papaya is a flesh-berry fruit of different sizes with thin skin, smooth, and majorly developed in much tropical and sub-tropical countries. Papaya is a non-seasonal fruit, and it is available throughout the year and has nutrients like vitamins A and C, potassium, iron, calcium, etc, [10]. The manual estimation of papaya, still it is challenging due to labour-dependency, time-consuming and extended task that relies specialized knowledge frequently inaccessible to farmers in rural areas or small processing facilities [11-13]. In recent times, there have been used Machine Learning (ML) based algorithms for predicting fruit disease. The ML-based algorithms are categorised into two kinds such as supervised and unsupervised [14]. The unsupervised ML algorithms are generally utilized to data visualization and clustering in input information and the supervised ML algorithms are considered to predict the known outcome from a group of inputs [15]. Detecting the diseases in fruits in initial phase is essential to overcome the yield losses, reduce economic damage for farmers and ensures a health and quality of fruits. But, the disease detection task is challenging because of varying formats, sizes, shapes and colours in which a similar disease appears [16-18].

1.1 Research Gap

Existing algorithms for fruit disease classification faces the challenges like limited generalization, overfitting and high computational cost because of training numerous methods. Many methods rely on conventional feature extraction techniques like LBP or SURF that struggles to capture difficult disease patterns. Feature selection algorithms in existing algorithms filed to remove redundant data that affects the method performance. Additionally, traditional optimization strategies generally converge to one solution, missing much optimum alternatives. There is also limited utilization of ensemble strategies which explores different method states efficiently. In this article, the Snapshot ensemble classifier is proposed to classify the different classes of papaya fruit disease. In Snapshot Ensemble classifier, learning rate is scheduled to be cyclic maximized and minimized over time, overfitting to a single solution and allowing exploration of multiple high-quality solutions. The Random Opposition Based Learning – Tuna Swarm Algorithm (ROBL-TSA) based feature selection algorithm is developed, which chooses the appropriate features to classify the different disease classes of papaya. The purpose of the research is explained below.

- The Histogram of Oriented Gradients (HOG) is developed for feature extraction, which extracts the meaningful features that support the differentiation of the different diseased classes.
- The Random Opposition Based Learning – Tuna Swarm Algorithm (ROBL-TSA) based features selection technique is proposed, which selects suitable features for classification to enhance a performance.
- The Snapshot ensemble classifier is used to classify the different classes of papaya fruit disease with high classification accuracy and reduced complexity.

The research paper is organized as follows: Section 2 analyses existing research. Section 3 explains details of developed technique. Section 4 provides outcomes and a discussion of developed method. Finally, conclusion is in Section 5.

Research Questions and Hypotheses

Based on identified research gaps, presented study addressed following research questions

- RQ1 – Can HOG efficiently extracts discriminative texture features of papaya fruit diseases compared to traditional feature extraction algorithms?
- RQ2 – Does integration of Random Opposition-Based Learning with Tuna Swarm Algorithm (ROBL-TSA) enhance feature selection by minimizing redundancy and improving classification performance?
- RQ3 – Can a Snapshot Ensemble classifier with cyclic cosine annealing outperforms traditional classifiers in terms of accuracy, generalization and robustness?

Accordingly, the following hypotheses are formulated

- H1 – HOG-based feature extraction will provide higher accuracy than traditional model like Local Binary Pattern (LBP), Local Ternary Pattern (LTP) or Speeded-Up Robust Features (SURF)
- H2 – ROBL-TSA feature selection will significantly enhance classification metrics comparing with other metaheuristic feature selection approaches.
- H3 – The proposed Snapshot Ensemble classifier will obtain superior performance when comparing with individual classifiers and conventional ensemble algorithms.

2. LITERATURE REVIEW

Habib et al. [19] suggested a novel method for jackfruit disease classification. Initially, the k-means clustering algorithm was used for segmentation, which detected the disease-affected image regions of disease-attacked jackfruit and extracted the features from these areas. Next, the disease classification was performed by utilizing the nine classification techniques for completely assessing the benefits of classifiers in the index of seven performance measures. The suggested method used segmentation based on clustering to identify the fruit disease, which was efficient for classification. But, the method doesn't resize the images, which increases the complexity of the model. Worasawate et al. [20] presented the four general ML classifiers such as k-mean, Naive Bayes, Support Vector Machine (SVM) and Feed-forward Artificial Neural Network (FANN) utilized for categorizing ripe phase of mangoes during harvest. ML classifiers were trained by bio-chemical information and next tested the electrical and physical information. The presented method classifies ripeness phase of mangoes effectively. However, it relies on a limited amount of

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training and faces the overfitting issue, which affects the classification accuracy. Moraes et al. [21] introduced the papaya fruit disease detection namely Yolo-Papaya was depended by YoloV7 detector and introduced Convolutional Block Attention Module (CBAM) for enhanced attention mechanisms. The introduced method attained the whole mean average precision (mAP) with different classes. The detector was utilized on practical applications to fruit quality handling as standard to papaya fruit disease detection. The introduced method has high precision, but the classification accuracy was less due to the complexity of features. Amin et al. [22] implemented an effective and correct fruit freshness classification technique that contains numerous interconnected phases. The fruit data was collected and it is pre-processed by utilizing color unfirming, resizing of the image, augmentation and labelling of the image. The AlexNet method was used, which has 8 layers, involves 5 convolutional layers and 3 fully connected layers. At last, softmax classifier was utilised for final classification. However, the method do not remove the noise in images which leads to classification error.Huang et al. [23] developed the neural network that integrated the Inception module with the present EfficientNetV2 for effective multi-scale feature extraction and identification of disease in citrus fruits. The VGG was utilised for replacing the U-Net backbone to improve performance of segmentation in network. The developed method has effective performance in terms of precision, but the model has less classification accuracy due to whole feature subsets utilized to classification.

S M Masfequier Rahman Swapno et al. [24] suggested the ViT-SENet-Tom that was hybrid vision transformer (ViT) method with Squeeze and Excitation (SE) module to quick, precise and effective fruit classification. Model process 3 tomato classes, ripe, unripe and reject. In suggested method, used a newly developed layers and functions. This combination developed the much difficult and sophisticated neural network, effectively enhances the overall performance.

The papaya quality and quantity are effectively impacted through different diseases. The diseases and physical classification of diseased fruit are expensive in agricultural files and causes to inappropriate errors. Detecting the diseases in fruits in initial phase is essential to overcome the losses and ensures a health and quality of fruits. Though, the task is challenging because of variant formats, sizes, shapes and colours that similar disease present.

Prior studies on fruit disease detection have explored variety of algorithms like clustering-based segmentation with classical classifier for jackfruit [19], machine learning classifier for mange ripeness [20], deep CNN-based YOLO-Papaya detection [21] and Alexnet-based freshness classification [22]. While these researches determined the feasibility of ML and DL models for fruit disease or quality detection, it reported limitations like high model complexity, overfitting dure to limited training data and sensitivity to noise. Additionally, conventional feature extraction algorithms like LBP, SURF or CNN-based global features failed to capture dine-grained texture variation in fruit diseases and feature selection strategies used lacked robustness and against redundancy. The motivation is to addressed overfitting, redundancy in features and limited generalization observed in previous works through developing hybrid model which integrates HOG-based feature extraction to extract discriminative textual patterns, ROBL-TSA for choosing most relevant features when maintaining diversity and Snapshot Ensemble learning with cyclic cosine annealing to explore multiple local minima, that enhancing generalization.

Study design and Research protocol

This research followed a structured research protocol to ensure reproducibility and systematic evaluation. The total of 214 papaya images belongs to five disease classes are gathered from online sources and divided into training and testing sets in an 80:20 ratio. To enhance generalization, data augmentation algorithm like rotation and zooming extended dataset to 6277 images. Pre-processing includes image resizing for uniformity and Gaussian blur filtering for noise reduction. Features are then extracted by HOG, generating 3584 descriptors per image, from ROBL-TSA chosen 2867 relevant features to reduce redundancy. These feature are classified using Snapshot Ensemble classifier with cyclic cosine annealing to improve robustness and prevents overfitting.

3. PROPOSED METHOD

An ensemble-based classifier is proposed to classify the different disease classes of papaya fruit. Initially, data was collected from the papaya fruit image and pre-processed using image resizing, Gaussian Blur filter and data augmentation. Then, the meaningful features are extracted by using the HOG method and from that, relevant features are chosen by the ROBL-TSA. Then, the classification is performed by using the Snapshot ensemble-based classifier. Figure 1 represents a process of developed methodology.

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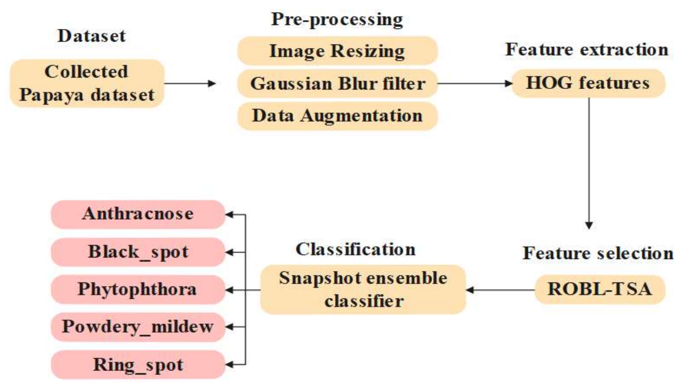

Figure 1: Process of developed snapshot ensemble classifier for papaya disease classification

3.1 Dataset

The papaya fruit images are gathered from different online sources. The dataset includes 214 samples with five classes such as Anthracnose includes 55 samples, Black_spot includes 24 samples, Phytophthora includes 43 samples, Powdery_mildew includes 42 samples and Ring_spot includes 50 samples. The training and testing set of dataset is divided to 80: 20. Figure 2 represents sample images in dataset

Figure 2: Sample images in the Papaya fruit disease dataset

3.2 Pre-processing

Pre-processing is an essential stage to enhance image quality, which better learns the patterns integrated with various diseases when decreasing the noise. Pre-processing techniques like image resizing, Gaussian blur and data augmentation are used in this research.

- Image Resizing - It ensures that all input images have uniform sizes compatible with feature extraction and minimises the execution complexity. All the images are resized to uniform size of 224×224 pixels for further process. The selected resolution balances between preventing significant features and minimising the execution cost.
- Gaussian Blur Filter - It minimises the unnecessary differences in images like noise without eliminating the significant features such as disease spots. This filter smooths the image by averaging the pixel values with its neighbours. This filter used the Gaussian function, which provides much weight for the pixels nearer to the target pixel. The 5×5 kernel size is utilized to eliminate the noise when preventing significant data. The smoothed image retained significant data like edges and disease spots as well as minimised the noise. Eliminating the Gaussian noise enhances the image quality and allows the model to concentrate on original features relevant to diseases like spots, texture and colour difference.
- Data augmentation - By employing random transformations to images, it extends the training dataset and helps to generalise and avoid overfitting. The image is rotated by random degrees, enabling the model to be invariant to the fruit orientation. The, randomly zooms in or out, allow the model to handle various image scales and capture precise data of diseases. After augmentation, the sample in the dataset is increased to 6277 images.

3.3 Feature extraction

Pre-processed images are fed to feature extraction stage that captures meaningful features to distinguish the various classes. The papaya fruit diseases are generally manifested by variations in texture like spots, rot and so on. The HOG captured edge and gradient data, which is crucial for highlighting these texture differences and executing gradients in little localized image regions and bins them to histograms depending on their orientations.

Papaya fruit diseases are typically characterized by texture variations such as spots, rot, and others. The Histogram of Oriented Gradients (HOG) captures edge and gradient information, which is crucial for highlighting these texture differences. HOG computes gradients in small localized image regions and groups them into histograms based on their orientations.

This supports detecting the edges that correlate with disease symptoms like leaf spots or rotting. Diseases like blights, which produce visible texture or edge variations, are easier to detect, while HOG emphasizes structural changes. In the process of HOG, the subsequent concatenation of 1-D histograms gives the feature vector. Consider the image intensity value to be analyzed is represented as L. When the image is divided into N × N cells, the gradients in the θxy directions at each pixel are measured for each orientation θ using the following Equation (1).

$$\theta_{x,y} = \tan^{-1}\frac{L(x,y+1)-L(x,y-1)}{L(x+1,y)-L(x-1,y)} \quad (1)$$

The successful orientations $\theta_i^j, i = 1,\ldots N2$ Belong to similar cells j quantized and associated with M-bins histogram. Next, every histogram was associated with one HOG histograms, which is represented as HOG features. By using the HOG technique, total 3584 features are extracted and given as input to the feature selection phase

3.4 Feature selection

The Tuna Swarm Algorithm (TSA) initializes with an optimization process through randomly and uniformly generated populations in search space [25]. The expression for initial population is in Equation (2).

$$X_i^{int} = rand \cdot (ub - lb) + lb,\ i = 1,2, \ldots, NP \quad (2)$$

In the above Equation (2), the X_i^{int} represents initial position of ith individual and ub and lb is the upper and lower boundaries of searching areas, and NP represents the number of tuna population. This score impacts rate of optimization in TSA and is uniformly distributed in the random vector. Spiral foraging is main foraging technique in tuna, which chases prey through makes tight spirals. With the prey chasing, the tuna exchanges the information with others. Each tuna is sequenced and highly relevance, therefore, adjacent tunes shared information. Mathematical expression for spiral foraging strategy is given in Equations (3) to (7).

$$X_i^{t+1} = \begin{cases} \alpha_1 \cdot (X_{best}^t + \beta \cdot X_{best}^t - X_i^t|) + \alpha_2 \cdot X_i^t, & i = 1 \\ \alpha_1 \cdot (X_{best}^t + \beta \cdot X_{best}^t - X_i^t|) + \alpha_2 \cdot X_{t-1}^i, & i = 2,3, \ldots, NP \end{cases} \quad (3)$$

$$\alpha_1 = \partial + (1-a) \cdot \frac{t}{t_{max}} \quad (4)$$

$$\alpha_2 = (1-a) - (1-a) \cdot \frac{T}{t_{max}} \quad (5)$$

$$\beta = e^{bl} \cdot cos(2\pi b) \quad (6)$$

$$l = e^{3cos(t_{max}+1/t)-1)\pi)} \quad (7)$$

In the above Equations (3-7), the $best$ represents the available good individual value, X_i^{t+1} denoted ith individual of $t+1$ iteration a is constant that determines extension to which an individual follows both best solution and a prior individual from earlier stage. The variable t and $t_{max} represent$ present and maximum number of iterations, respectively.

The α_1 and α_2 represents coefficients of weight that control movement trends of individual to good and past individuals and the b represents a random integer which is uniformly distributed in range [0,1]. If optimal individual fails to identify the food, blindly following it to ageing is not beneficial to group foraging. To address this, everyone is assisted with strong spatial search capabilities. The references stage for spiral search generates random coordinates within the search area, enabling TSA to maintain better global exploration capability. The mathematical expression is given in Equation (8).

$$X_i^{t=1} = \begin{cases} \alpha_1 \cdot (X_{rand}^t + \beta \cdot |X_{rand}^t - X_i^t|) + \alpha_2 \cdot X_i^t, & i = 1 \\ \alpha_1 \cdot (X_{rand}^t + \beta \cdot |X_{rand}^t - X_i^t|) + \alpha_2 \cdot X_{i-1}^t, & i = 2,3, \ldots, NP \end{cases} \quad (8)$$

In the above Equation (8), the X_{rand}^t represents random reference phase in search space, the TSA is explored globally in the initial phase and next transited for correct local exploitation. Therefore, with a high number of iterations, the TSA slowly modifies reference phase on spiral foraging from the random individual in the initial to the optimal individual. Mathematical formula for strategy of spiral foraging is in Equation (9).

$$X_i^{(t+1)} = \begin{cases} \begin{cases} \alpha_1 \cdot (X_{best}^t + \beta \cdot X_{best}^t - X_i^t|) + \alpha_2 \cdot X_i^t, i = 1, \\ \alpha_1 \cdot (X_{best}^t + \beta \cdot X_{best}^t - X_i^t|) + \alpha_2 \cdot X_{i-1}^t,\ i = 2,3,\ldots,NP, \end{cases} if rand \geq \frac{t}{t_{max}} \{ \\ \begin{cases} \alpha_1 \cdot (X_{rand}^t + \beta \cdot X_{rand}^t - X_i^t|) + \alpha_2 X_i^t, i = 1, \\ \alpha_1 \cdot (X_{rand}^t + +\beta \cdot X_{rand}^t - X_i^t|) + \alpha_2 X_{i-1}^t, i = 2,3,\ldots,NP, \end{cases} if rand < \frac{t}{t_{max}} \{ \end{cases} \quad (9)$$

Tuna selects for spiral foraging with parabolic cooperation foraging and creates the parabola to targeted food as reference for Z-point. Tuna identifies targeted food through searching the around parabola. Both foraging methods on tuna are processed depending on possibility allocation and chosen probability for two foraging methods is ½. The mathematical expression is given in Equations (10) and (11).

$$X_i^{t+1} = \begin{cases} X_{best}^t + (rand \cdot X_{best}^t - X_i^t) + TF \cdot 2 \cdot X_{best}^t - X_i^t, & if\ rand < 0.5 \\ TF \cdot p^2 \cdot X_i^t, & if\ rand \geq 0.5 \end{cases} \quad (10)$$

$$p = \left(1 - \frac{t}{t_{max}}\right)^{(t/t_{max})} \quad (11)$$

Where, the TF represents random number in range of [1, -1]. In this article, accuracy value is selected as fitness function and its mathematical expression is given in Equations (12) and (13).

$$Fitness = max(P) \quad (12)$$

$$P = \frac{TP}{TP+FP} \quad (13)$$

In the above Equation (13), the FP represents false positive and TP represents a value of a true positive.

3.4.1 Random Opposition Based Learning (ROBL)

The ROBL is the enhanced method of OBL that is included in TSA for enhancing diversity and support the population for being trapped into local optimal. The mathematical expression for ROBL is given as Equation (14).

$$\hat{S}_{ij} = x_{i,j} + y_{i,j} - rand \times S_{i,j},\ i = 1,2,3,\ \ldots, N \quad (14)$$

In the above Equation (14), the $x_{i,j}$ and $y_{i,j}$ represents lower and upper bounds, the $rand$ represents the random value in the range [0, 1]. The $\hat{S}_{ij}$ represents the opposite solution which is random enough for exploration. This process enhances diversity of population when assisting to avoid falling into local optimum. By utilizing the ROBL-TSA, a total of 2867 relevant features are selected and fed into the classification phase

3.5 Classification

Selected appropriate features are given as input to classification stage, which classifies different diseased classes of papaya. Here, 2 different ML algorithms Random Forest Classifier (RFC), Gradient Boosting Tree (GBT) and Adaboost are utilized for training to address the respective challenges and then integrated to provide better outcomes.

- Random Forest Classifier (RFC) – It is the predictive technique which utilized for regression and classification. The RFC is an ensemble of decision tress and every Decision Tree (DT) is trained utilizing random subset of training samples with replacing.
- At every phase in DT development, a good feature is selected from the random feature subsets. To predict testing data, each DT's initially generates its own prediction then predicted from all DT are combined.
- Gradient Boosting Tree (GBT) – It is the ensemble of tree-based predictors where every tree is developed sequentially. Every tree is subsequently included to the method, for prediction or fit to residual errors achieved from the past method. In this article, the XGBoost is used for implementing the gradient boosting tree.
- Adaboost – It is the ensemble method used for regression or classification. It develops the strong learner through continuously giving weak learners. In each cycle of learning, the new weak learner is attained for the ensemble and the weighting vector is changed to focus on samples that are mislabelled in the final cycles.

3.5.1 Snapshot ensemble classifier

Utilizing ensemble learning technique, it achieves high generalization capability compared to single method, thereby enhancing classification performance. The classical ensemble techniques produce effective training costs when the snapshot ensemble adjusts learning rate by cosine annealing without maximizing the training costs. In this research, snapshot ensemble examines changing procedure of cosine annealing learning rate and principles of training or testing.

3.5.1.1 Principles of Snapshot Ensemble

It generates set of correct and diverse methods by training process. Significance of the snapshot ensemble is the optimization procedure that visited the multi-local minima before converging for last minimum. Saving method parameters to various local minimums is the same as a snapshot of the method in various local minimums. In optimization process, the Stochastic Gradient Descent (SGD) is utilized and the mathematical formula for calculation is given in Equations (15) and (16).

$$g_t = \nabla_{\theta_{t-1}} f(\theta_{t-1}) \quad (15)$$

$$\Delta\theta_t = -\eta \times g_t \quad (16)$$

Where, η is learning rate and g_t is gradient. Although the trained network is not converged for global minimum, it exhibits better generalization capability, particularly about local minima. While utilizing the SGD to optimization, whether learning rate is too large, or convergence rate is delayed, that provides good local minima.

3.5.1.2 Cyclic Cosine Annealing Learning Rate

The cyclic learning rate is an essential technique to adjust the learning rate. This technique sets the upper and lower limits for learning rate so that a learning rate score modifies periodically among upper and lower limits. Hence, procedure of snapshot ensemble utilizes a cyclic cosine annealing learning rate. In an initial phase of training, learning rate is gradually minimized in accordance with cosine function. As a result, the method converges to an initial local minimum after 50th training epoch next, learning rate is changed for beginning value and process of optimization continues to high learning rate. This procedure was repeated several times to attain multi-convergence local minima. The mathematical expression for measuring the learning rate is in Equation (17).

$$\alpha(t) = f\left(mod\left(t-1, \left[\frac{T}{M}\right]\right)\right) \quad (17)$$

In the above Equation (17), the t is number of iterations, the T is whole amount of training and f is the monotonically minimizing function. The whole training procedure is separated to M cycles, every cycle initializes with a similar starting learning rate and that is annealed to small learning rate in single cycle. Beginning learning rate is $\alpha = f(0)$, that makes method jump out on present local minimum point.

3.5.1.3 Snapshot Incorporation of training and testing

In process of snapshot ensemble, cosine annealing learning rate is utilized for setting the less initial learning rate for train method. As training phase maximizes, learning rate simulates to minimize. In end of the training phase, learning rate reached minimum, and value of a loss function reached local minima, which converges to local optima. Before proceeding to a next training cycle, snapshot is taken, and method parameters are saved. Learning rate is then readjusted to highest initial values. Following this, optimization continues to target the next local optimum. In this process, training time of M snapshot methods is similar as the training time of networks in classic techniques and there is null extra training cost. Hence, utilizing snapshot ensemble technique saves efficient training costs, attains a method with high generalization capability and enhances classification accuracy.

In the testing stage, prediction output is the mean of softmax output in m snapshot methods. Let x is the test sample and the $h_i(x)$ is result value of softmax of i snapshot method. The mathematical expression for ensemble is given in Equation (18).

$$h_{ensemble} = \frac{1}{m}\sum_{0}^{m-1} h_{M-i}(x) \quad (18)$$

4. EXPERIMENTAL RESULTS

The performance of the snapshot ensemble model is simulated on Python environment and the required configurations are i5 processor, 8 GB RAM and Windows 10.

In Table 1, performance of snapshot ensemble technique is evaluated with different classes like Anthracnose, Blackspot, Phytophthora, Powdery mildew and Ringspot. The snapshot ensemble classifier obtained 90.00% precision on Anthracnose, 85.71% precision on Black_spot, 81.25% precision on Phytophthora, 100.00% precision on Powdery mildew and 94.12% precision on Ringspot class.

Table 1: Performance of Snapshot ensemble classifier with different classes

Classes	Precision (%)	Recall (%)	F1-score (%)
Anthracnose	90.00	94.74	92.31
Black_spot	85.71	66.67	75.00
Phytophthora	81.25	92.86	86.67
Powdery mildew	100.00	100.00	100.00
Ringspot	94.12	88.89	91.43

In Table 2, performance of feature extraction is evaluated with different feature extraction algorithms. The different feature extraction algorithms considered to evaluate performance of HOG are Speed Up Robust Features (SURF), Local Binary Pattern (LBP) and Local Ternary Pattern (LTP). While compared to these existing algorithms, the HOG has the ability to effectively capture the shape and structural patterns.

Table 2: Performance of HOG based feature extraction technique

Methods	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	AUC (%)
SURF	69.45	65.00	69.00	66.94	70.80
LBP	71.50	69.08	68.90	68.99	68.45
LTP	68.32	69.10	67.75	68.42	70.22
HOG	89.83	90.22	88.63	89.42	93.27

The HOG based feature extraction technique obtained accuracy 89.83%, precision 90.22%, recall 88.63%, an f1-score 89.42% and Area Under the Curve (AUC) 93.27% which is more effective than different feature extraction techniques. In Table 3, performance of feature selection is validated to various feature selection techniques. The different feature selection algorithms considered to validate performance of ROBL-TSA are Reptile Search Algorithm (RSA), Whale Shark Optimization (WSO) and Salp Swarm Algorithm (SSA). The ROBL-TSA introduced the potential solution to prevent from trap of local optima, this allows the algorithm for quick convergence and effective balance between exploration and exploitation. This ensures that the chosen feature subset is diverse and generalize better through choosing relevant features. The SSA based feature selection technique acquired an accuracy 89.83%, precision 90.22%, recall 88.63%, f1-score 89.42% and AUC 93.27% which is more effective than different feature selection algorithms.

Table 3: Performance of ROBL-TSA based feature selection algorithm

Algorithms	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	AUC (%)
RSA	67.45	68.32	66.85	67.58	70.25
WSO	70.58	71.22	69.80	70.50	72.89
SSA	73.10	74.05	72.45	73.24	74.65
ROBL-TSA	89.83	90.22	88.63	89.42	93.27

Table 4: Performance of developed Snapshot Ensemble Classifier

Classifiers	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	AUC (%)
RFC	63.00	64.00	65.00	62.00	76.92
Ada boost	60.00	64.00	60.00	51.00	75.00
Gradient Boosting	82.00	88.00	78.00	82.00	76.92
Snapshot Ensemble classifier	89.83	90.22	88.63	89.42	93.27

In Table 4, a performance analysis of various classifiers on papaya dataset. The different classifiers considered to evaluate the performance of ensemble method are Random Forest Classifier (RFC), Adaboost and Gradient Boosting. Developed algorithm works well on complex and high-dimensional data, this minimizes computation cost while comparing with multiple independent algorithms. This algorithm handled the overfitting issues than other conventional boosting algorithms. The ensemble technique acquired an accuracy 89.83%, precision 90.22%, recall 88.63%, f1-score 89.42% and AUC 93.27% which is more effective than different classifiers.

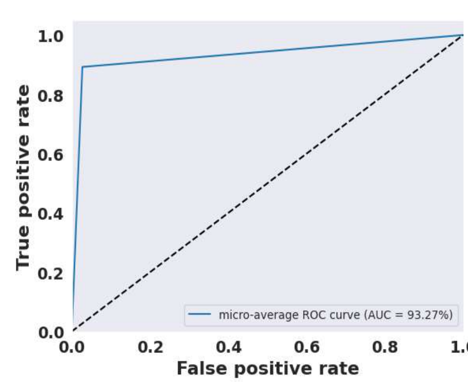

Figure 3: ROC Curve of snapshot ensemble classifier

In Figure 3, the AUC represents a separability of the degree attained through the snapshot ensemble

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classifier. The AUC of 93.27% was achieved, demonstrating excellent performance in differentiating between the positive and negative classes. The curve shows that a model performed well while maintaining high True Positive Rate (TPR) and less False Positive Rate (FPR).

The snapshot ensemble classifier is efficient in differentiating the different classes with high performance. Figure 4 represents a confusion matrix of Snapshot ensemble classifier. In Table 5, a performance of proposed ensemble classifiers is validated with various k-fold values. The k-fold values considered in this article to evaluate the proposed ensemble classifier are 2, 3 and 5. In the value of k=5, the proposed ensemble method showed the highest performance with high classification accuracy. Figure 5 represents the fitness graph for optimization algorithm.

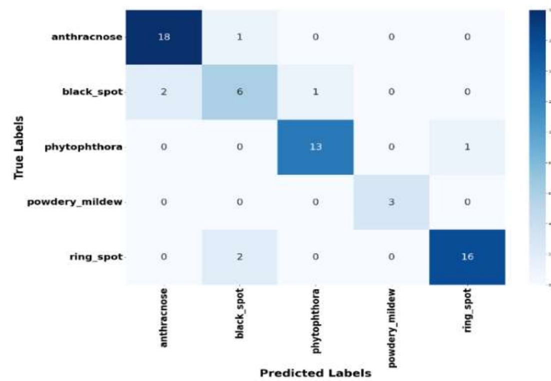

Figure 4: Confusion matric for Snapshot ensemble classifier

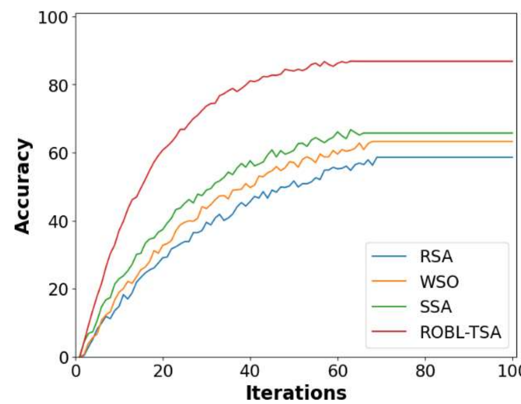

Figure 5: Fitness graph

Table 5: Performance of k-fold validation

K-fold values	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)	AUC (%)
2	65.00	67.00	64.00	65.47	78.00
3	67.75	69.00	66.00	67.47	80.50
5	89.83	90.22	88.63	89.42	93.27

4.1 Comparative Analysis

Performance of developed ensemble classifier is comparing to existing techniques like RFC [17], and FANN [18] with different fruit disease classifications. The RFC [17] method identified the disease in jackfruit with an accuracy of 89.59% and the FANN [18] identified the ripeness stage of mango with 89.6% accuracy. The Snapshot ensemble classifier is proposed to classify the different classes of papaya fruit disease. In a Snapshot ensemble classifier, a learning rate is scheduled to cyclically increase and decrease over time, preventing the method from overfitting to a single solution and allowing it to explore multiple high-quality solutions. The ROBL-TSA-based feature selection algorithm is developed which chooses the appropriate features to classify the different disease classes of papaya. The HOG-enabled feature extraction model is utilized to capture meaningful attributes from the images to differentiate different classes of diseases. In this article, papaya fruit diseases are identified with a high classification of 89.83%, precision of 90.22% and recall of 88.63% and proposed method outperforms existing techniques in terms of performance, which is shown in Table 6 and Table 7.

Table 6: Comparative analysis of developed model on the papaya dataset

Methods	Accuracy (%)	Precision (%)	Recall (%)
RFC [17]	89.59	74.20	73.61
FANN [18]	89.6	NA	NA
Proposed Snapshot ensemble classifier	89.83	90.22	88.63

Table 7: Comparative analysis of YOLO-Papaya [19]

Methods	Inference time (ms)	mAP (%)
YOLO-Papaya [19]	3.9	86.2
Proposed Snapshot ensemble classifier	4.3	88.5

4.2 Discussion

Results of a Snapshot ensemble model are validated with different techniques like SURF, LTP, LBP, RSA, WSA, SSA, RFC, GBT and Adaboost techniques. Moreover, a performance of the developed snapshot ensemble approach is compared to previous methods such as RFC [17], FANN [18] with different fruit disease classifications. The RFC [17] method identified the disease in jackfruit and the FANN [18] identified the ripeness stage of mango. The RFC [17] method doesn't resize the images which increases the complexity of the model. The FANN [18] method used only a small amount of training. The Snapshot ensemble classifier is proposed to classify the different classes of papaya fruit disease. In the Snapshot ensemble classifier, a learning rate is scheduled to cyclically increase and decrease over time, preventing the method from overfitting to a single solution and allowing it to explore multiple high-quality solutions. The ROBL-TSA-based feature selection algorithm is developed which chooses the appropriate features to classify the different disease classes of papaya. The HOG-enabled feature extraction model is utilized to capture meaningful features from images to differentiate the different classes of diseases.

Although, proposed model outperformed existing algorithms, that has certain drawbacks. Initially, dataset size is relatively small (214 images before augmentation), that restrict generalization ability. The research considered only five papaya diseases, whereas real-world scenarios include more different classes and environmental variations. HOG is handcrafted feature extractor and not completely captured deep semantic features when compared to advanced CNNs.

4.3 Research Problems and Open Issues

This manuscript addressed key problems in papaya fruit disease detection include challenges of capturing discriminative features from variable textures and colors, removing redundant feature which minimize efficiency and mitigating overfitting and limited generalization in conventional classifiers. When proposed HOG-based feature extraction with ROBL-TSA feature selection and Snapshot Ensemble classification enhanced accuracy and robustness. The size of dataset is relatively small and limited to five papaya diseases, that affect generalization ability to broad real-world scenarios. Scalability for real-time deployment on IoT devices is obtained and combining deep feature learning algorithms like CNNs or Vision Transformers with optimization-based feature selection remains challenging.

5. CONCLUSION

In this study, we developed an efficient and accurate method to classify papaya fruit diseases using a Snapshot Ensemble-based learning approach. The proposed model integrates HOG for feature extraction, the ROBL-TSA for selecting important features, and a Snapshot Ensemble classifier with a cyclic learning rate to improve generalization and reduce overfitting. This approach successfully classified five types of papaya fruit diseases and achieved superior performance compared to traditional classifiers. Key conclusions are:

- Pre-processing techniques such as Gaussian blur and data augmentation improved the input quality and model robustness.
- HOG effectively captured structural and textural features of diseased papaya regions.
- ROBL-TSA selected the most relevant features, improving classification accuracy and reducing computation time.
- The Snapshot Ensemble classifier achieved an accuracy 89.83% and an AUC 93.27%, outperforming standard models.

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- The proposed method is scalable, cost-effective, and suitable for precision agriculture applications.

Future Work involves expanding dataset with much different samples and extending model to additional papaya diseases and other crops. Including Transformers with advanced feature selection will improve the semantic learning. Segmentation model will integrate for accurate lesion detection, when lightweight models support for real-time deployment. Moreover, embedding uncertainty quantification and explainability will enhance reliability for precision agriculture applications.

REFERENCES

[1] Gulzar, Y., 2025. PapNet: An AI-Driven Approach for Early Detection and Classification of Papaya Leaf Diseases. *Applied Fruit Science*, *67*(4), p.256.

[2] Gani, R., Rashid, M.R.A., Ahmed, J., Isty, M.N., Islam, M., Hasan, M., Ferdaus, M.H. and Ali, M.S., 2024. Smartphone image dataset to distinguish healthy and unhealthy leaves in papaya orchards in Bangladesh. *Data in Brief*, *55*, p.110599.

[3] Parmar, M. and Degadwala, S., 2024. Deep learning for accurate papaya disease identification using vision transformers. *International Journal of Scientific Research in Computer Science, Engineering and Information Technology*, *10*(2), pp.420-26.

[4] Biswas, R., Sahu, P., Manwal, M., Mohapatra, S.K., Goyal, H. and Mohanty, J., 2025. Papaya diseases classification using fuzzy CNN network. In *Intelligent Computing and Communication Techniques* (pp. 377-384). CRC Press.

[5] Britto, I.O., Fernandes, P.M.B. and Santos, A.M.C., 2024. Stage-Specific Biomarkers for Papaya Sticky Disease Using the Molecular Profile of Carica papaya (L.) Leaf Extracts: A Chromatographic Approach. *Food Analytical Methods*, *17*(11), pp.1581-1591.

[6] W. Wang, A. Zhu, H. Wei, and L. Yu, "A novel method for vegetable and fruit classification based on using diffusion maps and machine learning", *Current Research in Food Science*, Vol. 8, 2024, p. 100737.

[7] Chen, D., Lin, F., Lu, C., Zhuang, J., Su, H., Zhang, D. and He, J., 2025. YOLOv8-MDN-Tiny: A lightweight model for multi-scale disease detection of postharvest golden passion fruit. *Postharvest Biology and Technology*, *219*, p.113281.

[8] Zayani, H.M., Ammar, I., Ghodhbani, R., Maqbool, A., Saidani, T., Slimane, J.B., Kachoukh, A., Kouki, M., Kallel, M., Alsuwaylimi, A.A. and Alenezi, S.M., 2024. Deep learning for tomato disease detection with YOLOv8. *Engineering, Technology & Applied Science Research*, *14*(2), pp.13584-13591.

[9] Karki, S., Basak, J.K., Tamrakar, N., Deb, N.C., Paudel, B., Kook, J.H., Kang, M.Y., Kang, D.Y. and Kim, H.T., 2024. Strawberry disease detection using transfer learning of deep convolutional neural networks. *Scientia Horticulturae*, *332*, p.113241.

[10] Lv, M. and Su, W.H., 2024. YOLOV5-CBAM-C3TR: an optimized model based on transformer module and attention mechanism for apple leaf disease detection. *Frontiers in Plant Science*, *14*, p.1323301.

[11] J. Wang, Z. Li, G. Gao, Y. Wang, C. Zhao, H. Bai, Y. Lv, X. Zhang, and Q. Li, "BerryNet-Lite: A Lightweight Convolutional Neural Network for Strawberry Disease Identification", *Agriculture*, Vol. 14, No. 5, p. 665, 2024.

[12] Sankaran, S., Subbiah, D. and Chokkalingam, B.S., 2024. CitrusDiseaseNet: An integrated approach for automated citrus disease detection using deep learning and kernel extreme learning machine. *Earth Science Informatics*, *17*(4), pp.3053-3070.

[13] Tewari, V., Azeem, N.A. and Sharma, S., 2024. Automatic guava disease detection using different deep learning approaches. *Multimedia tools and applications*, *83*(4), pp.9973-9996.

[14] Al-Shahari, E.A., Aldehim, G., Aljebreen, M., Alqurni, J.S., Salama, A.S. and Abdelbagi, S., 2024. Internet of Things Assisted Plant Disease Detection and Crop Management using Deep Learning for Sustainable Agriculture. *IEEE access*, *13*, pp.3512-3520.

[15] Moupojou, E., Retraint, F., Tapamo, H., Nkenlifack, M., Kacfah, C. and Tagne, A., 2024. Segment anything model & fully convolutional data description for plant Multi-disease detection on field images. *IEEE Access*.

[16] Wang, H., Nguyen, T.H., Nguyen, T.N. and Dang, M., 2024. PD-TR: End-to-end plant diseases detection using a transformer. *Computers and Electronics in Agriculture*, *224*, p.109123.

[17] U. Premchand, R.K. Mesta, M.P. Basavarajappa, Venkataravanappa, V., Narasimha L.R.C. Reddy, and K.S.

Shankarappa, "Epidemiological studies on the incidence of papaya ringspot disease under Indian sub-continent conditions", *Scientific Reports,* Vol. 15, No. 1, 2025, p. 6973.

[18] Y. Akhter and S. Saxena, "Association of Catharanthus Yellow Mosaic Virus and a Novel Tomato Leaf Curl Lucknow Betasatellite with Papaya Leaf Curl Disease (PaLCD) in India", *The Microbe,* Vol. 6, 2025 p. 100256.

[19] M. T. Habib, M. J. Mia, M. S. Uddin, and F. Ahmed, "An in-depth exploration of automated jackfruit disease recognition," *Journal of King Saud University, Computer and Information Sciences,* Vol. 34, No. 4, 2022, pp. 1200-1209.

[20] D. Worasawate, P. Sakunasinha, and S. Chiangga, "Automatic classification of the ripeness stage of mango fruit using a machine learning approach", *AgriEngineering,* Vol. 4, No. 1, 2022, pp. 32-47.

[21] J.L. de Moraes, J. de Oliveira Neto, C. Badue, T. Oliveira-Santos, and A. F. de Souza, "Yolo-papaya: a papaya fruit disease detector and classifier using cnns and convolutional block attention modules", *Electronics*, Vol. 12, No. 10, 2023, p. 2202.

[22] U. Amin, M.I. Shahzad, A. Shahzad, M. Shahzad, U. Khan, and Z. Mahmood, "Automatic fruits freshness classification using CNN and transfer learning," *Applied Sciences*, Vol. 13, No. 14, 2023, p. 8087.

[23] Z. Huang, X. Jiang, S. Huang, S. Qin, and S. Yang, "An efficient convolutional neural network-based diagnosis system for citrus fruit diseases," *Frontiers in Genetics*, Vol. 14, 2023, p. 1253934.

[24] S.M.R. Swapno, S.N. Nobel, M.B. Islam, P. Bhattacharya, and E.A. Mattar, "ViT-SENet-Tom: machine learning-based novel hybrid squeeze–excitation network and vision transformer framework for tomato fruits classification", *Neural Computing and Applications,* Vol. 37, 2025, pp. 6583-6600.

[25] M. Obayya, M.A. Arasi, N. Alruwais, R. Alsini, A. Mohamed, and I. Yaseen, "Biomedical image analysis for colon and lung cancer detection using tuna swarm algorithm with deep learning model", *IEEE Access*, Vol. 11, 2023, pp. 2169-3536.