

Classification of Paddy Crop Disease Using SVM from GLCM Features Obtained from Wavelet Sub-Band Decomposed Images

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Abstract: Rice serves as a primary dietary staple in many nations, prompting the establishment of expansive rice fields to meet escalating food requirements. Yet, biotic and abiotic stressors impose various health afflictions on crops, significantly compromising both quality and yield. Early-stage disease detection and preventive measures are thus critical in agriculture. Traditional diagnostic approaches, however, are often labor-intensive and financially burdensome. Advanced image processing techniques offer refined solutions for disease detection, severity grading, and prompt intervention, proving highly suitable for extensive farming practices. This work rigorously explores the application of wavelet decomposition (5-level and 7-level) using the db4 mother wavelet, feature extraction by Grey-Level Co-occurrence Matrix (GLCM), and classification through a range of classifiers (such as: support vector machine (SVM), KNN, ensemble, decision tree, and Naive's Baye) for efficient and precise disease identification. Wavelet decomposition helps capturing the disease information in different wavelet sub-bands. By selecting proper sub-band for a particular level of decomposition helps identifying disease features. Fourteen GLCM features are computed from the selected wavelet sub-band for classification. This approach was experimented on customized dataset, which is comprising of healthy class and seven distinct diseased classes. The performance of the proposed method is evaluated by accuracy, area under the curve (AUC), true positive rate (TPR), false negative rate (FNR), positive predictive value (PPV), false discovery rate (FDR) and MCC. SVM with cubic kernel achieved a training-accuracy and testing-accuracy of 98.12% and of 90.64% for 5-level decomposition. For 7-level decomposition, the training and testing accuracy are found to be 94.48% and 84.45%, respectively.

Keywords: gray level co-occurrence matrix (GLCM); image processing in agriculture; rice disease diagnosis; wavelet decomposition (db4); support vector machine (SVM)

1 INTRODUCTION

Rice constitutes the prime food source for majority of people living globally [1]. Being a source of nutrition, it contributes to culture, economy, and livelihoods to millions of people around the world. Cultivating rice has also shaped landscapes, ecosystems, and agricultural practices for centuries. Diseases, biotic, and abiotic stress significantly affects the production of rice to a great extent [2]. Biotic stress arises from organisms like pathogens and pests, whereas abiotic stress is due to environmental factors devoid of life [3]. Prompt paddy disease diagnosis helps farmers take timely and suitable agricultural disease control strategies [4]. Diagnosing and preventing common rice diseases relies on recognizing characteristic symptoms and demanding field expertise [5]. Discrimination of crop diseases is challenging one because of their similar symptoms. However, this process is laborious, expensive, and cumbersome. Pattern recognition [6, 7], SVM classifier, feature matching, and membership function etc., are some of the techniques used earlier in the literature for paddy disease classification. Image segmentation, feature extraction, and deep learning (DL) techniques are employed to improve the accuracy of disease classification models. Automatic detection of crop disease involves preprocessing, segmentation of diseased region, feature extraction, and classification. Researchers have proved that machine learning (ML) and DL model provide better classification results than the traditional approach.

Joseph et al., [8] demonstrated rice disease classification using the Xception and Inception V3 models and attained testing accuracies of 0.9728 and 0.9620, respectively. They have used their own dataset having four classes of paddy diseases (such as: bacterial and fungal diseases). Isaac et al., [9] used DL and transfer learning approach for identifying 9 diverse diseases out of 5932-images taken from the regional paddy fields. Based on the infection level, the diseases were classified as mild and

severe after inspection by experts. Modified VGG16 model architecture produced a remarkable accuracy of 99.94% for classification. AI interpretability was used for better visualization of layer-wise information.

Bharanidharan et al., [10] computed statistical features from thermal imaging followed by modified Lemurs optimization algorithm (MLOA) for feature selection and various ML classifiers (out of which, KNN recorded the highest balance accuracy of 90%) for classification of rice diseases. Mathulapransan et al., [11] identified five prevalent rice crop diseases by VGG16 and VGG19, from the rice crop images collected from local fields. Authors used static and dynamic learning for improving performance. This method reported an accuracy of 98.62% for 5-fold cross-validation.

Kumar et al., [12] analysed temperature, moisture, and humidity of rice fields using ML and DL techniques for rice disease prediction and reported the highest accuracy of 90.79%. Patil et al., [13] used attention mechanism in DL based transformer system to identify the crop diseases from a custom dataset, having 4200 images and reported an accuracy of 97.38%. MobInc-Net (an enhanced version of Inception and MobileNet) was developed by Chen et al., [14] for detecting various crop diseases and reported an average classification accuracy of 99.21% and 97.89% for public and local dataset, respectively. This model used a densely connected softmax layer and an SSD block for classification.

Azim et al., [15] incorporates saturation thresholding for eliminating background and hue thresholding for segmenting the disease regions from paddy images followed by extreme gradient boosting decision tree ensemble for classification. Authors computed local- and global-statistical features from shape, colour, and texture of the images. This method reported an accuracy of 86.58%. Shrivastava et al., [16] extracted 172-features (highlighting the color features) from 619-paddy images followed by classification using various classifiers.

Authors reported the highest accuracy of 94.65% using SVM classifier.

Sethy et al., [17] used transfer learning by 13-pre-trained CNN models for feature extraction followed by SVM classifier to identify 4-different rice diseases from 5932-images collected from paddy crops. This method recorded the highest F1 score of 0.984 for ResNet-50 pre-trained network and SVM classifier. Zhou et al. [18] addressed the challenges (such as: image noise, blurred edges, and background interference) from the paddy crops using faster region based the CNN for identifying rice blast, bacterial blight, and blight from 3010-images and reported the highest accuracy of 96%.

Gogoi et al., [19] proposed a 3-Stage CNN with transfer learning, incorporating progressive resizing and PReLU techniques for detection of 4 rice diseases with 94% accuracy on limited datasets. Padhi et al., [20] employs the EfficientNet B4 deep learning model, achieving remarkable accuracy of 96.91% on the paddy doctor dataset for diagnosing nine paddy diseases. Precise features are extracted using the MBConv layers and swish activation function.

Amitabha Chakrabarty et al., [21] presented an advanced transformer model integrated with pre-trained CNNs for rice leaf diseases, with a precision of 0.97 and an F1-score of 0.97. Explainability is incorporated in the model through segmentation and LIME approach.

From the above discussed literature, it may be concluded that: Only few classes of rice diseases were classified. Severity of grading of rice diseases is not carried out in the literature. Publicly available datasets are limited. Results for real time data are very few.

Rice diseases include bacterial blight, brown spot, leaf spot, narrow brown spot, neck blast, rice hispa, and tungro etc. These diseases mainly affect the leaf, sheath, and panicles. Considering the differences among various diseases, a novel approach using wavelet decomposition and Grey level co-occurrence matrix (GLCM) is used for accurate and efficient disease feature identification followed by classification with various ML classifiers (such as: SVM, KNN, ensembled, decision tree, and Naive-Bayes).

In this work, wavelet decomposition is used to identify the important changes related to the paddy crop diseases in different wavelet sub-bands depending on their frequency content. This occurs due to the time-frequency resolution of wavelet using scaling and translation. Different mother wavelets (Daubechies and symlet) have been used to study the disease information in different wavelet sub-bands in three levels to nine levels wavelet decomposition.

Daubechies wavelet is asymmetric, orthogonal. This mother wavelet has the highest number of vanishing moments for a given support width. In this case energy is concentrated near the start of their support. Db1, db2, and db3 are similar to symlet. Db4 has 4 moments and offers a good balance between localization in time and frequency domain, enables precise feature extraction from spatial variations in the images. This capability enhances the model's performance in identifying and classifying the subtle differences in disease-related textures. Due to the above mentioned reasons, db4 mother wavelet is used in this manuscript.

In this manuscript, three level, five level, seven level, and nine level wavelet decompositions have been performed to analyse the disease features in different wavelet sub-bands. Sub-bands contributing highest disease informations are considered for feature extraction. From the analysis it is found that fifth level and seventh level wavelet sub-bands contribute higher disease features compared to the other decomposition levels. Due to this reason the seventh level wavelet decomposition and fifth level wavelet decomposition have been used for extracting the features and classification. From the analysis, it is found that fifth level and seventh level attended the highest testing accuracy of 90.64% and 84.45%, respectively. Due to this, the fifth level and seventh level wavelet decomposition have been used for classification.

5-level and 7-level wavelet decompositions are used to emphasize the disease regions from the paddy images using Daubechies-4 (db4) mother wavelet. The highlighted disease regions are subjected to GLCM for calculating 14-different features. GLCM helps identifying the patterns from grey scale images. This helps improving the discrimination ability of classifiers by computing various features.

Rest part of manuscript is structured as follows. The proposed methodology along with the dataset is represented in Section 2. Section 3 elaborates the experimentation carried out and analysis of results for various classifiers. Section 4 provides conclusion and future directions for the research.

2 METHODS AND MATERIALS

The proposed approach for identifying rice crop diseases (represented in Fig. 1) consists of data preprocessing, followed by wavelet decomposition, feature extraction by GLCM, classification by ML classifiers, and performance evaluation.

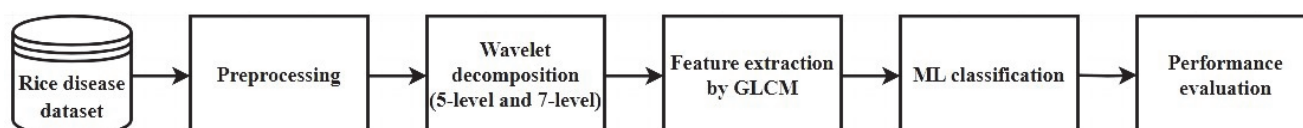


Figure 1 Proposed block diagram for paddy disease classification approach.

This method was experimented on the images available in the customized dataset. This dataset consists of images corresponding to seven diseases (such as: bacterial blight, brown spot, leaf blast, narrow brown spot, neck blast, rice hispa, and tungro) and healthy crops, captured using digital camera (specification: Canon EOS 1200D,

3456 × 2304 pixels, 55 mm focal length) from paddy fields located nearby Lalgudi district, Tiruchirappalli, Tamilnadu, India. These images are captured during daytime in bright sunlight. A total of 7857-paddy crop images are collected and the number of images for each class is represented in Tab. 1. For overcoming the problem

of over-fitting, images in each class have been increased by augmentation (such as: rotating the images from -45 degree to $+45$ degree).

Table 1 Description about the dataset

S. No.	Class	No. of Images
1	Bacterial blight	981
2	Brown spot	963
3	Leaf blast	993
4	Narrow brown spot	975
5	Neck blast	981
6	Rice hispa	989
7	Tungro	977
8	Healthy leaves	998

The red channel of the RGB images available in the database are resized to 512×512 and subjected to wavelet decomposition for extracting intricate details based on the frequency components. Discrete wavelet transform (DWT) decomposes the image into one low frequency approximation band (A) and three high frequency detail bands (horizontal (H), vertical (V), and diagonal (D)). The N -level wavelet decomposition will generate $3N + 1$ bands (one approximation band at the final level and $3N$ detail bands). The disease information is distributed in different bands based on the frequency content and selective bands are combined for reconstructing the image for feature extraction by GLCM. In this work, 5-level and 7-level wavelet decomposition are performed by db4 mother wavelet. 5-level wavelet decomposition generates one approximation band and fifteen detail bands. The band corresponding to disease information is checked by reconstructing the image after altering one detail band coefficients and keeping the rest detail bands coefficients. Further analysis is performed with the reconstructed image by keeping one band coefficients and altering the rest band coefficients. The wavelet decomposition is extended to 7-level and the reconstructed images are obtained. Subsequently, segmentation techniques are applied to generate a binary mask. This masking operation highlights foreground of the image in extracting useful features for categorizing the paddy crop diseases. The reconstructed images are subjected to analysis by GLCM, which helps identifying useful features (such as: angular second moment (ASM), contrast, correlation, variance, inverse difference moment (IDM), sum average (SA), sum entropy (SE), sum variance (SV), entropy, difference variance (DV), difference entropy (DE), information measure of correlation-1 (IMC-1), information measure of correlation-2 (IMC-2), and maximal correlation coefficient (MCC)) from the images [22]. GLCM examines the likelihood of pixel pairs with specific values in given distance and direction to identify intricate details about texture for classification [23].

Tab. 2 represents the 14-GLCM features. It helps extracting features in the presence of noise. After feature extraction by GLCM, classification is performed using various ML classifiers (such as: SVM, KNN, ensemble, decision tree, and Naive-Bayes). SVM classifier computes a hyperplane for better discrimination of classes in an N -dimensional space for handling non linear data. It transforms the input data into a higher-dimensional space for linear separation [24].

Table 2 Features computed from GLCM

Features	Formula
ASM	$ASM = \sum_{i=0}^{N-1} \sum_{j=0}^{M-1} GLCM(i, j)^2$
Contrast	$Contrast = \sum_{i,j=0}^{N-1} i-j ^2 GLCM(i, j)$
Correlation	$Correlation = \frac{\sum_{i,j=0}^{N-1} GLCM(i, j) - \mu_x \mu_y}{\sigma_x \sigma_y}$
Variance	$Variance = \sum_{i,j=0}^{N-1} (i - \mu)^2 GLCM(i, j)$
IDM	$IDM = \sum_{i,j=0}^{N-1} \frac{1}{1 + (i-j)^2} GLCM(i, j)$
SA	$SA = \sum_{k=2}^{2N} k \cdot p_{x+y}(k)$
SE	$SE = - \sum_{k=2}^{2N} p_{x+y}(k) \log_2(p_{x+y}(k))$
SV	$SV = \sum_{k=2}^{2N} (k - SA)^2 \cdot p_{x+y}(k)$
Entropy	$Entropy = - \sum_{i,j=0}^{N-1} GLCM(i, j) \log_2(GLCM(i, j))$
DV	$DV = \sum_{i,j=0}^{N-1} (i-j)^2 \cdot GLCM(i, j)$
DE	$DE = - \sum_{i,j=0}^{N-1} GLCM(i, j) \log_2(i-j)^2$
IMC-1	$IMC-1 = \frac{HXY - HXY1}{\max(HX - HY)}$
IMC-2	$IMC-2 = \sqrt{1 - \exp(-2(HXY2 - HXY))}$
MCC	$MCC = \frac{\lambda_1 - \lambda_2}{\lambda_1 + \lambda_2 - \lambda_3}$

The dimension of the hyperplane depends on the number of features analyzed. The selection of hyperplane is used to categorize the data. The kernels (such as: linear, quadratic, cubic, fine Gaussian, medium Gaussian, and coarse Gaussian etc.) are used. Each kernel has distinct properties and its choice depends on the unique features of the dataset and type of classification problem. The hyperplane equation for SVM is given by:

$$w \cdot x + b = 0 \quad (1)$$

where, w is the weight vector and controls the orientation of hyperplane and its direction. x is the input vector representing feature values of data points in feature space. $w \cdot x$ measures the projection of the input vector x onto the weight vector w . b represents the bias adjusting the position of hyperplane.

K-nearest neighbour (KNN) separates the classes based on k number of nearest neighbours by calculating Euclidean distance. It uses various kernels (such as: fine, medium, coarse, cosine, cubic, and weighted etc.) for transforming non-linear separable data to linear one. The general equation for KNN is given by:

$$\hat{y}(x) = \text{majority vote}(\{y_i : (x_i, y_i) \in N_k(x)\}) \quad (2)$$

where, $\hat{y}(x)$ represents the predicted class or value for the new data point x . x_i is the feature vector of the i^{th} training sample. y_i denotes the class or value of the i^{th} training sample. $N_k(x)$ represents set of k nearest neighbours of x , based on a chosen distance metric. The Euclidean distance function between two points in KNN is calculated by:

$$d(x, y) = \sqrt{\sum_{i=1}^d (x_i - y_i)^2} \quad (3)$$

where, $x = (x_1, x_2, \dots, x_d)$ and $y = (y_1, y_2, \dots, y_d)$ are feature vectors in a d -dimensional space. x_i and y_i represent the i^{th} components of x and y , respectively.

Decision tree (DT) can be used for both classification & regression and has the ability to model non-linear relationships to produce clear, and understandable rules. Ensemble model uses a diverse array of algorithms having individual strengths for improving accuracy, robustness against overfitting, and ability to capture intricate patterns within data that may elude simpler models. This method uses averaging predictions (e.g., in bagging methods like random forest classifier), boosting the importance of harder-to-predict instances (e.g., in AdaBoost), or combining the strengths of different models through stacking.

Naive Bayes classifier simplifies complex probability calculations for making the model computationally simpler for large datasets. The calculation is given by:

$$P(C_k | x) = \frac{P(C_k) \prod_{i=1}^n P(x_i | C_k)}{P(x)} \quad (4)$$

where, $P(C_k | x)$ denotes the posterior probability of class C_k given the features $x = (x_1, x_2, \dots, x_n)$. $P(C_k)$ represents the prior probability of class C_k . $P(x_i | C_k)$ signifies the likelihood of feature x_i given class C_k . $P(x)$ stands for the evidence or marginal probability of the features x .

2.1 Performance Metrics

The proposed method's ability for identifying crop diseases from the paddy images is objectively evaluated by training accuracy, testing accuracy, area under the curve (AUC), confusion matrix, true positive rate (TPR), positive predictive value (PPV), false discovery rate (FDR), false negative rate (FNR), Matthews correlation coefficient (MCC) etc. Training and testing accuracy are the gold standard measures and represent the ability of the model for correctly classified samples to the total number of samples in training and testing, respectively. It ranges [0,1]. TPR is known as sensitivity or recall and computes the correctly classified positive samples to the total number of positive samples. FNR represents the portion of positive class incorrectly classified by the classifier. PPV denotes the precision in classification task. FDR (1-precision) represents the proportion of incorrect classifications per

predicted class. TNR is known as specificity and represents the portion of the negative samples correctly classified. FPR (1-specificity) represents the portion of negative class incorrectly classified by the classifier. A good classifier has higher TNR, TPR, but lower FNR and FPR. AUC is a single metric that computes the classifier performance based on receiver operating characteristic curve (ROCC), which is a graphical plot representing the trade-off between FPR and TPR for various threshold levels of the classifier. AUC represents the area under the curve and is computed by the average of sensitivity and specificity. Intersection over union (IoU) represents the total number of correctly classified samples to the sum of TP, FP, and FN. The mathematical representation of these measures is given in Tab. 3.

Table 3 Performance metrics and their mathematical representation

S. No	Metrics	Mathematical representation	Range	Remarks
1.	Accuracy	$\frac{TP + TN}{TP + TN + FP + FN}$	[0, 1]	Classification success rate
2.	Sensitivity	$\frac{TP}{TP + FN}$	[0, 1]	Rate of correctly predicted positives
3.	Specificity	$\frac{TN}{TN + FP}$	[0, 1]	Rate of correctly predicted negatives
4.	Precision	$\frac{TP}{TP + FP}$	[0, 1]	Prediction accuracy
5.	IoU	$\frac{TP}{TP + FP + FN}$	[0, 1]	Area overlap metric
Note: TP: True Positive, TN: True Negative, FP: False Positive, FN: False Negative				

3 RESULTS AND DISCUSSION

Red component of the paddy crop images has been considered for extracting the information related to paddy crop diseases and subjected to the fifth-level and seventh-level wavelet decomposition.

Fifth level wavelet decomposition generates one approximation band at the fifth level and three detail bands in each level. The total number of bands is equal to sixteen. The images are reconstructed in two ways. In the first approach, one of the sub-band coefficients are altered by keeping the other sub-band coefficients. In the second approach, one of the sub-band coefficients remain unaltered by altering the other sub-band coefficients. These reconstructed images in both approaches are represented in Fig. 2.

Fig. 2a and Fig. 2b represent the reconstructed images (i.e R and RZA5) obtained after 5-level wavelet decomposition and altering only the approximation band coefficients at 5 levels, respectively. Fig. 2c, Fig. 2d, Fig. 2e, Fig. 2f, and Fig. 2g represent the reconstructed images (i.e RZD1, RZD2, RZD3, RZD4, and RZD5), whose detail coefficients are altered in levels-1, 2, 3, 4, and 5, respectively. These images are deprived of approximation band coefficients at the fifth level. Fig. 2h represents the reconstructed image (i.e RA5), which is reconstructed by keeping the approximation coefficients and altering the rest band coefficients. Fig. 2i, Fig. 2j, Fig. 2k, Fig. 2l, and Fig. 2m illustrate the reconstructed images (i.e RD1, RD2, RD3, RD4, and RD5) with the detail coefficients set to zero except those at levels 1, 2, 3, 4, and 5, respectively. Fig. 2n

illustrates the reconstructed image (i.e RD125) having the detail coefficients set to zero except the coefficients at levels 1, 2, and 5. RD12 (illustrated in Fig. 2o) represents the reconstructed image with all the detail coefficients set to zero, except those at levels 1, and 2. Among these, RD125 (illustrated in Fig. 2n) reconstructed image (consists of sub-band coefficients 1, 2, and 5) provides detailed information about the diseased region in paddy crop. This experiment has been extended to 7-level wavelet decomposition. The images high lighting the disease informations have been considered for extracting the GLCM features. In this work, 14-GLCM features have been computed. These features have been passed through various classifiers incorporating different kernels. The classifiers (such as: SVM, KNN, ensemble, decision tree, and Naive's Baye) are trained with 80% of the images and tested with the rest of 20% images present in the database for a cross validation of 5, 10, and 20. For 5-level wavelet decomposition, GLCM features attained the training accuracies of 98.12% (for SVM with cubic kernel, 10 fold), 99.7% (for KNN with fine kernel, 20 fold), 99.46% (for ensemble with bagged trees kernel, 10 fold), 79.59% (for decision tree with fine kernel, 5 fold), and 52.97% (for Naive Baye's, kernel, 20 fold). In a similar manner, the experiment was extended to 7-level wavelet decompositions and training accuracies of 94.48% (for SVM with cubic kernel, 20 fold), 98.54% (for KNN with fine kernel, 20 fold), 98.15% (for ensemble with bagged trees kernel, 20 fold), 65.27% (for decision tree with fine kernel, 10 fold), and 42.54% (for Naives Baye's, kernel, 5 fold) were obtained. These above discussed values are precisely represented in Tab. 5 and Tab. 6.

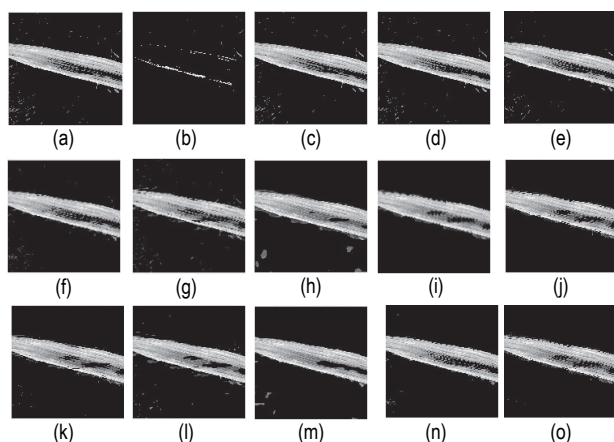


Figure 2 Reconstructed images in 5-level wavelet decomposition: (a) R, (b) RZA5, (c) RZD1, (d) RZD2, (e) RZD3, (f) RZD4, (g) RZD5, (h) RA5 (i) RD1, (j) RD2, (k) RD3, (l) RD4, (m) RD5, (n) RD125, and (o) RD12

From these results, it may be concluded that SVM classifier with cubic kernel obtained the highest training accuracy of 98.12% for 5-level decomposition. For 7-level decomposition, SVM classifier with cubic kernel obtained the highest training accuracy of 94.48%. For 5-level wavelet decomposition, the proposed method attained testing accuracies of 90.64% (for SVM with cubic kernel), 93.57% (for KNN with fine kernel), 93.13% (for ensemble with bagged trees kernel), 76.13% (for decision trees with fine kernel), and 46.18% (for Naives Baye's). In a similar manner, the experiment was extended to 7-level wavelet decompositions and attained testing accuracies of 84.85% (for SVM with cubic kernel), 87.58% (for KNN with fine kernel), 86.76% (for ensemble with bagged trees

kernel), 64.48% (for decision trees with fine kernel), and 43.09% (for Naives Baye's kernel) for 20 fold cross validation. From the above result, it may be concluded that SVM classifier with cubic kernel obtained the highest testing accuracy of 90.64% and 84.85%, for 5-level and 7-level wavelet decompositions, respectively. Various performance measures (such as: TPR, FNR, PPV, FDR, and MCC) are evaluated and represented in Tab. 6 for identifying the classification performance of the proposed method. The AUC values for all the disease classes during training and testing are tabulated in Tab. 4 and Tab. 5.

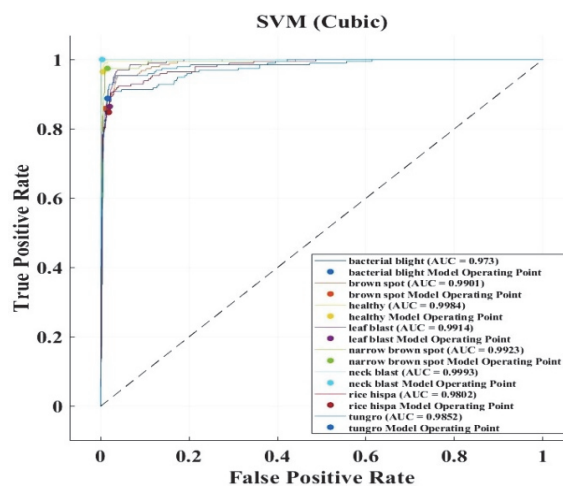


Figure 3 AUC for SVM classifier with cubic kernel for 20 fold cross validation obtained on 5-level wavelet decomposition for testing

		SVM (cubic)							
True class	bacterial blight	167	2		4	5	4	9	5
	brown spot	5	165		7	7		3	5
	healthy		3	192				3	1
	leaf blast	2	9		172	6		6	4
	narrow brown spot				2	190		1	2
	neck blast						197		
	rice hispa	10		6	8	1		167	5
	tungro	5	3	1	7	2	1	3	174
	Predicted class	bacterial blight	brown spot	healthy	leaf blast	narrow brown spot	neck blast	rice hispa	tungro

Figure 4 Confusion matrix for SVM classifier with cubic kernel for 20 fold cross validation obtained on 5-level wavelet decomposition for testing

From the experimental results, it may be concluded that maximum AUC of 1 is achieved for neckblast diseases by SVM classifier with cubic kernel (20 fold cross validation). The receiver operating characteristics are illustrated in Fig. 3 for 5-level wavelet decomposition.

The confusion matrix represented in Fig. 4 clearly indicates the classification accuracy of paddy crop diseases by the proposed method. It is evident that misclassification is less for neck blast disease. It was inferred that SVM classifier with cubic kernel achieved the highest TPR of 100% (for healthy, narrow brown spot, and neck blast) for 5-level and 7-level wavelet decomposition during training and testing.

In 5-level and 7-level wavelet decomposition, the proposed method attained 0% FNR (for neckblast) with SVM classifier having cubic kernel during training and testing.

In training, SVM classifier with cubic kernel (20 fold cross validation) attained the highest PPV of 99.9% and 98.7% for neck blast in 5-level and 7-level wavelet decomposition respectively, whereas in testing the highest PPV of 97.5% and 94.7% was achieved for neck blast in 5-level and 7-level wavelet decomposition respectively, using SVM classifier with cubic kernel for 20 fold cross validation.

For 5-level and 7-level wavelet decomposition, the proposed method attained the least FDR of 0.1% and 1.3%, respectively, for identifying neckblast disease by SVM classifier with cubic kernel having 20 fold cross validation during training. For 5-level and 7-level wavelet decomposition, the minimum FDR of 2.5% and 5.3%, respectively, have been recorded for identifying neck blast crop disease by SVM classifier having cubic kernel during testing.

Table 4 Training accuracy and AUC for various classifiers with 5-level wavelet decomposed images

S. No	K-fold	Classifier	Type	AUC training								
				Accuracy training	Bacterial blight	Brown spot	Healthy	Leaf blast	Narrow brown spot	Neck blast	Hispa	Tungro
1	5	SVM	Linear	69.39	0.9315	0.9369	0.9673	0.8975	0.9237	0.9994	0.9495	0.934
			Quadratic	86.67	0.9825	0.9817	0.9949	0.9789	0.9892	1	0.9847	0.9795
			Cubic	97.22	0.9979	0.9982	0.9993	0.9983	0.9996	1	0.9969	0.9966
			Fine Gaussian	95.50	0.9971	0.999	0.9982	0.9999	0.9994	1	0.9954	0.9961
			Medium Gaussian	73.11	0.9551	0.9475	0.971	0.9379	0.9636	1	0.9436	0.9546
			Coarse Gaussian	57.24	0.9032	0.8984	0.9016	0.812	0.8728	0.9982	0.897	0.9002
	10	SVM	Linear	70.31	0.9326	0.9383	0.9691	0.9017	0.9267	0.9997	0.9526	0.9244
			Quadratic	86.96	0.983	0.9815	0.9915	0.9797	0.9888	1	0.9858	0.9826
			Cubic	98.12	0.9991	0.9992	0.9997	0.9996	0.9996	0.9998	0.9987	0.9983
			Fine Gaussian	96.04	0.9976	0.9992	0.9984	0.9999	0.9992	1	0.9955	0.997
			Medium Gaussian	73.67	0.9562	0.9489	0.9731	0.9419	0.9649	1	0.9459	0.9563
			Coarse Gaussian	57.94	0.9058	0.9014	0.9038	0.8122	0.8751	0.9983	0.9881	0.9018
	20	SVM	Linear	70.63	0.9332	0.9379	0.9705	0.9025	0.9276	0.9996	0.9532	0.9358
			Quadratic	87.24	0.9846	0.9833	0.9954	0.9812	0.99	1	0.9863	0.9839
			Cubic	98.06	0.9988	0.9986	0.9995	0.9993	0.9995	1	0.9987	0.9974
			Fine Gaussian	96.37	0.9978	0.9991	0.9985	0.9999	0.9996	1	0.9962	0.9971
			Medium Gaussian	73.94	0.9572	0.9494	0.9738	0.943	0.9657	1	0.9473	0.957
			Coarse Gaussian	58.43	0.9071	0.9022	0.9042	0.8139	0.875	0.9984	0.9	0.9034
2	5	KNN	Fine	99.59	0.9968	0.9996	1	0.9997	0.9997	0.9999	0.9993	0.9859
	10		Fine	99.67	0.9989	0.9996	1	0.9997	0.9997	0.9999	0.9995	0.9872
	20		Fine	99.70	0.9989	0.9996	1	0.9999	0.9997	0.9999	0.9995	0.9885
3	5	Ensemble	Bagged Trees	99.25	0.9998	1	1	1	1	1	0.9999	0.9996
	10		Bagged Trees	99.46	1	1	1	1	1	1	0.9999	0.9992
	20		Bagged Trees	99.36	1	1	1	1	1	1	0.9999	0.9998
4	5	DT	Fine	79.59	0.9382	0.9549	0.9827	0.9646	0.9557	1	0.9415	0.9292
	10		Fine	79.06	0.9392	0.9477	0.9842	0.9592	0.9563	1	0.9427	0.9394
	20		Fine	79.24	0.9428	0.9511	0.9857	0.9585	0.9558	1	0.9411	0.9348
5	5	Naïve Baiye's	Kernel	52.66	0.7782	0.795	0.7528	0.7239	0.8339	0.9998	0.8624	0.7406
	10		Kernel	52.85	0.7775	0.7942	0.7614	0.7271	0.836	0.9998	0.8609	0.7426
	20		Kernel	52.97	0.7784	0.7944	0.7618	0.7281	0.8352	0.9999	0.8618	0.7447

Table 5 Testing accuracy and AUC for various classifiers with 5-level wavelet decomposed images

S. No	K-fold	Classifier	Type	AUC testing								
				Accuracy testing	Bacterial blight	Brown spot	Healthy	Leaf blast	Narrow brown spot	Neck blast	Hispa	Tungro
1	20	SVM	Linear	63.65	0.9275	0.9286	0.9355	0.8722	0.9173	0.9991	0.9326	0.9183
			Quadratic	83.26	0.9617	0.9674	0.9878	0.9732	0.9755	0.9993	0.9654	0.9723
			Cubic	90.64	0.973	0.9901	0.9984	0.9914	0.9923	0.9993	0.9802	0.9852
			Fine Gaussian	88.22	0.9691	0.9836	0.993	0.9951	0.9908	1	0.9658	0.9836
			Medium Gaussian	68.49	0.9385	0.9232	0.9445	0.8963	0.9439	0.9998	0.9258	0.9325
			Coarse Gaussian	50.41	0.8475	0.8609	0.8916	0.7743	0.8659	0.9851	0.8846	0.8518
2	20	KNN	Fine	93.57	0.9362	0.9625	0.9824	0.9877	0.9905	1	0.9249	0.9213
			Medium	69.57	0.9218	0.9152	0.9542	0.9421	0.9542	1	0.9184	0.917
			Coarse	47.10	0.8297	0.8084	0.8605	0.7556	0.8924	0.9904	0.8406	0.8173
			Cosine	72.44	0.9377	0.9247	0.9514	0.9508	0.9578	0.9996	0.916	0.923
			Cubic	70.34	0.9138	0.915	0.9572	0.9468	0.9532	0.9996	0.9187	0.9235
			Weighted	91.53	0.987	0.99	0.9958	0.999	0.9986	1	0.99	0.9886
3	20	Ensemble	Boosted Trees	63.72	0.8838	0.8546	0.9342	0.8854	0.9048	0.9985	0.8975	0.8811
			Bagged Trees	93.13	0.9814	0.993	0.99	0.997	0.992	0.9996	0.9903	0.987
			Subspaced Discriminant	54.74	0.8725	0.8607	0.8434	0.7403	0.8842	0.9993	0.8977	0.8573
			Subspace KNN	90.71	0.9902	0.9862	0.9924	0.9946	0.9984	1	0.9819	0.9792
			RUSBoostedtrees	54.11	0.8411	0.8148	0.8742	0.8415	0.8351	0.9986	0.8381	0.8527
4	20	DT	Fine	76.83	0.8944	0.9352	0.9689	0.9574	0.9552	0.9996	0.8971	0.8713
			Medium	52.83	0.8127	0.795	0.8626	0.8068	0.8325	0.998	0.821	0.8287
			Coarse	36.66	0.5674	0.7101	0.7712	0.669	0.6966	0.9969	0.7376	0.6384
5	20	Naïve Baye's	Gaussian	41.18	0.6318	0.746	0.5827	0.5887	0.8073	0.9773	0.7988	0.7331
			Kernel	48.19	0.7422	0.7491	0.7339	0.6517	0.8289	0.9981	0.8536	0.7551

Table 6 Performance measures (TPR, FNR, PPV, FDR, and MCC) for various classifiers

S. No	Performance metrics in %	K-fold	Paddy crop diseases							
			Bacterial blight	Brown spot	Healthy	Leaf blast	Narrow brown spot	Neck blast	Hispa	Tungro
1	TPR		Training							
		5	96.2	95.1	100	97.4	100	100	93.1	96
		10	97.5	94.9	100	98.7	100	100	97	96.8
		20	97.6	95.6	99.9	98.2	100	100	96.6	96.5
2	FNR	5	3.8	4.9	0	2.6	0	0	6.9	4
		10	2.5	5.1	0	1.3	0	0	3	3.2
		20	2.4	4.4	0.1	1.8	0	0	3.4	3.5
3	PPV	5	95.1	98	98	95.6	97.9	99.1	95.8	98.3
		10	97	99.2	98.9	97.1	98.2	99.5	97	98.2
		20	96.4	98.3	98.8	97.1	98.1	99.9	97.2	98.7
4	FDR	5	4.9	2	2	4.4	2.1	0.9	4.2	1.7
		10	3	0.8	1.1	2.9	1.8	0.5	3	1.8
		20	3.6	1.7	1.1	2.9	1.9	0.1	2.8	1.3
5	MCC	5	0.950	0.960	0.989	0.959	0.988	0.995	0.936	0.968
		10	0.968	0.966	0.994	0.976	0.989	0.997	0.965	0.971
		20	0.965	0.965	0.993	0.973	0.989	0.999	0.965	0.973
			Testing							
1	TPR	20	85.2	85.9	96.5	86.4	97.4	100	84.8	88.8
2	FNR	20	14.8	14.1	3.5	13.6	2.6	0	15.2	11.2
3	PPV	20	88.4	90.7	96.5	86	90	97.5	87	88.8
4	FDR	20	11.6	9.3	3.5	14	10	2.5	13	11.2
5	MCC	20	0.849	0.867	0.960	0.842	0.927	0.986	0.839	0.872

4 CONCLUSION AND FUTURE SCOPE

In this manuscript, a novel method (comprising wavelet decomposition and GLCM based feature extraction) for classifying paddy diseases is proposed. Fourteen GLCM features are calculated from the sub-bands of 5-level and 7-level wavelet decomposed images performed by db4 mother wavelet. The extracted features are used by SVM, KNN, ensemble methods, decision trees, and Naive Bayes classifiers for classification. The experiment was performed on paddy crop images (80% for training and 20% for testing) obtained from Tiruchirapalli area of Tamilnadu. SVM classifier reported the highest accuracy of 98.12% and 90.64% for training and testing, respectively, for 5-level wavelet decomposition with 20 fold cross validation. In 7-level wavelet decomposition the testing accuracy was found to be 84.85%. MCC was reported to be 0.999 and 0.986 during training and testing, respectively. This method was robust to other crop diseases.

The proposed method needs a pre-processing stage for improving the performance by highlighting the contrast of edge regions of the disease. In our future work, the classification needs to be performed among various diseases in different plants along with the level of severity. Significant challenges in rice disease classification include cases, where multiple diseases occur on a single leaf or diseases exhibiting similar symptoms, and limited datasets for training deep learning models. In future research these complexities need to be addressed along with explainability for severity level of disease identification. This will help actionable insights for disease management to provide substantial support to farmers involved in large-scale crop cultivation by enhancing precision in disease mitigation strategies.

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