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# A NOVEL HYBRID APPROACH FOR PADDY LEAF DISEASE SEVERITY CLASSIFICATION USING SPATIAL BIDIRECTIONAL CONVOLUTIONAL NEURAL NETWORK CLASSIFIER

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## Abstract

Bacterial, viral, and fungal pathogens that cause Paddy Leaf Diseases (PLD) result in significant yield losses in rice crops. Early detection and effective management are crucial for ensuring optimal growth and productivity. For severity analysis, they used the publicly accessible Mendeley Rice Leaf Disease Dataset, which contains images of the illnesses Brown Spot, Blight, Blast, and Tungro. Gaussian Blur is a multi-step pre-processing technique that smoothens noisy images by identifying regions where intensity changes rapidly.Further image segmentation using Otsu's thresholding, which automatically determines the optimal threshold to separate the foreground and background based on image histogram analysis and feature extraction using an autoencoder, can be used to learn high-level features, and Scale-Invariant Feature Transform (SIFT) can capture local spatial information, enhancing the overall feature set for downstream tasks. Select KBest for the feature selection method that selects the top k features, evaluates each feature's relevance to the target variable, and retains the most informative ones. The proposed Spatial Bidirectional Convo Neural Feedforward Net (SBCNFN) integrates Convolutional Neural Networks (CNN) for spatial feature extraction, Feedforward Neural Networks (FNN) for nonlinear feature mapping, and Bidirectional Long Short-Term Memory (Bi-LSTM) networks for capturing bidirectional temporal dependencies in spatial sequences. Grid Search optimizes the model by fine-tuning hyperparameters to achieve the best performance. Python tools and libraries were used for model development. The proposed model used to classify the severity levels of paddy leaf disease, like Mild 98.62%, Average 96.7%, Severe 98.12%, and Profound Accuracy of 98.66%. The findings demonstrate that the suggested approach works better than the current approaches by offering more precise and trustworthy estimates of disease severity.

***Keywords: Paddy Leaf Disease, Gaussian Blur, Otsu's Thresholding, Autoencoder, Spatial Bidirectional Convo Neuro Feedforward Net Classifier, Grid Search, Disease Severity Prediction, Deep Learning (DL), Python.***

## 1. Introduction

The worldwide consumption of paddy rice amounts to half of the human diet because it plays an essential role in securing nutritional supplies and supporting rural economies. Different diseases attacking paddy leaves reduce photosynthetic activity and cause growth impediments that result in yield reduction [1]. Suboptimal environmental conditions allow quick disease expansion of PLD bacterial leaf blight, blast, and sheath rot, which results in severe agricultural harm [2]. These diseases can be effectively diagnosed in a short period and accurately, which allows the stakeholders to achieve the intended measures not only to reduce losses in agriculture but also to improve management practices. The visual examination is one of the ways used by experts to detect diseases through traditional methods but this is rather time consuming and may be subjective when dealing with large agricultural areas [3].

Advancements in the field of computer vision and the artificial intelligence have created a high level of interest in the development of automatic systems to detect diseases and the level of their severity [4]. Image processing and ML approaches have automated disease identification and symptom classification performance that operates at scale to provide the accurate analysis of the paddy leaf images [5]. The potential of complex visual data processing with the technology called DL brings a lot of benefits due to the possibility to find hard to detect features of the disease stage and extract repetitive patterns [6]. A hybrid approach combines decision trees and randomized processing layers and grid-based convolutional operations to provide the advantages of multiple learning approaches [7]. The combination develops the potential performance adaptive ability and the strong operations in various agricultural settings to the exact identification of disease in smart agriculture systems. The purpose was to create an effective model of the severity of rice leaf diseases classification using the SBCNFN Classifier based on the hybrid method to increase the accuracy of the study by incorporating CNN, FNN, and Bi-LSTM.

The paper describes the design and assessment of a rice leaf disease severity classification framework by the use of the Spatial Bidirectional Convo Neuro Feedforward Net (SBCNFN). Section 2 summarizes the related literature, paying attention to ML and DL methods of agricultural disease detection. Section 3 outlines the proposed model, which will entail the incorporation of CNN, FNN, and Bi-LSTM into the SBCNFN. Section 4 shows the experimental data comparing the proposed classifier with the conventional models in terms of accuracy and robustness. Section 5 ends with observations on future enhancements, such as model scalability, real-time field application and generalizability to other crop diseases.

## 2. Related Works

The automated image acquisition and processing system, used to estimate the severity of paddy disease of leaves, was created by [8]. The system measured the infection using pixels, using MATLAB. The percentages of infection were found to range between 15.53 and 41.23 pointing to higher detection levels than the results of leaf area meter but variation was noted. According to [9], AI-based models have been created to estimate the severity of three diseases affecting rice crop using image analysis. A CNN (Faster Region-based CNN (FRCNN)) and EfficientNet-B0 was optimized to reach an accuracy of 96.43, which is the highest among CNNs, and, therefore, field images allow predicting disease severity, leading to better management of organic crops.

Bacterial leaf streak (BLS) Net, an automatic system of recognizing and segmenting rice BLS lesions with a U-Net network, was investigated by [10]. The findings indicated that, BLSNet worked better than DeepLabv3+ and U-Net in area of segmentation accuracy and are highly promising to be reliable in estimating the severity of BLS diseases. It was [11] that formulated the technique of recognizing rice-leaf diseases and estimating the degree of severity of the various diseases in the paddy fields. The technique was the most accurate in the classification of three diseases and healthy rice leaves with a score of 0.43 more than the approaches of DL. As discussed by [12], the recognition of rice leaf disease was improved through the application of the DL and transfer learning methods using a dataset consisting of 5932 images. The VGG16 model (custom) was found to be more accurate in detecting different leaf diseases compared to existing models and had better generalization abilities. A study by [13] investigated the Efficient DL-based Fusion Model-Rice Plant Disease (EDLFM-RPD) detection and classification. It used the median filtering, K-means segmentation, Gray-Level Co-occurrence Matrix (GLCM), and Inception features, and Fuzzy Support Vector Machine (FSVM) classification. EDLM-RPD method resulted in a highest level of accuracy of 96.170% which was higher than the latest techniques.

Image processing methods were used to determine the occurrence of PLD. It consisted of preprocessing, feature extraction and evaluation of infected leaf images as discussed by [14]. The findings indicate the correct classification of diseased plants, which proves the high efficiency of the method in the identification of the affected areas and decreases the processing time with an enhanced signal-noise ratio. [15] studied the automated approach to the classification and recognition of PLD that includes bacterial blight and blast through the use of ML techniques. The approach had a 98.64 percent accuracy rate with Naive Bayes classification with firefly optimization.

## 3. Methodology

The dataset that was obtained was the Mendeley Rice Leaf Disease Dataset which included 5,932 labelled rice leaf images with the disease. Preprocessing entailed using a Gaussian Blur as a way of improving quality of images and to show areas of disease. The Otsu thresholding was used to segment the image and separate the foreground and background. AutoEncoder and SIFT were used to extract features of deep and local features. Relevant features were chosen by SelectKBest. SBCNFN combined grid search optimization with FNN, Bi-LSTM, and CNN in the classification of severity. This model was trained to give four degrees (Mild, Average, Severe, Profound) of the visual symptoms of disease spread, lesion coverage, and color degradation on the leaves. The general flow of the methodology is presented in Figure 1.

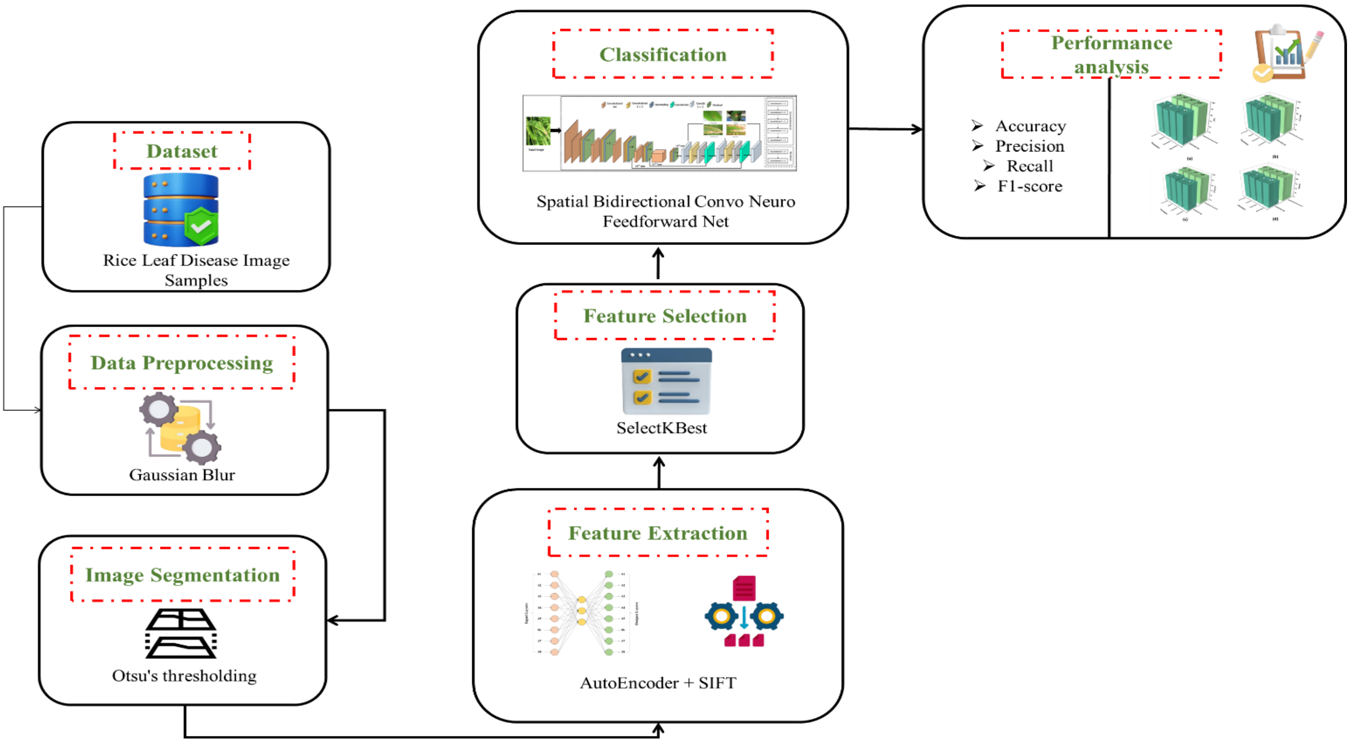


**Figure1: General Outline of the Methodological Approach**

### 3.1 Data Collection

The data consists of 5,932 pictures of rice leaves with four disease types, Brown Spot, Blast, Tungro and Bacterial Blight. It will help analyze images to identify these diseases, which will help in agricultural research and disease control. The dataset is to be used in the application of ML, specifically, the enhancement of disease detection. The training and validation images were developed with respect to the classes, as shown in Table 1. The sample images are indicated in figure 2. Every picture was graded with an equivalent degree of severity at harm level: Mild (less than 10 percent affected), Average (10-25 percent), Severe (26-50 percent), and Profound (over 50 percent). These were the labels as multi-class target outputs of the model.

**Source:** https://data.mendeley.com/datasets/fwcj7stb8r/1.

**Table 1: Training and Validation Image Distribution per Disease Class**

| Class Name | Training Images | Validation Images | Total Images |
|---|---|---|---|
| Bacterialblight | 1296 | 288 | 1584 |
| Blast | 1143 | 297 | 1440 |
| Brownspot | 1269 | 331 | 1600 |
| Tungro | 1038 | 270 | 1308 |

**a) Bacterial blight**

**b) Blast**

**c) Brown spot**

**d) Tungro**

**Figure 2: Sample rice leaf diseases**

### 3.2 Data Preprocessing using Gaussian Blur

Data preprocessing using Gaussian Blur smoothens noisy images in paddy leaf disease severity classification. This technique enhances feature extraction by reducing high-frequency noise, facilitating more accurate predictions with the classifier. One data processing method for smoothing the gathered values in the collection of data is blurring. The vectorized non-coding RNA sequence was smoothed using a Gaussian function. In Equation (1), the data were reprocessed with a Gaussian blur to increase accuracy.

$$g(y) = 1/\left(\sigma sqrt(2\pi)\right) f^{-1/2\left(\frac{y-\mu}{\sigma}\right)^2} \quad (1)$$

Sigma was set at 1, which is frequently used since it offers a reasonable level of blurring, computational efficiency, and customization flexibility. Gaussian Blur helped to enhance the regional contrast between diseased and healthy tissues, making it easier for subsequent segmentation and classification of the severity level.

### 3.3 Image Segmentation using Otsu's thresholding

Image segmentation using Otsu's thresholding effectively isolates the disease-affected regions of paddy leaves. This method helps in the accurate classification of disease severity by distinguishing relevant features. Assume that a grayscale image's intensity is represented in $K$. Grayscale levels$[\,1, 2, \dots, K]$. The total number of points can be written as $W\ = w1\ +\ w2\ + \cdots\ w_K$, and the number of elements with gray level at $j$ is shown by $w_j$. This grayscale image's histogram is thought of as a probability occurrence distribution in equation (2).

$$o(j) = \frac{w_j}{W}, \quad w_j \geq 0 \sum_{j=1}^{K} w_j = 1 \quad (2)$$

A threshold separates the image's pixels into the foreground and background, or $D_0$and $D_1$. Whereas $D_1$ indicates pixels within levels $D_0[1, 2, \dots, s]$ indicates pixels within levels $D_1[s + 1, \dots \dots, K]$. The average and this class's occurrence probabilities can be written in equations (3)-(6)

$$\omega_0 = \omega(s) = \sum_{j=1}^{s} o(j) \quad (3)$$

$$\omega_1 = 1 - \omega(s) = \sum_{j=s+1}^{K} o(j) \quad (4)$$

$$\mu_0 = \sum_{j=1}^{s} \frac{j.o(j)}{\omega_0} = \frac{1}{\omega(s)} \sum_{j=1}^{s} j.\, o(j) \quad (5)$$

$$\mu_1 = \sum_{j=s+1}^{K} \frac{j.o(j)}{\omega_1} = \frac{1}{1-\omega(s)} \sum_{j=s+1}^{K} j.\, o(j) \quad (6)$$

The overall mean can be expressed in equations (7)& (8).

$$\mu_S = \sum_{j=1}^{K} j.\, o(j) \quad (7)$$

$$\mu_S = \omega_0\mu_0 + \omega_1\mu_1 \tag{8}$$

Where the probability of the foreground and background parts is indicated by the symbols of $\omega_0$and $\omega_1$. Additionally, $\mu_0, \mu_1$and, and µS denote the average gray level of the gray image's foreground, background, and total gray level image.

The two classes $D_0$ and $D_1$ between-class variance $\sigma_A^2$are provided in Equation (9).

$$\sigma_A^2 = \omega_0(\mu_0 - \mu_S)^2 + \omega_1(\mu_1 - \mu_S)^2 \tag{9}$$

According to the discrimination analysis, the class's separability degree $\eta$is expressed in Equation (10).

$$\eta = \max_{1\le s\le K} \sigma_A^2 \tag{10}$$

To determine the ideal threshold $s^*$, $\sigma_A^2$is maximized, as shown in Equation (11).

$$s^* = arg\max_{1\le s\le K} \sigma_A^2 \tag{11}$$

Segmentation helped separate infected regions based on pixel intensity histograms. The resulting binary maps were essential in measuring lesion areas, which directly influenced the severity labeling.

### 3.4 Feature Extraction using AutoEncoder + SIFT

Feature extraction using AutoEncoder + SIFT combines deep and handcrafted features, capturing both global and local patterns in paddy leaf images to improve disease severity classification accuracy.

#### 3.4.1 AutoEncoder

Feature extraction using an AutoEncoder learns compact and informative representations of paddy leaf images, enabling efficient classification of disease severity. An unsupervised learning technique called AutoEncoder uses hidden layers to examine input images and then reconstruct the image as an output. During the reconstruction stage, it transfers the internal structure features of the input images to the output layer. Three layers make up the model, which carries out encoder and decoder functions. Though the hidden layer uploads the features that were collected as input, the encoder operation expands the size of the data. AutoEncoder improves classification performance by lowering image noise. Generating data near the input image through the use of backpropagation during the processing of images also reduces the error rate. The autoencoder model lowers the chance of errors and produces more effective outcomes by updating the weight parameters. Additionally, it recreates the compressed features using the loss methods. The $y$ variable's value converges to $y$, minimizing the loss rate. Equation (12) provides a mathematical expression for this. Equations (13) and (14) are used to determine the output layer value $(y')$ and the hidden layer value $(t)$. The $\sigma$was an activation function that had a bias vector $X.c$ is the weight matrix. Figure 3 shows the structure of an autoencoder.

$$M(y, y') = ||y - y'||^2 \tag{12}$$

$$z = \sigma(Xy + c) \tag{13}$$

$$y' = \sigma'(X't + c') \tag{14}$$

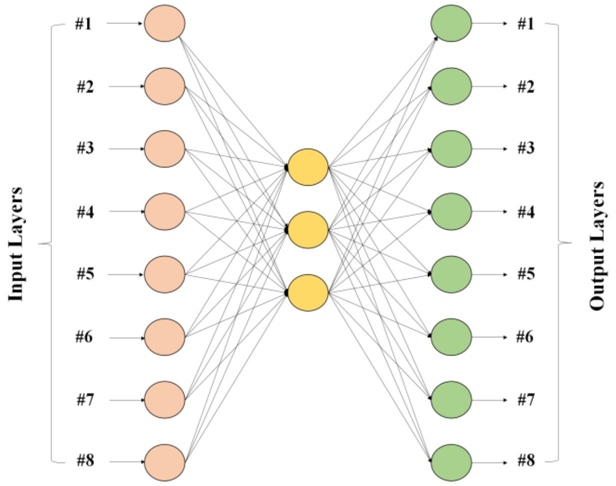


**Figure 3: Structure of AutoEncoder**

### 3.4.2 SIFT

Feature extraction using SIFT identifies key local features in paddy leaf images, enabling efficient classification of disease severity by capturing distinct patterns. The SIFT has various benefits and is typically used to extract local features from a picture. SIFT features remain constant when images are rotated, scaled, and illuminated; they remain somewhat stable when perspectives change, affine transformations occur, and they are resilient to noise. SIFT features are distinctive and instructive.

- Construct the DOG scale-space in Equation (15).

$$C(w,z,\sigma) = \left(H(w,z,l\sigma) - H(w,z,\sigma)\right) * J(w,z) = K(w,z,l\sigma) - K(w,z,\sigma) \qquad (15)$$

Where $H(w,z,\sigma) = \frac{1}{2\pi\sigma^2} e^{-\frac{w^2+z^2}{2\sigma^2}}$, $J(w,z)$ is the original image and $K(w,z,\sigma) = H(w,z,\sigma) * J(w,z)$.

- Get the key points: The critical spots in the difference of the Gaussian function, organized with the image, are obtained in the dimension space.
- For every key point, assign a gradient modulus and an orientation in equations (16) and (17).

$$n(w,z) = \sqrt{\left(K(w+1,z) - K(w-1,z)\right)^2 + \left(K(w,z+1) - K(w,z-1)\right)^2} \qquad (16)$$

$$\theta(w,z) = tan^{-1}\left(\frac{K(w,z+1)-K(w,z-1)}{K(w+1,z)-K(w-1,z)}\right) \qquad (17)$$

- Construct the descriptor of SIFT features: The gradient orientation histogram yields a 128-dimensional vector known as the descriptor, with eight bins in each child window. Figure 4 displays the paddy leaf image pre-processing and feature extraction output.

The features extracted by AutoEncoder captured high-level representations of disease spread patterns, while SIFT identified key local points that help differentiate subtle differences in disease intensity, both crucial for classifying severity levels.

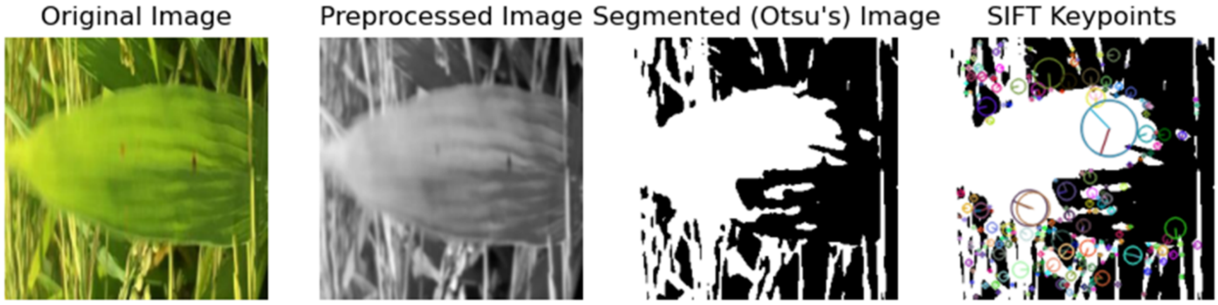


**Figure4: Output of preprocessing and feature extraction in Paddy Leaf Image**

### 3.5 Feature Selection using SelectKBest

Feature selection using SelectKBest ranks and selects the most significant features from paddy leaf data, reducing dimensionality and enhancing the efficiency and accuracy of disease severity classification models. ML specialists use the SelectKBest method to select the most relevant or instructional features from a given dataset. To increase computational efficiency, reduce over-fitting, and enhance model performance, it is frequently employed in supervised learning tasks where choosing the most important features is essential. Finding the top '$k$' characteristic based on their statistical scores is the primary objective of SelectKBest. Each feature is rated independently, and the '$k$' features with the highest ratings are chosen. It is important to understand that multiple scoring systems are used to evaluate feature importance. The mutual_info_classif function from the sci-kit-learn library is employed as a scoring function. The degree of interdependence between characteristics determines their ranking.SelectKBest was applied to retain features most relevant to distinguishing between the four severity classes, improving classifier focus and efficiency.

### 3.6 Spatial Bidirectional Convo Neuro Feedforward Net (SBCNFN)

The SBCNFN is a hybrid framework of deep learning for the classification of paddy leaf disease severity. Spatial feature extraction occurs through integrating CNN capabilities, feature transformation in the nonlinear space can occur due to the use of FNN, and bidirectional information learning occurs due to incorporating Bi-LSTM. Together, these models will learn spatial, contextual, and sequential patterns in an effective manner to maintain strong and highly accurate classification of disease development. The multilayer hierarchical approach allows for precision in identifying disease severity at various levels.

#### 3.6.1Convolutional Neural Network (CNN) for Spatial Feature Extraction

A Convolution Neural Network (CNN) was chosen as the primary method for spatial feature extraction and was able to learn representative and discriminative features from the paddy leaf image dataset. Through the application of convolutions and pooling in multiple layers, CNNs capture visual spatial patterns that are hierarchical and reflect characteristics of leaf images, such as the orientation of edges, morphology of lesions, and intensity of chlorosis. The spatial abstractions created by the CNN contain locally-based texture variation, which is important for discerning the level of disease severity. The convolutional kernels automatically adapt to identify indicators of infection, region-specific to each leaf image, and deeper layers synthesize global structural features and patterns. In summary, CNNs transform raw image input into high-dimensional patterns in a spatial dimension system. CNN is a family of neural networks with biological inspiration that solves Equation (18) by subjecting $W$ to several simple nonlinearities and convolutional filters. The architecture of a CNN is hierarchical. From the input signals, each layer $w_i$ is calculated as follows:

$$w_i = \rho X_i w_{i-1} \tag{18}$$

$\rho$ is a non-linearity, while $X_i$ is a linear operator. Usually, $\rho$ is a rectifier $\max(w, 0)$, or sigmoid $1/1 + \exp(-w)$, and $X_i$ is a convolution in a CNN. The operator $X_i$ is more easily conceptualized as a stack of convolutional filtering algorithms. Thus, each layer can be expressed as a sum of the convolutions of the one before it, and the layers are filter maps in Equation (19).

$$w_i(v, l_i) = \rho(\textstyle\sum_l \left(w_{i-1}(.,l) * W_{i,l_i}(.,l)(v)\right)] \tag{19}$$

The discrete convolution operator in this case is $*$ in Equation (20):

$$(e * h)(w) = \textstyle\sum_{v=-\infty}^{\infty} e(v)h(w - v) \tag{20}$$

A CNN defines an extremely non-convex optimization problem. Therefore, stochastic gradient descent is usually used to learn the weights$X_i$, with gradients being computed using the back propagation process. Figure 5 shows that the architecture of a CNN is indispensable for learning hierarchical visual features that are pertinent to disease severity. CNN naturally picks up fine nuances in paddy leaf texture, lesion propagation, and chlorosis patterns reflecting severity development. Shallow layers, for example, detect edges and leaf boundaries, while deeper layers perceive intricate disease symptoms related to greater severity grades such as 'Severe' or 'Profound'. These learned representations are crucial for the multi-class classification of paddy disease severity.

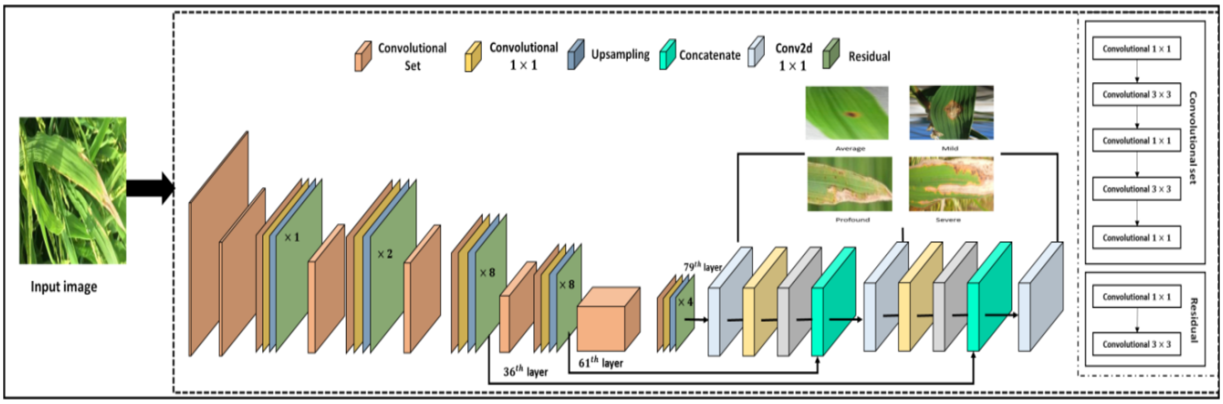


Figure5: Architecture of a CNN

### 3.6.2 Feedforward Neural Network (FNN) for Nonlinear Feature Mapping

Feedforward Neural Networks (FNNs) operate by transmitting information in one direction from input to output through interconnected layers of neurons. Each layer performs weighted summations followed by nonlinear activation, enabling complex pattern recognition. In this research, FNNs interpret spatial features extracted from paddy leaf images, transforming them into decisive representations that distinguish varying disease severity levels with high precision and computational efficiency. Where $y$ is the output neuron value, $y_j$ denotes input signals, $v_j$ represents connection weights, $a$is bias, $g$is activation function, and $c$is exponential constant as equation (21-23).

$$y = \textstyle\sum_{j=1}^{m_j} y_j v_j + a \tag{21}$$

$$a = y(\gamma) = g(\textstyle\sum_{j=1}^{m_j} y_j v_j + a) \tag{22}$$

$$a = y(\gamma) = \frac{1}{1+c^{-g}} \tag{23}$$

Where $a$ is neuron activation output, $y(\gamma)$is activation function output, $c$ is exponential constant, $\gamma$ is input signal, $k$ and $l$ denote summation indices, and $b'$is derivative output as equations (24 and 25).

$$a = y(\gamma) = \frac{c^{g}}{\sum_{k=0}^{l} c^{\gamma k}} \tag{24}$$

$$b' = y'^{(\gamma)} = \frac{c^{-\gamma}}{(1+c^{-\gamma})^{2}} = \frac{1}{1+c^{-\gamma}}\frac{c^{-\gamma}}{1+c^{-\gamma}} = \frac{1}{1+c^{-\gamma}}\left(1 - \frac{c^{-\gamma}}{1+c^{-\gamma}}\right) = y(\gamma) \tag{25}$$

By efficiently converting extracted spatial data into nonlinear decision visualizations, the FNN improves classification accuracy. Its layered structure allows for complicated feature interaction learning, resulting in reliable distinction of paddy leaf and the severity of diseases across many progression levels.

### 3.6.3 Bidirectional Long Short-Term Memory (Bi-LSTM) for Sequential Feature Learning

Bi-LSTM networks handle sequential data both forward and backward in a way that can capture contextual dependencies throughout time or feature sequences. In an LSTM unit, information that may be crucial to the LSTM's prediction is retained using gated components, thus preventing loss of gradient during training. The Bi-LSTM in this study is tasked with learning features based on sequential feature patterns derived from the CNN and FNN outputs, subsequently learning temporal relationships between spatial features that indicate the progressions in infection severity on the paddy leaf, as evaluated in Equations (26-28).

$$\vec{g}_s = tanh(X_{w\vec{g}}w_s + X_{\vec{g}\vec{g}} + a_{\vec{g}}) \tag{26}$$

$$\overleftarrow{g}_s = tanh(w_s + X_{\overleftarrow{g}\overleftarrow{g}} + a_{\overleftarrow{g}}) \tag{27}$$

$$g_s = X_{\vec{g}}\vec{g}_s + X_{\overleftarrow{g}z}\overleftarrow{g}_{+}a_z \tag{28}$$

In Bi-LSTM, $\vec{g}_s$ and $\overleftarrow{g}_s$ denote forward and $backward\ hidden\ states, tanh$ shows backward hidden states, $X$ represents input features, $w$ are weights, and $a, z, and\ s$ indicate bias terms for transformation computations. The forward and backward LSTM stages that constitute the Bi-LSTM structure process input sequences in both directions. This framework improves feature interpretation for precise categorization of paddy leaf disease severity by capturing historical contexts, both past and potential situations, in Figure 6.

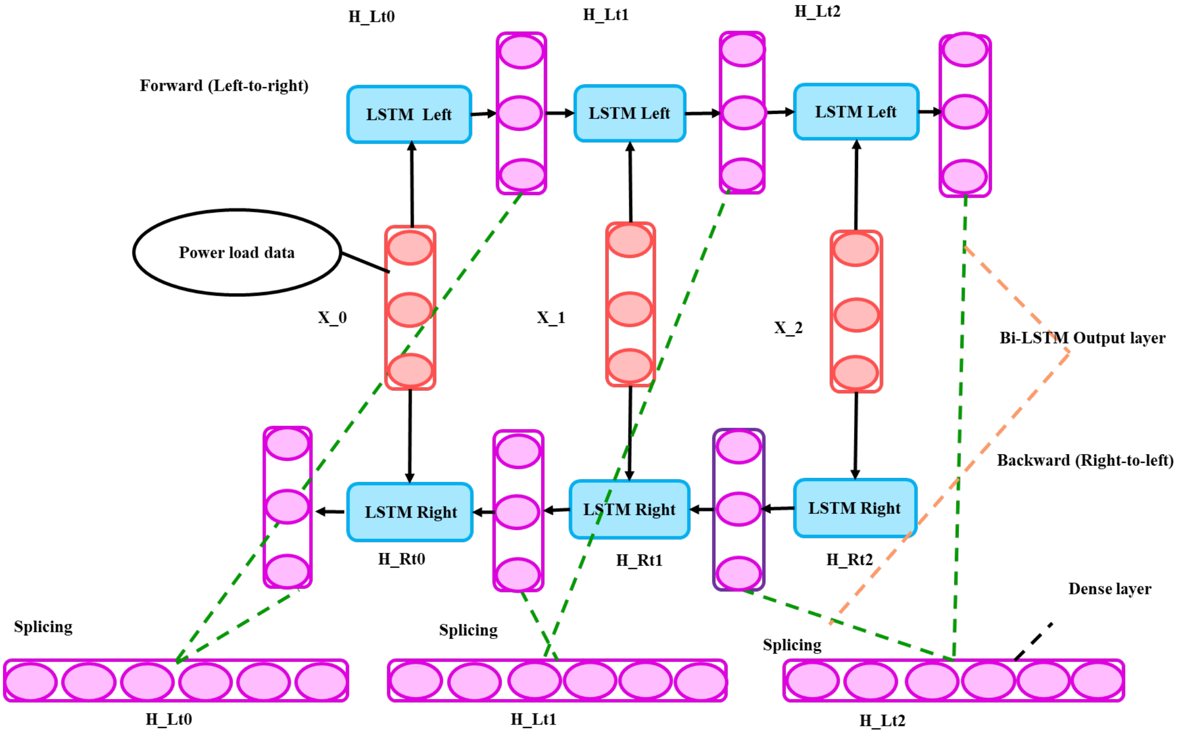


Figure 6: BiLSTM Architecture for Sequential Feature Processing

The SBCNFN algorithm operates as a deep learning framework that is hybrid in nature by including CNN, FNN, and BiLSTM for classifying paddy leaf disease severities with high accuracy.The CNN extracts the spatial and textural patterns from leaf images while the FNN maps those features into nonlinear feature representations to improve discriminative power. The Bi-LSTM preserves sequential dependencies over spatial-temporal features to achieve a better understanding of the progression patterns of infection. By combining spatial, contextual, and sequential learning, the SBCNFN algorithm provides comprehensive feature representation, increases individual classification accuracy at all severity levels, and provides a trustworthy analytical tool for pre-symptomatic detection and management of crop diseases.

**Algorithm : Spatial Bidirectional Convo Neuro Feedforward Net (SBCNFN)**

```
Input:
    - Paddy leaf image dataset D = {I1, I2, ..., In}
    - Labels L = {l1, l2, ..., ln} indicating disease severity levels
Output:
    - Trained SBCNFN model for severity classification
    - Predicted severity class y_pred for each image
1. Initialize CNN, FNN, and BiLSTM model parameters:
       W_cnn, W_fnn, W_bilstm, learning_rate, batch_size, epochs

2. For each image I in dataset D:
       a. Preprocess image I:
              - Resize and normalize pixel intensities
              - Augment (rotation, flipping, zoom) to reduce overfitting
3. CNN Feature Extraction:
       a. For each convolutional layer l in CNN:
```

```
            F_l = Conv2D(W_cnn[l], Input)
            F_l = Activation(ReLU(F_l))
            F_l = MaxPooling(F_l)
        b. Flatten final spatial feature map F_cnn
4. FNN Nonlinear Feature Transformation:
        a. Input F_cnn → Fully Connected Layers
        b. For each hidden layer h:
            F_fnn = Activation(σ(W_fnn[h] * F_cnn + b_fnn[h]))
        c. Output transformed feature vector F_nonlin
5. BiLSTM Sequential Feature Learning:
        a. Split F_nonlin into temporal feature sequence S = {s1, s2, ..., sm}
        b. Forward pass: h_fwd = LSTM_forward(S)
        c. Backward pass: h_bwd = LSTM_backward(S)
        d. Concatenate hidden states: H_seq = [h_fwd ⊕ h_bwd]
6. Classification Layer:
        a. y_pred = Softmax(W_out * H_seq + b_out)
7. Model Optimization:
        a. Compute loss = CrossEntropy(y_pred, L)
        b. Update {W_cnn, W_fnn, W_bilstm} using Adam optimizer:
            θ ← θ - learning_rate * ∇(loss)
8. Repeat steps 2–7 for all epochs until convergence
9. Evaluate performance on the test set using metrics:
        Accuracy, Precision, Recall, F1-score
Return:
Trained the SBCNFN model and final classification results
```

## 4. Result

To carry out the proposed approach, the Python language was used as the experiment platform. The section will give a detailed commentary of the experimental results. The offered strategy was evaluated, and the effectiveness was calculated with the help of the following indicators: F1 score, accuracy, recall, and precision. Also, the other available methods, such as Support Vector Machine (SVM) [16] were also compared and investigated.

### 4.1 Confusion Matrix (CM)

The confusion matrix shows that the SBCNFN model has a classification performance concerning the levels of the paddy leaf disease severity of Average, Mild, Profound and Severe. The majority of the misclassifications are between neighboring levels of severity, and this implies the existence of visual similarities in the symptoms that fall within the boundaries of the levels of severity. Even though the model has slight overlaps in the severity, it is strong in classifying disease progression in the categories of disease severity and proves to be quite strong in analyzing the multiclass severity of disease symptomology. The confusion graph of the classification results is presented in Figure 7.

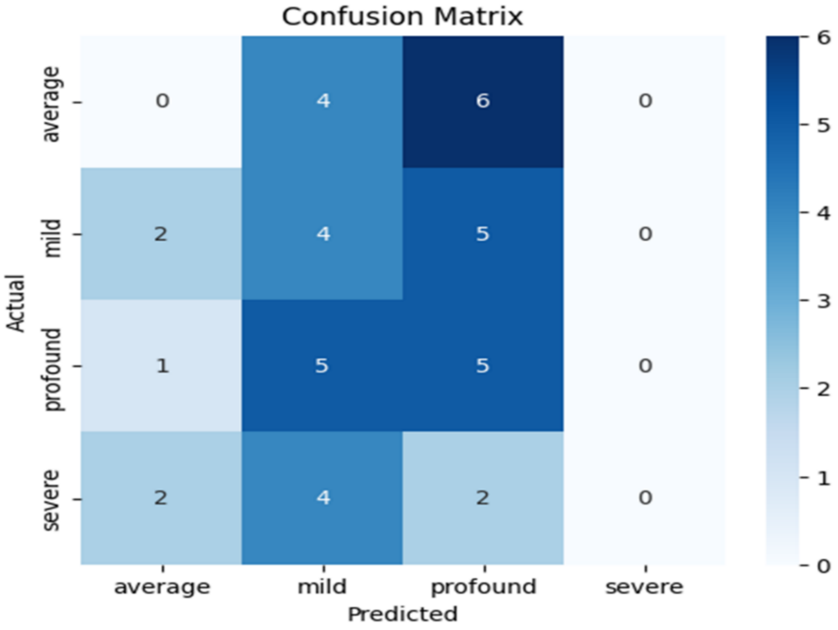


**Figure7: Confusion matrix evaluation outcomes**

## 4.2 Receiver Operating Characteristic (ROC) Curve

The ROC graph is used to evaluate the performance of the paddy leaf disease severity classification model. An Area under the Curve (AUC) value of 1.00 indicates perfect categorization performance. The ROC curve reaches the top-left corner of the graph, demonstrating that the classifier can distinguish between disease severity classes with no errors. Figure 8 displays the outcome of the ROC analysis.

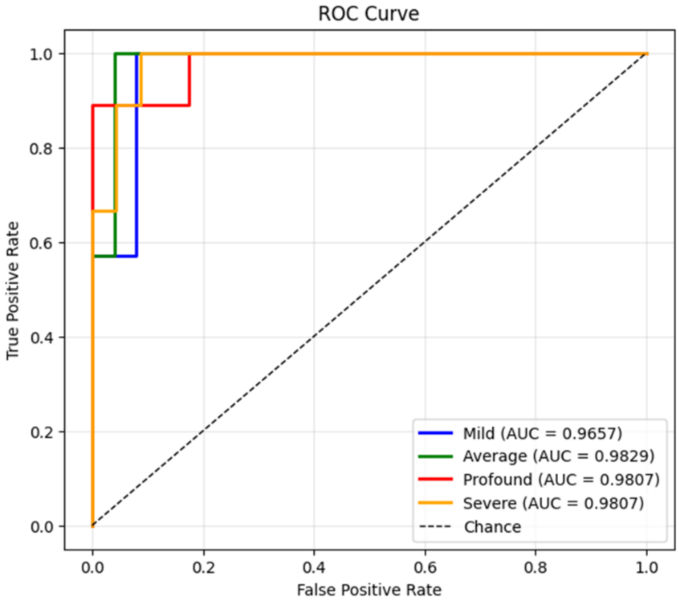


**Figure 8: Outcome of the ROC Analysis**

- **Accuracy**

Precision in the classification of PLD severity will translate in the determination of the model as accurate in identifying the levels of disease in order to manage crops effectively. Equation (30) is the accuracy of the context to classification tasks.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (30)$$

True Negatives (TN) are accurate negative forecasts, whereas True Positives (TP) are accurate positive forecasts. False Negatives (FN) are inaccurate negative forecasts, whereas False Positives (FP) is inaccurate positive forecasts. The SBCNFN method outperforms SVM across all blast severity levels, showing higher precision scores: 98.62% (mild), 96.7% (average), 98.66% (severe), and 98.12% (profound), compared to SVM 97.4%, 95.6%, 96.86%, and 97%, respectively.

- **Precision**

Precision is the percentage of correctly determined positive cases out of all the predicted positives in the PLD severity classification. The accuracy estimates the right positive predictions of all the positive predictions in Equation (31).

$$precision = \frac{TP}{TP+FP} \tag{31}$$

The SBCNFN method outperforms SVM across all blast severity levels, showing higher precision scores: 98.73% (mild), 96.73% (average), 98.13% (severe), 98.58% (profound), and, compared to SVM 97%, 95%, 94%, and 96%, respectively.

- **Recall**

The recall of the model measures how well the model can identify all cases of actual disease severity and this is a measure of the sensitivity of the model in classification tasks. Recall is correct positive predictions divided by the total actual positives in Equation (32).

$$Recall = \frac{TP}{TP+FN} \tag{32}$$

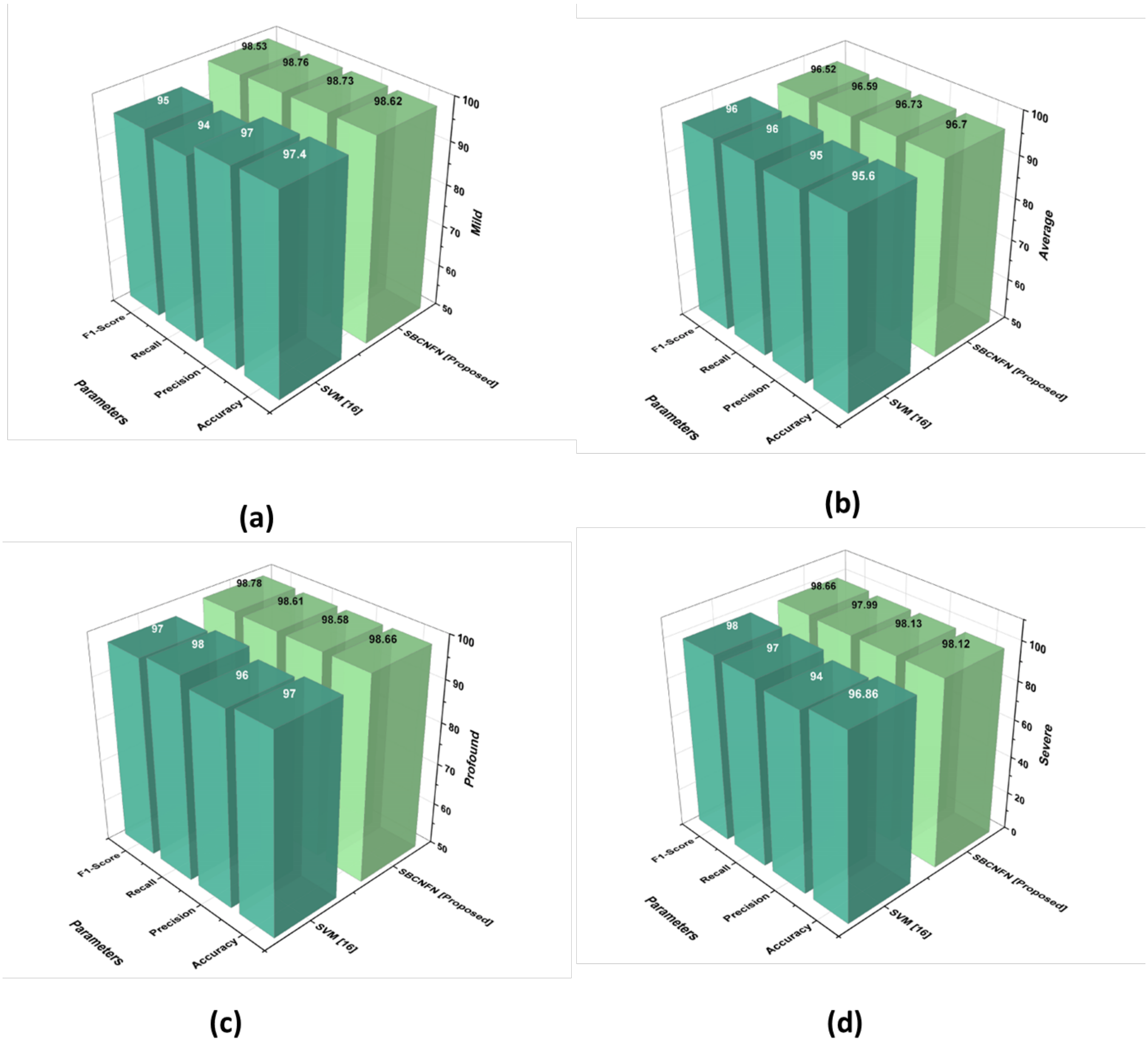
The results show that SBCNFN outperforms SVM in blast severity classification, with precision values of 98.76% (mild), 96.59% (average), 97.99 % (severe), and 98.61% (profound) compared to SVM's 94%, 96%, 97%, and 98%, respectively.

- **F1 score**

The F1 score is used to measure the ability to classify by weighing the recall and precision which is needed to assess the performance of the paddy leaf disease severity classification. In equation (33), F1 score balances both precision and recall so as to reduce false positives and falses.

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall} \tag{33}$$

The results show F1 scores for blast severity detection: mild (SVM 95%, SBCNFN 98.53%), average (SVM 96%, SBCNFN 96.52%), severe (SVM 98%, SBCNFN 98.66%), and profound (SVM 97%, SBCNFN 98.78%), indicating that SBCNFN performs slightly better. Figure 9 illustrates the outcome of (a) mild, (b) average, (c) severe, and (d) profound. Table 2 shows the comparison of classifier performance evaluation results.



(a)

(b)

(c)

(d)

**Figure 9: Outcome of (a) Mild, (b) Average, (c)Profound, and (d) Severe**

**Table 2: Comparison of Classifiers: Performance Evaluation Results**

| Blast Severity | Method | Accuracy (%) | Precision (%) | Recall (%) | F1 Score (%) |
|---|---|---|---|---|---|
| Mild | SVM [16] | 97.4 | 97 | 94 | 95 |
| | SBCNFN [Proposed] | 98.62 | 98.73 | 98.76 | 98.53 |
| Average | SVM [16] | 95.6 | 95 | 96 | 96 |
| | SBCNFN [Proposed] | 96.7 | 96.73 | 96.59 | 96.52 |
| Severe | SVM [16] | 96.86 | 94 | 97 | 98 |
| | SBCNFN [Proposed] | 98.12 | 98.13 | 97.99 | 98.66 |
| Profound | SVM [16] | 97 | 96 | 98 | 97 |

| | | | | | |
|---|---|---|---|---|---|
| | SBCNFN [Proposed] | 98.66 | 98.58 | 98.61 | 98.78 |

### 4.3 Discussion

The classification of PLD severity with the help of ML and image processing technologies aims to determine and categorize the severity of the disease in the leaf images and enable timely intervention and the following enhancement of the agricultural productivity. The results of SVM based paddy leaf disease severity classification are highly dependent on the selection of kernel and the parameter fine-tuning to avoid over-fitting or under-fitting. The SVM is also not suitable in processing large size of data as it demands high computational complexity and large memory which is in particular when large sizes of features are used. The model provides poor performance in cases where there is noise in data and the distribution of classes is unequal, hence making it less useful in the real world of agriculture. The SBCNFN is characterised by large datasets and computational gains and better performance on noisy or imbalanced data. The randomized search of parameters of this method has optimal performance due to its ability to increase classification robustness.

## 5. Conclusion

The proposed framework on the severity classification of paddy leaf disease has a powerful and full pipeline that optimally integrates the data pre-processing phase, high-level features extraction, and ensemble-based classification. The dataset used in this model is 5,932 rice leaf images afflicted with common diseases such as Blast, Brown Spot, Bacterial Blight and Tungro, whereby has been used to reduce noise, and thresholding by Otsu, respectively, to provide quality segmentation of disease-infected regions. The hybrid approach that is used to extract features is a combination of AutoEncoder and SIFT, which helps retain the global and local patterns of the image, which are critical in successful classification. SelectKBest is a feature selection technique that focuses on the most informative features, hence making computational effectiveness effective. The SBCNFN novel is highly effective in defining four levels of severity (Mild, Average, Severe, and Profound) of various kinds of diseases. In particular, the model shows great costs in the Blast severity classification at extremely large costs on each category up to Mild 98.62%, Average 96.7%, Severe 98.12%, and Profound Accuracy 98.66%. The results show the abilities of the model to recognize small visual differences and a high degree of reliability when grade the severity with much greater precision than the traditional models do.

**Limitations and Future Scope:** The model can impair performance in changing lighting conditions, leaf area occlusion or problematic backgrounds as found in the field. The training dataset, which is diverse, may also not capture the regional and seasonal differences in disease manifestations which may affect the model generalizability in different agroecological regions. Future studies would be directed at eliminating these problems with the help of drone aerial imagery and real-time monitoring systems in field implementation on a large scale. Multi-spectral or hyperspectral imaging and combining of the time data in the detection of a disease and the prediction of the early severity would be a potentially more accurate method of detecting a disease and leading the severity of the disease. Also, expanded datasets will be used to aid in building a scalable, intelligent disease management system capable of facilitating precision agriculture and improved food security by responding to disease outbreaks and managing resources in a timely manner and across geographic regions.

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