TELKOMNIKA Telecommunication, Computing, Electronics and Control
Vol. 19, No. 2, April 2021, pp. 463~470
ISSN: 1693-6930, accredited First Grade by Kemenristekdikti, Decree No: 21/E/KPT/2018
DOI: 10.12928/TELKOMNIKA.v19i2.16488

An effective feature extraction method for rice leaf disease classification

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Article Info

Article history:

Received Apr 28, 2020
Revised Sep 25, 2020
Accepted Oct 7, 2020

Keywords:

Classification
Extreme gradient boosting
Image processing
Machine learning
Plant disease detection
Rice leaf diseases
XGBoost

ABSTRACT

Our society is getting more and more technology dependent day by day. Nevertheless, agriculture is imperative for our survival. Rice is one of the primary food grains. It provides sustenance to almost fifty percent of the world population and promotes huge amount of employments. Hence, proper mitigation of rice plant diseases is of paramount importance. A model to detect three rice leaf diseases, namely bacterial leaf blight, brown spot, and leaf smut is proposed in this paper. Backgrounds of the images are removed by saturation threshold while disease affected areas are segmented using hue threshold. Distinctive features from color, shape, and texture domain are extracted from affected areas. These features can robustly describe local and global statistics of such images. Trying a couple of classification algorithms, extreme gradient boosting decision tree ensemble is incorporated in this model for its superior performance. Our model achieves 86.58% accuracy on rice leaf diseases dataset from UCI, which is higher than previous works on the same dataset. Class-wise accuracy of the model is also consistent among the classes.

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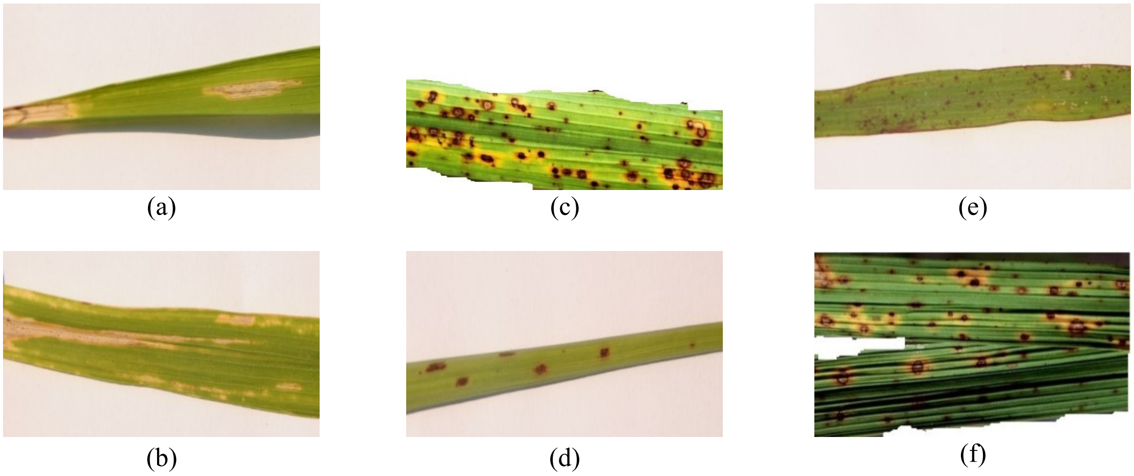
1. INTRODUCTION

Being the primary food of more than three billion people of the world, rice is one of the most important crops. It is the staple food of Bangladesh, China, India, Indonesia, Vietnam, and Nigeria. Anything that influences the quality and quantity of rice production affects the mass population. Hence, continual monitoring and detection of diseases is essential for proper mitigation. Without timely intervention, diseases can severely affect the production. Thus, automatic plant disease detection is a topic of great interest in agro-informatics. bacterial leaf blight (BLB), brown spot (BS), leaf blast, sheath blight, tungro, and leaf smut (LS) are some of the most prevalent rice plant diseases. Affected plants produce rice of less amount and lower quality than that of healthy plants. This loss of yield has direct and negative effect on mass people, food security, and national economy. According to International Rice Research Institute, bacterial leaf blight can reduce the yield up to 70% [1]. Brown spot disease can damage rice production up to 45% [2]. It is one of the primary reasons behind the "Great Bengal Famine" of 1943. Some of these diseases have similar symptoms which confuse the untrained farmers and cause loss of harvest. Had there been a simple, automated, and reliable disease detection facility, this production loss could have been avoided. Such a system can surely bring tangible results in short time. In this paper, we intend to devise a set of effective features to classify rice leaf diseases with higher accuracy. The approach presented in this paper is briefly laid out in five steps. Firstly, rice leaf disease image dataset is collected from [3] which is prepared and published by Prajapati *et al.* [4]. After image acquisition, backgrounds of the images are removed and then disease affected portions are segmented. Color, shape, and texture features are extracted from the images. Finally, extreme gradient boosting decision tree ensemble (XGBoost) classifier is used for classification.

2. BACKGROUND AND RELATED WORK

2.1. Background

The dataset used in this work is prepared by Prajapati *et al.* [4] which contains 120 RGB images of three classes e.g., bacterial leaf blight, brown spot, and leaf smut each containing 40 images. Images are taken on a white background under natural lighting. Among them BLB disease is caused by a bacterium named Xanthomonas oryzae. Hot and humid area is congenial for the spread of the disease. That is the reason behind its prevalence in rice-producing areas of Asia, Africa, and the Caribbean. During a BLB epidemic, crop loss can be as high as 75%. It can affect paddy leaves and seedlings; oozing milky juice at the primary stage and finally drying out the leaves to wilt and die. Brown spot (BS) disease is caused by Cochliobolus miyabeanus, a fungus. It affects the rice plant in various parts like leaves, seedlings, sheath, and stems. The loss of yield can be up to 45% or more. On paddy leaves, the disease affected spots are circular or oval in shape. It causes the affected part of the plant to die, effectively diminishing the quality and quantity of harvest. Leaf smut (LS) is also caused by a fungus named Entyloma oryzae. Though it is not a major disease, it can make way for other diseases by creating a favorable environment for other fungi. The lesions are circular to oval or non-uniform in shape with a rough texture. Figure 1 shows a few sample images of these diseases from the dataset. To develop a reliable classification model, extracting important features is essential. For that purpose, the most vital characteristics of the diseases are briefly presented in Table 1 [1, 2]. These color and shape information can be analyzed to generate distinctive features.



(a) (c) (e)

(b) (d) (f)

Figure 1. Rice leaves affected with various diseases; (a)-(b) BLB, (c)-(d) BS, (e)-(f) LS

Table 1. Rice leaf disease lesion comparison

Name of disease	Symptom color	Lesion shape
BLB	Yellow to Gray-White	Long spots, non-uniform shape
BS	Light Brown to Gray at the center, Reddish Brown surrounding	Circular to oval
LS	Dark Reddish Brown to Dark Gray	Circular to oval or non-uniform

2.2. Related work

Application of computer and information technology in agricultural domain is a prominent field of study nowadays. Various researchers are working in different sections of this field. Garcia *et al.* [5] carried out a survey on various image processing and classification techniques of this domain, while Prajapati *et al.* [6] surveyed various techniques used in rice plant disease detection. Shimamura *et al.* [7] worked on automatic detection of tipburn in artificially illuminated plant factories using CNNs. Sugimoto *et al.* [8] addressed the yield loss due to the presence of weeds in paddy fields. They developed a technique of paddy weed removal using robotics. A lot of researchers undertook the problem of automatic detection of plant diseases from the leaf images. Khirade *et al.* [9] used hue-saturation thresholding for image segmentation and SVM for classification in their method. Wang *et al.* [10] extracted 50 features from a dataset containing two grape leaf classes and two wheat leaf classes. They used K-means for segmentation and PCA for dimensionality reduction with back propagation neural network for disease classification. Orillo *et al.* [11] also used back propagation neural network with statistical features from color image dataset containing Blast, Brown Spot, and bacterial leaf blight diseases. Suman *et al.* [12] worked with bacterial leaf blight, brown spot, narrow brown spot, and rice blast diseases. They used 8-connected component analysis for disease segmentation and SVM for classification. They extracted various color and shape features for their model which achieved 70% accuracy. K-means clustering was used by Singh *et al.* [13] for affected spot segmentation. They used SVM for classification and gained 82% classification accuracy. K-means was also used by Sethy *et al.* [14]. Yao *et al.* [15] used shape and texture features with SVM as the classifier. Phadikar *et al.* [16] worked with rice blast and brown spot diseases. They extracted color and shape features like radial distribution of hue. Segmentation was carried out using Ostu's segmentation technique with hue threshold. For 10-fold cross validation, they achieved 79.5% accuracy with Bayesian classifier and 68.1% accuracy using SVM. Phadikar *et al.* [17] worked with four disease classes and achieved 82% accuracy with pattern recognition technique. Charliepaul [18] segmented the disease affected areas using Fermi energy, extracted color and shape features and acquired 75% accuracy. Fermi energy was also used by Phadikar *et al.* [19]. Kurniawati *et al.* [20] used Ostu's method for segmentation and extracted statistical features from images of three rice leaf diseases. They used production rule-based classifier for achieving superior accuracy. Anthonys *et al.* [21] processed rice blast, brown spot, and sheath blight diseases. They used mathematical morphology for segmentation and membership function as classifier. With color, shape, and texture features, they acquired over 70% accuracy. Various color and shape features were also extracted as features in the work of Chawathe [22]. Majid *et al.* [23] used fuzzy entropy for feature extraction and probabilistic neural network as classifier on a dataset of four diseases. Prajapati *et al.* [4] worked with bacterial leaf blight, brown spot, and leaf smut diseases. They used K-means clustering algorithm for disease segmentation. They used morphological operations for region filling, region masking and noise removal. They extracted a total of 40 features from color, shape, and texture. Their dataset contained 40 images of each disease, out of which 35 were used for training and 5 for testing. They used an SVM classifier with radial basis function (RBF) kernel and obtained 73.33% classification accuracy. It is observed that there is no standard dataset for rice leaf disease. All the researchers mentioned above prepared and used their own dataset. An open and standard rice leaf disease image dataset would immensely help the researchers of this field. It is also noted that K-means clustering algorithm is the prime algorithm for disease affected spot segmentation, as utilized in [4, 10, 13].

3. PROPOSED METHOD

Figure 2 shows the block diagram of our proposed approach. It consists of background removal, affected spot segmentation, feature extraction, and classification. For the sake of comparison with other research works, we use the images of the dataset used in Prajapati *et al.* [4] as input. The images of the used dataset are captured with a white background, which are usually saturation dominated. Hence, we convert an RGB image to HSV and remove its background. This ensures that shadows and other outliers do not affect the feature extraction process. Next step is extracting those portions of leaves where disease symptoms are located. It is done by using a threshold mask on the hue plane of the HSV images. To generate a signature of a disease we extract various features from color, shape, and texture of the infected areas. Finally, extreme gradient boosting decision tree ensemble is used for classifying the diseases. The following sections illustrate these steps in detail.

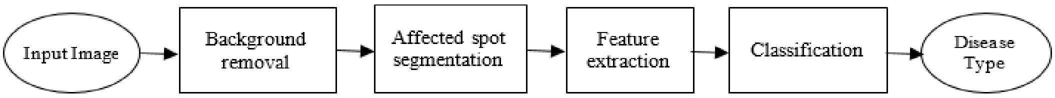


Figure 2. Overview of proposed methodology

3.1. Background removal

The images in the dataset belong to RGB color space. Also, the backgrounds are white in all images. For background removal, images are first converted from RGB to HSV colorspace. The saturation of a background is completely different from that of a leaf. Binary thresholding is carried out on the saturation plane of the images. We set threshold to 71 for background separation. The original image is then masked with the thresholded image to get the background removed image. Figure 3 illustrates the background removal procedure and Figure 4 shows the output image.

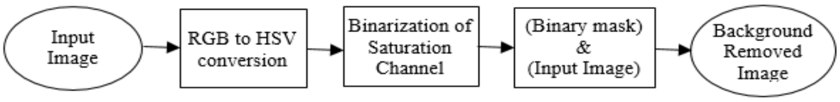


Figure 3. Background removal process


(a) (b)

Figure 4. Background removal; (a) original image and (b) background removed image

3.2. Disease affected spot segmentation

The affected area of a leaf turns brown, gray, dark gray, or reddish brown which are completely dissimilar to the unaffected green portion of the leaf. In our work, hue based segmentation is found effective and time efficient compared to K-Means. Binary thresholding is applied on the hue plane of the images with a threshold value of 22, which is found suitable from histogram analysis. Figure 5 shows the block diagram of the segmentation step and Figure 6 illustrates an output after using the process.

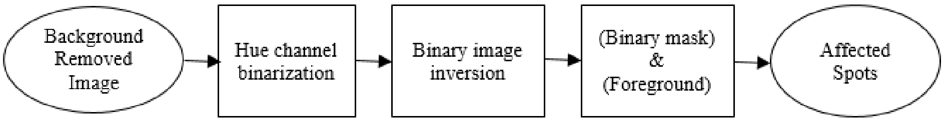


Figure 5. Disease spot segmentation process

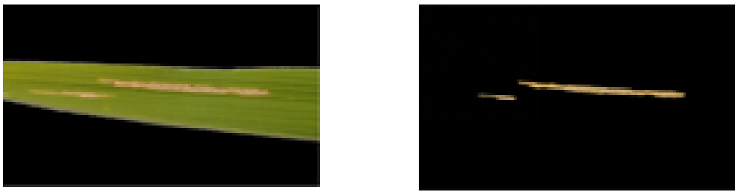

(a) (b)

Figure 6. Disease spot segmentation; (a) background removed image and (b) affected spots

3.3. Feature selection and extraction

The researches, using the same dataset, tried to decrease the number of features to reduce model complexity and achieve higher classification accuracy. We have thoroughly investigated the features of diseases on the leaves. Finally, we have come up with a set of 26 features from the color, shape, and texture domain that can robustly describe disease affected leaf spots. These are mentioned below.

Color features: these features describe color properties of the segmented leaf spots as well as global color properties of the images. 12 color features are extracted from the segmented images. These are: i) mean of red channel, ii) mean of green channel, iii) mean of blue channel, iv) mean of hue channel, v) mean of saturation channel, vi) standard deviation of red channel, vii) standard deviation of green channel, viii) standard deviation of blue channel, ix) normalized hue-saturation histogram, x) skewness, xi) kurtosis, and xii) standard deviation of the intensity values.

Shape features*:* shape features are very helpful where colors of multiple disease symptoms are similar. We use Hu moment invariants [24] as shape features. These are seven mathematical moments of the images which are invariant to rotation, translation, scale, and brightness. We extract a total of 9 shape features from the affected areas of leaf images. These are: i) average contour perimeter, ii) average contour area, and iii-ix) 7 Hu moment invariants.

Texture features: robust texture features are tested on the dataset. We select gray-level co-occurrence matrix (GLCM) and local binary pattern (LBP) as textural feature descriptors. GLCM shows the co-occurrence of gray-level patterns in the segmented spots. We calculate the GLCM in 4 directions at a 3-pixel distance from the reference pixel. From GLCM, the four features used are contrast, correlation, energy, and homogeneity. We take the mean of these values in 4 specified directions e.g., 0, 45, 90, 135 degrees. We employ LBP feature in its basic form as proposed in [25] to capture the intensity pattern from the segmented images. LBP is brightness and rotation invariant. It represents the local change in intensity pattern. So, the texture features are: i) mean contrast, ii) mean correlation, iii) mean energy, iv) mean homogeneity, and v) normalized local binary pattern histogram. We extract a set of different features compared to Prajapati *et al.* [4] for classification. We utilize hue-saturation histogram which captures the relation of pixel colors. A completely different set of shape feature descriptor is used in this work. We find these to be highly robust and effective in distinguishing between disease classes with similar color symptoms. LBP histogram is also used for effective texture analysis.

3.4. Classification

Extreme gradient boosting or XGBoost is proposed by Chen *et al.* [26] in 2016 which is an extension of decision tree algorithm. This brings significant performance improvement over other supervised learning algorithms including the original gradient boosted tree algorithm. The objective function is given by (1).

$$Obj(\theta) = L(\theta) + \Omega(\theta) \tag{1}$$

where, $L(\theta)$ and $\Omega(\theta)$ represents training loss and regularization, i.e. model complexity of the ensemble respectively. The classifier builds a number of weak learners and ensembles them. The algorithm first builds a tree based on a feature. Using the objective function, it generates another tree which improves upon the errors or residuals of the previous tree. During new tree building, error or residual is calculated and minimized using gradient descent. Tree pruning is done greedily based on accuracy gain in each split. Depth-first tree pruning and gradient loss minimization boost the decision tree building process which results in faster execution and improved accuracy.

4. EXPERIMENTAL RESULTS

4.1. Experimental setup

For our implementation, Python 2.7.15 is used along with OpenCV 2.4.13 in a desktop environment. Scikit-learn and XGBoost python packages are used for machine learning tasks. We use standard model evaluation metrics like accuracy score, and f1 score. We tune three parameters e.g. learning rate, maximum depth, and minimum child weight of XGBoost classifier to obtain the best performance. The number of decision trees and tree levels are two very important parameters that control data fitting. Huge number of decision trees can make the ensemble model complex and extremely time consuming. High value of tree levels i.e. deeper trees can overfit the model. Minimum child weight indicates the minimum number of data samples that need to exist in a decision split. The loss function calculates the error during new iterations of tree building. Logistic loss function is used here for this purpose. 20% data is used for testing the model, while rest of the images is allocated for training. For optimal performance, the model needs to be accurate, robust, simple, and effective. Various combinations of the aforementioned parameter values are tested for accuracy improvement. Table 2 shows the values of the tuned parameters for the classifier.

Table 2. Tuned parameter values of XGBoost

Learning rate	Maximum depth	Minimum child weight
0.1	3	5

4.2. Results

We also classify with support vector machine using radial basis function (Gaussian) kernel. In our approach, SVM performs better than the findings of Prajapati *et al.* [4] by more than 8% accuracy. This improvement clearly demonstrates the effectiveness of our feature extraction method. Moreover, XGBoost outperforms SVM by an accuracy of about 5%, achieving overall accuracy improvement of about 13%. The result of classification process is given in Table 3. Figure 7 illustrates the class-wise and overall accuracy comparison between our approach and the previous work of Prajapati *et al.* [4] on the same dataset.

Table 3. Performance comparison between XGBoost and SVM with RBF kernel

Classifier	Accuracy (%)	Weighted average F-1 score
XGBoost	86.58	0.87
SVM with RBF kernel	81.67	0.82

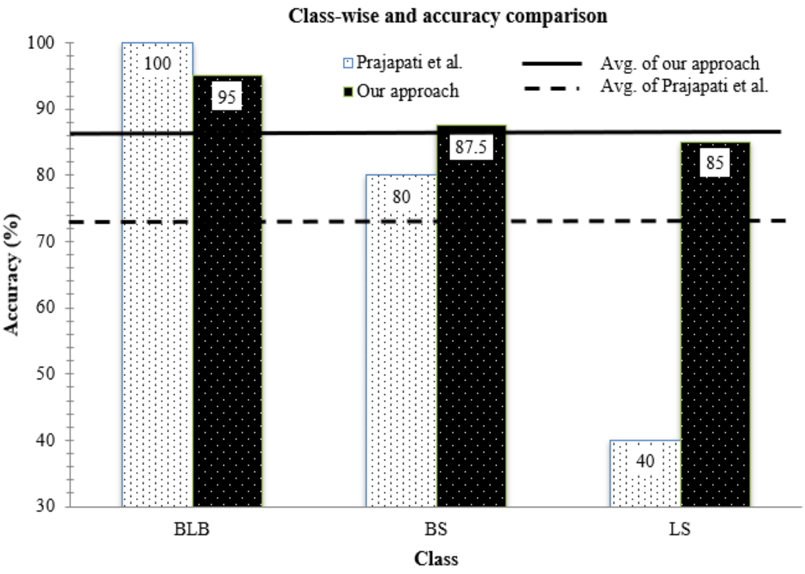


Figure 7. Class-wise and overall accuracy

4.3. Discussion

Among the selected features, some had significant impact on the model performance. Normalized Hue-Saturation histogram is worth mentioning. It is a strong feature descriptor of color domain. In our observation, Hue-Saturation 2D histogram highly contributed to the accuracy gain. GLCM features are also prominent with respect to accuracy gain. Mean correlation and contrast of the segmented image improved the successful classification rate of the proposed model. Brown spot and leaf smut diseases have almost similar effect on the rice leaves. Both of the diseases create symptoms of circular to oval shape. The lesion colors are also similar. Prajapati *et al.* [4] failed to extract proper features which could distinguish between the BS and LS classes according to their subtle shape distinction. Hence, class-wise accuracy of leaf smut was as low as 40% in their work. In our work, carefully selected shape features are found highly effective in differentiating between these two confusing classes. With the chosen features, both SVM and XGBoost achieve consistent class-wise accuracy. The detection rate of BLB is much higher than the others as it has distinct disease signature. On the other hand, BS and LS have similar disease spots. Furthermore, resolution of many LS images in the dataset is significantly lower than the average resolution of images of other classes. For this reason, the accuracy rate of LS detection, although comparable, yet is marginally lower than that of BS.

5. CONCLUSION

In this paper, we propose an approach for rice leaf disease classification. The approach detects three rice leaf diseases e.g. Bacterial Leaf Blight, Brown Spot, and Leaf Smut. In this work, backgrounds of the images are removed using saturation threshold, while affected portions are segmented using hue threshold. The diseases manifest different symptoms on infected leaves. Several statistical features pertaining color, shape, and texture domain are extracted from the images. XGBoost is used for classification process. Model parameters are tuned for optimal performance. The novel contribution of our approach is feature selection and combination. This resulted in higher accuracy of classification from previous researches on the dataset along with consistent class-wise accuracy. 86.58% accuracy on the test dataset is achieved with a small number of features (26 features). Proper feature selection resulted in a significant accuracy improvement over the previous works on the same dataset. We aim to continue our investigation for extracting a new set of distinctive features from the infected areas which will further increase the accuracy of disease detection. The proposed method will be implemented in mobile app format so that the farmers can use it on-field for detecting diseases.

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