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Research Article

Enhanced Deep Residual Network based Self-Learning framework for Mango leaf disease Classification: Focus on Anthracnose and Grey Blight

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ABSTRACT

In modern agriculture, ensuring early and accurate diagnosis of plant diseases is vital for crop health and yield. Deep learning has increasingly been utilized for diagnosing diseases in mango leaves using pathological images. Most existing solutions rely heavily on supervised learning models, which require extensive labeled data—a process that is both time-consuming and labor-intensive for agricultural experts. To ease this burden, a self-supervised learning approach has been developed that depends on minimal labeled data. This proposed work introduces a semi-supervised learning model for classifying mango leaf diseases, reducing the need for exhaustive manual annotation. The system is trained using 3,654 images of diseased mango leaves. BYOL (Bootstrap Your Own Latent), a self-supervised algorithm, was employed to train a ResNet with SE blocks network, enabling it to extract meaningful features from infected regions without relying entirely on labeled data. With only 30% of the dataset labeled, a self-supervised learning approach was used to develop a classification model for identifying Anthracnose, Grey Blight, and healthy leaves. This technique achieved an impressive classification accuracy of 98.11%, slightly surpassing the fully supervised ResNet-50 model's accuracy of 97.62%. The outcome demonstrates that accurate disease detection in mango leaves can be accomplished with reduced labeling effort, supporting more efficient and scalable agricultural diagnostics.

Keywords: efficient, technique, agricultural, minimal, annotation

INTRODUCTION

In agriculture fruit crops such as mango (Mangifera indica) have considerable commercial value due to their high demand, nutritional value and export potential. However, mango cultivation faces the constant threat of various foliar diseases such as Anthracnose and Grey Blight, which seriously affect the quality and quantity of the crop. Traditionally, crop disease diagnosis has relied on manual inspection by trained agricultural experts. While effective, this method is inherently subjective, laborious, and time-consuming, especially when applied to large-scale plantations. Deep learning models, particularly Convolutional Neural Networks (CNNs), have demonstrated significant success in extracting discriminatory features from diseased plant images for classification tasks. However, the performance of these models is highly dependent on large amounts of labeled data. Obtaining high-quality annotations for plant disease images requires domain expertise, which is a major obstacle to building scalable systems. In agricultural settings where expert time is limited and annotation costs are high, fully supervised learning techniques are often impractical[1].

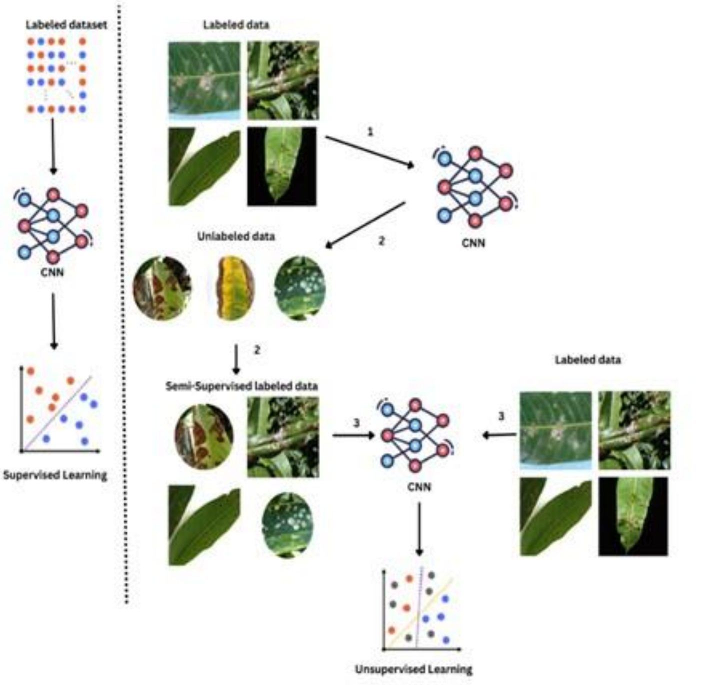
To overcome these challenges, semi-supervised learning (SSL) and self-supervised learning (self-SL) methods have attracted attention for their ability to use unlabeled data, thus reducing the annotation burden without significantly compromising model performance. Among these, adversarial learning frameworks such as SimCLR, MoCo, and BYOL (Bootstrap Your Own Latent) have emerged as powerful tools for learning visual representations in the absence of labels. These frameworks learn to map images into a feature space, where similar images are close together and dissimilar images are far apart, enabling efficient representation learning from unlabeled data.

In the proposed work a novel self-supervised learning approach for mango leaf disease classification is introduced. This approach uses a state-of-the-art self-supervised learning algorithm BYOL to pre-train a deep residual network enriched with Squeeze-and-Excitation (SE) blocks. This architecture is designed to improve feature recalibration by adaptively highlighting informative regions of the input images. The pre-training phase allows the network to extract rich and meaningful features from mango leaf images with minimal label supervision. The system was developed from a dataset of 3,654 high-resolution images representing mango leaves affected by Anthracnose, Grey Blight, and healthy samples. In the self-supervised training phase, only 30% of the dataset was manually labeled, leaving the remaining 70% unlabeled. A pre-trained model was fine-tuned using this small subset of labeled data to perform disease classification. The proposed method achieved a classification accuracy of 98.11%, outperforming the performance of the fully supervised ResNet-50 baseline model, which achieved an accuracy of 97.62%.

LITERATURE REVIEW

KHAOULA TAJI et.al. [2] presents a hybrid deep learning framework for early detection and classification of plant leaf diseases in apple and maize crops. It combines CNN and LBP features, optimized using BDA, ACO, and MFO meta-heuristic algorithms. The ensemble feature vector is classified using advanced machine learning techniques. The proposed method achieves 99.8% accuracy, surpassing existing models. V. K. Vishnoi et.al.[3]work proposes a lightweight CNN with fewer layers to reduce complexity and enhance efficiency. Data augmentation techniques—such as shift, shear, scale, zoom, and flip—are used to expand the training set. Trained on the PlantVillage dataset, the model accurately identifies Scab, Black Rot, and Cedar Rust in apple leaves, achieving 98% accuracy. It outperforms many deep CNNs in terms of speed and storage, making it ideal for handheld device deployment. EWEES, A. A. et al. A novel approach utilising the crossover-salp ensemble and locust optimisation algorithm (cSG) is proposed in two parts. This approach uses advanced SSA as a local search to enhance the GOA exploration phase once SSA filling is completed using crossover operators. This enhancement subsequently prevents cSG from experiencing halting in local minima, high computation time, and premature convergence. The suggested cSG approach is tested on a range of optimisation tasks to verify its efficacy. Lastly, the outcomes are contrasted with a number of popular algorithms on feature selection datasets, global optimisation, and six actual engineering challenges. The experimental findings show that CSG outperforms SSA in resolving various optimisation issues because of the incorporation of crossover operators, which enhances its flexibility and performance [6]. The Ebola virus disease transmission model was enhanced by Akinola et al. and subsequently converted into a mathematical model. The novel metaheuristic algorithm EOSA is designed using the obtained model. Two sets of benchmark functions—47 classical benchmark functions and over 30 constrained IEEE CEC benchmark functions—were subjected to EOSA. The outcome of a comprehensive test to evaluate the algorithm's performance revealed that it is comparable to other population-based techniques. This performance is thought to be on par with other cutting-edge literary techniques. In several situations, the metaheuristic algorithm EOSA did not perform well [8]. Using methods for picture segmentation, feature extraction, optimisation, and classification, Jain et al. describe an autonomous disease diagnosis system. In order to determine the ideal number of features that provide the highest classification accuracy, this research suggests a Memetic Swarm Optimisation Algorithm (MSSOA), which converts into a binary MSSOA. The suggested feature selection algorithm's performance is evaluated against the UCI benchmark datasets in comparison to five metaheuristic feature selection algorithms (BSSA, BPSO, BMFO, BCOA, and IBHHO). The findings show that the suggested approach works better than the others by lowering the feature size and improving classification accuracy. The proposed algorithm was implemented for automatic detection of corn, rice and grape plant diseases and achieved classification accuracy of 90.6%, 67.9% and 91.6% and best classification accuracy of 93.6%, 79.1% and 95% [4][5].

PROPOSED METHODOLOGY



Train the CNN using the labeled dataset.
Use the trained CNN to generate pseudo-labels for the unlabeled data.

Fine-tune the CNN by retraining it with a combination of labeled and pseudo-labeled data.

Figure 1: Supervised Learning vs Proposed Methodology

Deep transfer learning approaches are currently the most commonly applied method for plant identification diseases in agriculture. A novel and unique method, which takes advantage of leaf disease image enhancement, semi-supervised learning is designed to exploit the contrast information embedded in images for addressing mango diseased leaf image classification. Strategies such as Deep Contrastive Learning and simCLR, have attempted to improve robust pattern recognition and feature extraction. However, such a target is limited due to curing non-satisfactory effects resulting from the absence of designing effect-enhanced operators. To address that, the new SE-ResNet structure is introduced by integrating the sensitivity-enhanced mechanism in a residual block.

The dataset with various light intensity leaf images of different sizes has been considered for performance analysis on Anthracnose and Grey blight diseased leaf images. The suggested novel Semi Supervised learning-based SE-ResNet technique provides a simple yet efficient performance to address the test issue and congenial diseased leaf image datasets, and it may have excellent potential for broad agricultural applications. Proposed approach has a primary goal of classifying the acquired dataset of images into Anthracnose, Grey Blight or Healthy leaves. The results demonstrate the effectiveness of the proposed method.

A semi-supervised learning method with a contrastive loss function is customized to classify the leaves affected by Anthracnose and Mango Grey Blight. Most existing deep learning methods for leaf classification and disease detection show high accuracy but rarely focus on mango leaves—likely due to limited datasets. To address this, a deep learning approach using a dataset of mango leaves affected by grey blight and anthracnose diseases is applied, leveraging a semi-supervised learning setup that utilizes both labeled and unlabeled data. However, there is a lack of labeled deep learning data in several fields of application because it often requires expensive and time-consuming labeling efforts. Semi-supervised learning is effective when sequentially labeled data is available, reducing labeling costs and enabling time-based data classification. It requires only a small portion of accurately labeled data to generalize well Figure 1.

A. *Preprocessing*

Pre-processing images to transform the images to provide to the semi-supervised model includes:

a) Random Resized Crop:

Randomly crop a portion of the image and resize it to a fixed size 224×224.

I(x,y,c): Input image of size H*W*C (H: Height, W: Width, C: Number of Channels)

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s~U(smin,smax): random scale factor (area of crop relative to original image)

r~U(rmin,rmax): Random aspect ratio

A=H*W: Area of original image

A′=s·A:Target area of the crop

$$w' = \sqrt{A' \cdot r} \qquad (1)$$

$$h' = \sqrt{A'/r} \qquad (2)$$

where w' and h' : width and height of the crop Equation (1) and (2).

x0~U(0, W−w′) and y0~U(0, H−h′)

where x0 and y0 : Top-left corner of the crop

Crop function Euqation(3):

Icrop (x,y,c) = I(x+x0, y+y0,c) 0≤x<w′,0≤y<h′ (3)

Resize Operation to 224×224:

$$Iout(u, v, c) = Icrop + (x = \frac{w'}{224} \cdot u, y = \frac{h'}{224} \cdot v, c) \qquad (4)$$

where 0≤u, v < 224

b) Random Horizontal Flip:

Flip the image with a probability.

I input image; F(I) horizontally flipped image.

P~U(0,1) : random variable sampled from a uniform distribution.

p∈[0,1] : probability of flipping.

Then the Random Horizontal Flip operation T(I) is defined as in Equation (5):

T(I)= $\{F(I) \quad if\ P < p\ I \quad otherwise$ (5)

Where, F(I)(x,y)=I(W−x−1,y)

image width W.

This flips the image horizontally by mirroring pixels across the vertical axis.

c) Color Jittering:

Randomly change brightness, contrast, saturation, and hue.

I(x,y)=[R(x,y), G(x,y), B(x,y)] be the original RGB image at pixel (x,y).

Let αb, αc, αs, αh be random variables sampled from defined jitter ranges:

Brightness: αb~U(1−βb,1+βb)

Contrast: αc~U(1−βc,1+βc)

Saturation: αs~U(1−βs,1+βs)

Hue: αh~U(−βh, βh)

d) Random Grayscale conversion:

Convert to grayscale with a certain probability Equation (8).

I(x,y)=[R(x,y),G(x,y),B(x,y)] be the RGB color image at pixel (x,y).

P~U(0,1) is a random variable.

p∈[0,1] is the probability of applying grayscale. The grayscale intensity is computed using the luminance formula as in the Equation (6) and (7):

$L(x,y)=0.299\cdot R(x,y)+0.587\cdot G(x,y)+0.114\cdot B(x,y)$ (6)

$G(x,y)=[L(x,y),L(x,y),L(x,y)]$ (7)

$T(I)(x,y) = \{G(x,y) \quad if\ P < p\ I(x,y) \quad otherwise$ (8)

e) Gaussian Blur: Applying blur randomly

Gaussian blur with random application, we need two components:

The Gaussian blur itself (a convolution with a Gaussian kernel).

A random application rule that applies the blur based on some probability.

The 2D Gaussian function used to create the blur kernel is Equation (9):

$$G(x,y) = \frac{1}{2\pi\sigma^2} \cdot e^{-\frac{x^2+y^2}{2\sigma^2}} \tag{9}$$

Where:

x,y are the pixel distances from the center of the kernel.

σ is the standard deviation (controls the amount of blur).

The blurred image Iblurred is computed via convolution Equation (10):

$$I_{\text{blurred}}(i,j) = \sum_{m=-k}^{k} \sum_{n=-k}^{k} G(m,n) \cdot I(i-m, j-n) \tag{10}$$

where, I(i,j)is the original image pixel at (i,j)

G(m,n) is the Gaussian kernel

k is half the kernel size (5×5 kernel, k=2)

Bernoulli random variable B~Bernoulli(p) Equation (11).

where,

$B = \{1 \quad probability\ p\ 0 \quad probability\ 1 - p$ (11)

Final output image Iout is Equation (12) and (13):

$I_{out}=B\cdot I_{blurred}+(1-B)\cdot I$ (12)

Where,

I is the original image,

$I_{blurred}$ is the blurred version

p is the probability of applying the blur (p=0.5).

$$I_{\text{out}}(i,j) = B \cdot \left(\sum_{m=-k}^{k} \sum_{n=-k}^{k} G(m,n) \cdot I(i-m, j-n) \right) + (1-B) \cdot I(i,j) \tag{13}$$

B. Model Architecture

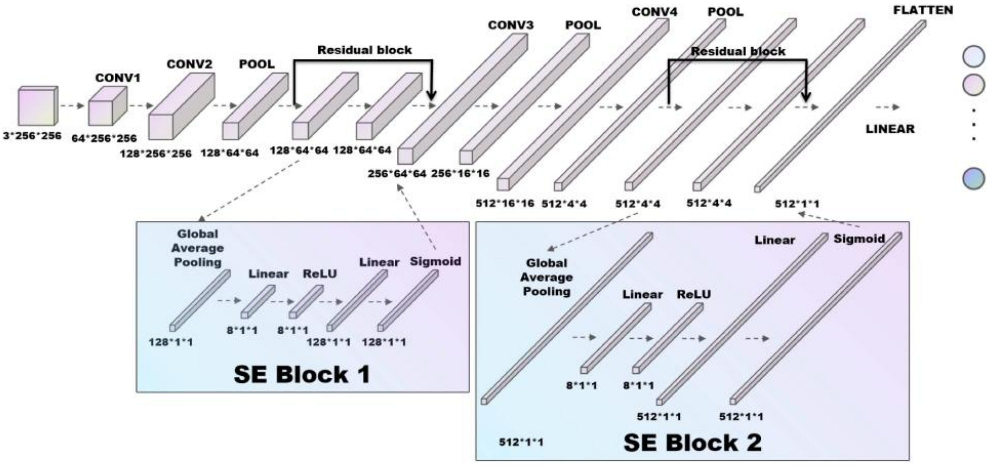


Figure 2: SE-Resnet9 backbone network

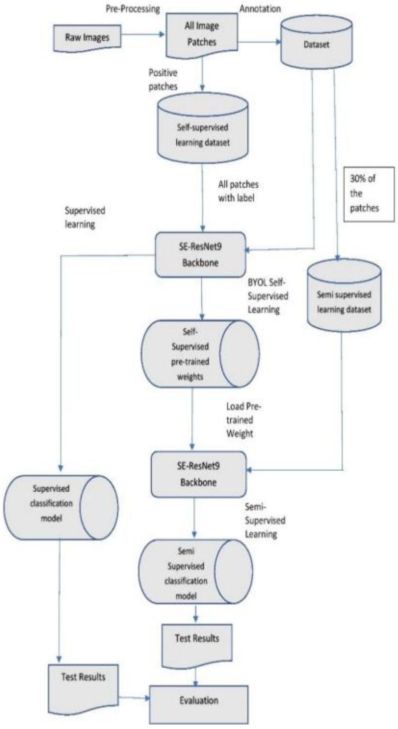


Figure 3: Proposed Classification model based on self-supervised pre-trained weights

a. SE-ResNet9 backbone network

Many variants of the ResNet model have been proposed in the literature. Among them, ResNet9 has a relatively shallow version of the ResNet architecture compared to deeper variants such as ResNet50 or ResNet101. In situations where data or computing resources are limited (as in our case), a shallow network may be more practical while still benefiting from the advantages of remaining connections. Factors such as dataset size, computational resources, and specific application requirements should be considered when choosing a neural network architecture for plant disease diagnosis. ResNet9 balances performance and efficiency, making it an acceptable choice for image classification tasks, including plant disease diagnosis.

ResNet-9 is a 9-layer deep Convolutional Neural Network (CNN) and a simplified variant of the ResNet (Residual Network) architecture. Though shallower than models like ResNet-50, ResNet-9 retains the core innovation of residual blocks, which use skip connections. These connections help in training deeper networks by mitigating the vanishing gradient problem, allowing for more stable and faster convergence. Despite its smaller size, ResNet-9 is effective in tasks such as image classification.

ResNet-9 with SE (Squeeze-and-Excitation) Blocks is a 9-layer convolutional neural network that combines the efficiency of the ResNet-9 architecture with the enhanced representational power of SE blocks Figure 2. SE blocks are attention mechanisms that adaptively recalibrate channel-wise feature responses by explicitly modeling the interdependencies between channels. SE Blocks are used to enhance feature representation via channel-wise attention. In this architecture, SE blocks are integrated into the residual blocks of ResNet-9 Figure 3. The SE module performs two key operations: Squeeze: Global average pooling is applied to generate channel-wise statistics. Excitation: A small fully connected network learns non-linear interactions and produces channel weights that emphasise informative features and suppress less useful ones.

b. BYOL-based self-supervised learning

BYOL (Bootstrap Your Own Latent) is a novel self-supervised learning approach that aims to learn representations that can be used for low-level tasks. BYOL has achieved peak performance on several benchmarks, including ImageNet linear evaluation. Its efficiency has also been demonstrated for transfer learning and semi-supervised learning. In this study, BYOL was used to learn representations of mango leaf images.

BYOL uses two neural networks of similar structures, classified into an online network and a target network. One of the significant innovations of BYOL is that instead of relying on negative pairs, the online network and the target network are trained to predict the representation of the same image under different magnifications.

Given an input image x, two augmented views x1 and x2 are created using data augmentation. These are passed through an encoder network n_θ:

$l_1=n_\theta(x_1)$ and $l_2=n_\theta(x_2)$ where l_1 and l_2 are latent representations.

A non-linear projector g_θ maps the latent representations into a different space:

$p_1=g_\theta(l_1)$ and $p_2=g_\theta(l_2)$ where p_1 and p_2 are projected embeddings.

The target network, parameterized by ξ with encoder and projector:

$l'_1=n_\xi(x_1)$ and $l'_2=n_\xi(x_2)$

$p'_1=g_\xi(l'_1)$ and $p'_2=g_\xi(l'_2)$

The target network undergoes continuous refinement using an Exponential Moving Average (EMA) to ensure smoother and more stable updates Equation (14).

$$\xi \square \tau\xi + (1+\tau)\,\theta \tag{14}$$

τ is the momentum parameter.

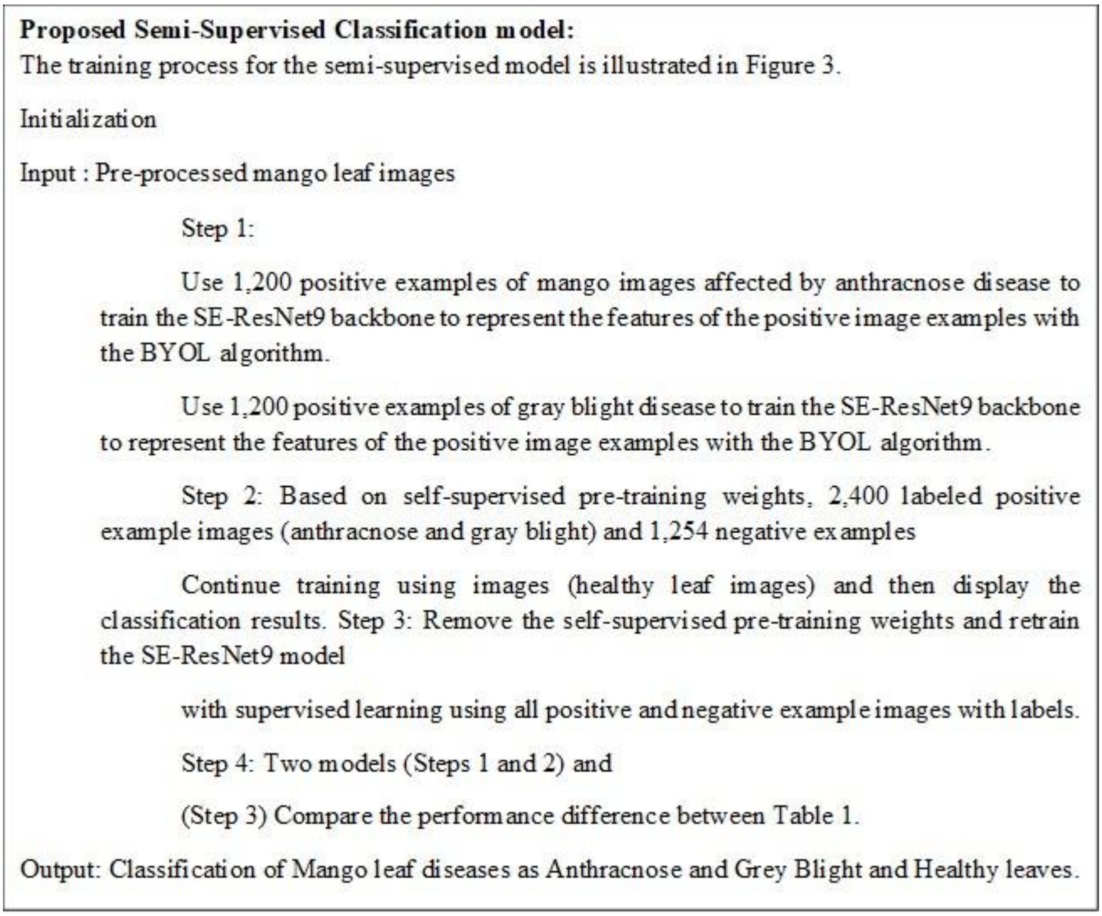
BYOL uses cosine similarity loss to enforce similarity between the online network's predictions and the target network's representations Equation (15) and (16):

$$L(p_1, p'_2) = -\frac{p1}{||p1||} \cdot \frac{p'2}{||p'2||} \tag{15}$$

$$L(p_2, p'_1) = -\frac{p2}{||p2||} \cdot \frac{p'1}{||p'1||} \tag{16}$$

The final loss is the sum of $L(p_1, p'_2)$ and $L(p_2, p'_1)$ Equation(17).

$$L_{BYOLFinal} = L(p_1, p'_2) + L(p_2, p'_1) \quad (17)$$



Proposed Semi-Supervised Classification model:
The training process for the semi-supervised model is illustrated in Figure 3.

Initialization

Input : Pre-processed mango leaf images

Step 1:

Use 1,200 positive examples of mango images affected by anthracnose disease to train the SE-ResNet9 backbone to represent the features of the positive image examples with the BYOL algorithm.

Use 1,200 positive examples of gray blight disease to train the SE-ResNet9 backbone to represent the features of the positive image examples with the BYOL algorithm.

Step 2: Based on self-supervised pre-training weights, 2,400 labeled positive example images (anthracnose and gray blight) and 1,254 negative examples

Continue training using images (healthy leaf images) and then display the classification results. Step 3: Remove the self-supervised pre-training weights and retrain the SE-ResNet9 model

with supervised learning using all positive and negative example images with labels.

Step 4: Two models (Steps 1 and 2) and

(Step 3) Compare the performance difference between Table 1.

Output: Classification of Mango leaf diseases as Anthracnose and Grey Blight and Healthy leaves.

RESULTS AND DISCUSSION

In the proposed work, a self-supervised classification model is proposed to recognise images containing Anthracnose and Grey Blight. Performance of the SE-ResNet9 semi-supervised model based on BYOL self-supervised pre-training weights was evaluated and compared with the SE-ResNet9 model without self-supervised pre-training weights. It can be concluded that the SE-ResNet9 backbone based on the BYOL algorithm self-supervised training can approach the classification accuracy of supervised learning with a small amount of labelled data. In plant pathology image classification, the BYOL-based self-supervised learning model offers two key advantages over supervised learning. Firstly, it facilitates full use of existing data. The images are interesting, pathologists are referred to as positive images containing corresponding tissue structures or lesions in plant pathology research. Therefore, the labelling and materials of positive images are usually readily available. The challenge of data labelling is greatly reduced. The semi-supervised model fine-tunes the weights of the self-supervised model by introducing 30% of the training set labels, and trains a fully connected layer to enhance classification accuracy. It greatly minimises the annotation burden on data engineers and pathologists while approaching the accuracy of supervised learning..

The model performance is evaluated in respect of various metrics Figure 3:

1) Accuracy: Accuracy is a commonly used performance metric that provides the ratio of correct prediction and the total no. of data samples or the total prediction made by the classifier. Both overall and individual class accuracy can be determined from the confusion matrix as in Equation 18.

$$\text{Accuracy}_{BYOL} = \frac{\sum_{i=1}^{N} 1\,(yi=\hat{y}i)}{N} \quad (18)$$

Where,

- yi is the true label
- $\hat{y}i$ is the predicted label from the classifier trained on BYOL embeddings
- 1(·) is the indicator function (1 if true, else 0)
- N is the number of samples.

2) Precision: It gives the fraction of all positive predictions that are actually positive Equation 19.

$$\text{Precision}_{\text{BYOL}} = \frac{TPBYOL}{TPBYOL+FPBYOL} \tag{19}$$

3) Recall or Sensitivity: It is the measure of ratio of correctly predicted positive samples and all positive samples Equation 20.

$$\text{Recall}_{\text{BYOL}} = \frac{TP_{\text{BYOL}}}{TP_{\text{BYOL}} + FN_{\text{BYOL}}} \tag{20}$$

4) Specificity or True Negative Rate (TNR): It defines the ratio of correctly predicted negative samples and all negative samples Equation 21.

$$\text{Specificity}_{\text{BYOL}} = \frac{TN_{\text{BYOL}}}{TN_{\text{BYOL}} + FP_{\text{BYOL}}} \tag{21}$$

5) F1-Score: It gives the harmonic mean of the precision and recall, and refers to the no. of correctly classified instances. It ranges from 0 to 1 Equation (22).

$$\text{F1}_{\text{BYOL}} = \frac{2 \cdot TP_{\text{BYOL}}}{2 \cdot TP_{\text{BYOL}} + FP_{\text{BYOL}} + FN_{\text{BYOL}}} \tag{22}$$

6) Cohen Kappa: Cohen Kappa is a measure of inter-rater reliability. Its higher value defines the model to be more reliable. It ranges from 0 to 1 Equation (23) and (24).

$$\kappa_{\text{BYOL}} = \frac{P_o - P_e}{1 - P_e} \tag{23}$$

Where:

- $P_o = \text{Accuracy}_{\text{BYOL}}$
- $P_e = \frac{(TP+FP)(TP+FN)+(TN+FN)(TN+FP)}{(TP+TN+FP+FN)^2}$

(24)

The Convolutional Neural Network model was trained with mini-batch gradient descent, in which the training set is broken down into subsets of smaller batches. This technique calculates the gradient of the loss function and adjusts the model weights accordingly, allowing for fast and stable convergence. Two very important hyperparameters—batch size and learning rate—are involved in this process and are highly interconnected. During this experiment, the model's performance was compared with varying batch sizes (50, 100, 150, and 200) and learning rates (0.0001, 0.001, and 0.01), as seen in Figure 4. The model performed best at a particular learning rate during these experiments.

To tackle overfitting, dropout regularization was utilized, which drops out a set of neurons randomly during training. The influence of various Dropout Rates (DR) was analyzed by changing the dropout rate from 0.0 to 0.8 with a step of 0.2. The model achieved a maximum validation accuracy of 97.62% at the dropout rate of 0.6.

In addition, the confusion matrix demonstrated that the majority of predictions were in close agreement with the actual labels, showing high classification performance. From the matrix, critical evaluation measures like precision, recall, F1-score, and Cohen's Kappa coefficient were calculated to thoroughly review the performance of the model.

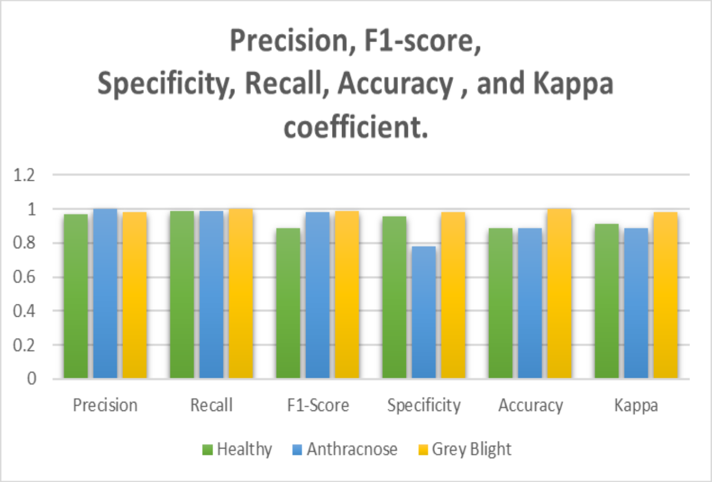


Figure 3: Evaluation of the model using parameters Precision, Recall, F1-Score, Specificity, Accuracy, Kappa

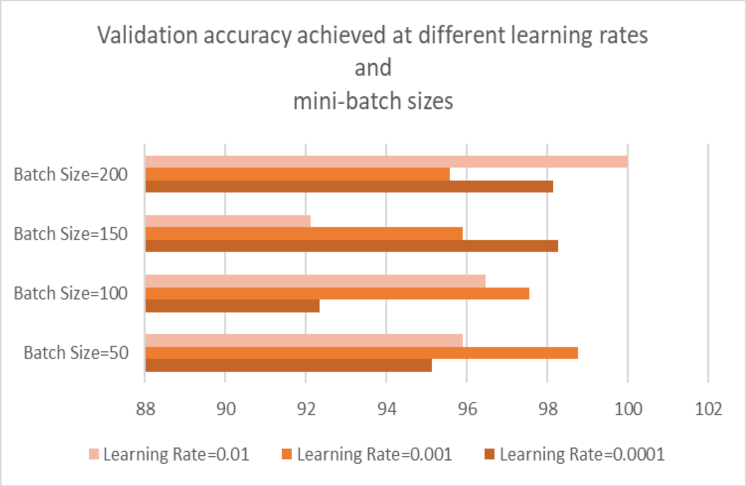


Figure 4: Validation accuracy achieved at different learning rates and mini-batch sizes

Dataset Description

The diseases used in this study are Mango Anthracnose and Grey Blight. These diseases were chosen because two diseases are prevalent in India. Standard Mango Leaf Disease (MLD) dataset is used which includes four types of images corresponding to the raw images captured from the field, corresponding to field images that were down-sampled to low resolution, background images used to generate synthetic images, and synthetic images. On the contrary, another dataset includes raw and processed images acquired under controlled conditions. This comparison is unfair because the processing and data collection of these datasets are different. Plant diseases are a significant factor reducing the quality and quantity of crops. With the advancement in computer vision, identification and analysis of diseased plant leaves through leaf images is becoming more and more attractive. However, it is difficult to obtain a dataset with a sufficient number of images. It is expected that the proposed dataset will contribute to the development of computational models for the identification of anthracnose and Grey Blight in mango leaves. This dataset consists of 3,654 images in JPEG format containing Anthracnose, Grey Blight and healthy leaves.

Comparison with Baseline Models

BYOL is a self-supervised learning model that learns useful visual representations from unlabeled data by predicting one augmented view of an image from another. In contrast, traditional CNN models rely on labeled data to learn directly from input-output mappings. Comparisons of supervised learning, and semi-supervised learning RestNet-9, ResNet-50, MobileNet, DenseNet, VGGNet, Inception and EfficientNet for disease diagnosis in Mango leaves is provided in Table 1.

Table 1: Comparison of proposed model with different supervised learning CNNs

Model	Accuracy	Precision	Recall or Sensitivity	Specificity or True Negative Rate	F1-Score	Kappa
RestNet-9	93.67	92.12	94.88	92.74	93.49	92.91
ResNet-50	97.62	90.67	91.55	90.88	91.11	90.90
AlexNet	88.02	86.43	89.32	86.94	87.85	86.73
Inception	86.77	85.54	87.12	86.38	86.32	85.90
VGGNet	92.63	91.88	92.35	92.01	92.11	91.75
DenseNet	94.45	93.57	94.92	94.11	94.24	93.98
MobileNet	95.81	95.03	96.34	95.18	95.68	95.42
EfficientNet	93.22	92.45	93.79	92.88	93.13	92.63
Proposed Model	98.11	97.78	98.23	99.34	97.65	92.45

CONCLUSION

This study focuses on the automatic identification of mango leaf diseases, specifically Grey blight and Anthracnose, using semi-supervised learning techniques. A Self-supervised approach is explored, leveraging a contrastive autoencoder for feature representation. The study evaluates a SE-ResNet9 model enhanced with BYOL self-supervised pre-training and compares it to a different CNN model. The results show that BYOL-based self-supervised learning achieves classification accuracy of (97.11%) similar (98.62%) to supervised learning while requiring significantly fewer labeled images. By labeling only 30% of the training data, the model effectively fine-tunes pre-trained representations, reducing the annotation workload while maintaining high accuracy. This approach enhances data efficiency and facilitates automated disease detection in agricultural research.

FUTURE WORK

Despite its effectiveness, this study has several limitations. The small dataset size limits the scalability evaluation of semi-supervised models, and only basic image preprocessing was applied, potentially affecting training efficiency. Additionally, alternative backbone networks were not explored for validation. Future research will implement advanced preprocessing techniques, introduce more detailed classification labels, and compare semi-supervised and supervised models more objectively.The dataset includes only Anthracnose and Grey blight images, lacking coverage of other mango leaf diseases. A broader study could examine dataset transferability for real-world applications. While the dataset is balanced, real-world data often lack class balance, affecting model performance. Semi-supervised learning expands natural class differences but may not always generate correct distinctions. Exploring alternative contrast learning methods and integrating class relationship labels through Contrast Label Learning (CLL) could enhance generalization and improve semi-supervised disease classification.

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