

Detection of Rice Diseases by the Fusion of Optimization based K-means Clustering Algorithm and Faster Region based Convolutional Neural Network

A. Pushpa Athisaya Sakila Rani

Research Scholar, Department of Computer Science, Malankara Catholic College, Affiliated to Manonmaniam Sundaranar University, Tamilnadu, India.

E-mail: pushpasakila@gmail.com

N. Suresh Singh

Associate Professor and Head, Department of Computer Applications, Malankara Catholic College, Affiliated to Manonmaniam Sundaranar University, India.

E-mail: sureshsinghn10@gmail.com

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Abstract

One of the most important food crops in the world is rice, which is highly affected by various plant diseases and pests. Even though there are so many methods to address the concern, detection accuracy is a hectic challenge, which needs to be boosted for an enjoyable farming environment. In the present study a rice disease detection technique was implemented by the fusion of Sailfish optimization – K-means (SCM-KM) and the Faster Region Based Convolutional Neural Network (Faster R-CNN) method. For the optimization of the KM clustering method, Sailfish Optimizer was coupled with the Maximum and Minimum distance algorithm, as well as Chaos theory. The 2D Filtering Mask and Weighted Multilevel Median Filter(2DFM-AMMF) were used to eliminate the sounds. With the aid of the Faster 2D-Otsu technique, the target leaf lesion was segmented from the image. The SCM-KM method is used for detection of rice disease. The Rice diseases were characterized and classified by Region Proposal Networks (RPN) and Faster R-CNN method. Comparative analysis of the SCM-KM+ Faster R-CNN method was performed using the metrics sensitivity, accuracy, and specificity. The proposed detection method produced elevated performance over similar bench marking frameworks.

Keywords

Rice Leaf Disease Detection, K-means, R-CNN, Sailfish Optimization.

Introduction

The science and practice of producing plants and livestock is known as agriculture. Agriculture is critical to the advancement of human civilization. Cultivating selected plant species created surplus food. It's evident that cultivating selected plant varieties started around 11500 years ago, but collecting wild grains for food was practised as long as 10500 years ago. Rearing of cattle started some 10000 years ago. From ancient times people depends on many plants as the source of staple food (Safety and health in agriculture, 1999). Having access to safe and nutritious food that meets people's dietary needs and tastes is essential for living an active and healthy life. The State of Food Insecurity in the World 2001. Rome, FAO, UN. 2002). Cereal crops are the most significant and largest feeders among them. Starch, a carbohydrate that supplies nutritional energy, is abundant in cereal crops (S. O. Serna-Saldivar (2012)). Cereals are the cheapest food source on the planet, accounting for 60% of the calories and proteins ingested.

Rice is the most significant human food, consumed by more than half of the world's population every day. Ensuring enough and affordable rice crops is most important especially for the Asian sub-continent where they alone consume 90% of rice. It's one of the most important crops among the food grain and it is scientifically termed as, *Oryzasativa* (S.K. De Datta (1981)). For over half the population in the world, food security is ensured by rice. The rice provides social stability, agricultural security, and national development as the production is stable. The productivity of paddy gets most affected due to diseases. Hence, it is necessary to detect the presence of disease for helping the farmers to save the crops (B. Chilwal and P.K. Mishra (2020)). Food safety may be accomplished through the prevention and treatment of paddy diseases that could only be done with the prompt detection of infections. Fast and precise diagnosis of plant disease should be successfully made in order to control this disease. In order to preserve crops without loss, the incidence of plant diseases must be detected in advance. The main issue is thus to quickly diagnose pest infestations and the frequency of the disease. Paddy disease from image recognition and automated disease severity categorization is done by the use of Image Processing Technologies.

Even if many classification frameworks brought to address this problem in the recent past, it is important to adopt state-of-art scientific methods such as machine learning (R. John Martin et al. (2018)) to enhance the performance. The major focus of the study is to develop a scientific method for detecting rice diseases by combining both Shadowed C-Means (SCM) (Sushmita Mitra et al. (2010); L. Kong and L. Chen (2017)) and Faster

R-CNN (D.A. Jasm et al. (2020); S. Shindo et al. (2019)) algorithms. First, image of the diseased leaf from the dataset is acquired and continued by removal of noise using 2DFM-AMMF. The denoised image is segmented using faster 2D Otsu that extracts the target leaf lesion from the image. Infections are identified using SCM and Faster R-CNN. Result obtained is subjected to classification by RPN and Faster R-CNN for specific diseases. Disease diagnosis systems including predictive modeling systems generally uses bottom up approaches (R. John Martin and S. Sujatha (2016)) for modeling decision making behavior (R. John Martin and S. Sujatha (2018)) of its intelligent agents. Different variants of K-means clustering methods for data mining are proposed by Md. Zakir Hossain et al. (2019) and R. Gustriansyah *et al.* (2020)) used a K-means clustering variant in a signal analysis application.

Zhou, G. *et al.* (2019) developed a rice disease prediction method by the fusion of Faster R-CNN and FCM-KM. In this approach, the noise was decreased by merging the 2D filter mask with the weighted multi-level median filter. The segmentation was done using the Faster 2D-Otsu method for separating the background from the target image. The optimal clustering class value was determined using the FCM-KM algorithm. Although this method had a higher recognition rate, it was not suitable for monitoring large-scale cultivation of rice.

C.R. Rahman et al. (2020) designed a rice plant disease detection method using a deep learning-based method. The detection of the disease was done by implementing the VGG16 architecture, whereas the rice diseases were recognized using the InceptionV3 architecture. Although this method achieved a reduced model size with good accuracy, it failed to implement the technique in the heterogeneous background.

N. Guchait et al. (2020) designed a neutrosophic logic based segmentation method for the detection of disease in leaf. Three membership elements were formed by distinguishing the segmented image. The new feature subset was formed based on the segmented regions using color, texture, and histogram. This method obtained better accuracy in classification by combining the discrimination power of texture and intensity. However, this method failed to determine the severity of the diseases.

A. Sony (2020) developed a rice disease detection method using the Convolutional Neural Network. This method used the R language in the rice plant leaves for the detection of the disease. Although this method provided an average detection rate, it failed to predict the name of the disease and recommend suitable pesticides.

Research Methods

Pre-processing Using 2D FM-AMMF

Pre-processing is carried out using 2DFM-AMMF for the reduction of noise. The weighted multistage filtering method integrates both the average weighting algorithm and the multilevel median filter to reduce the elimination of the edge information such that the shape and the size of the filtering window are determined. Let us consider, the square filter window of size $G=2D+1$ that is centered at (x,y) . The digital image sequence considered for the rice disease is given as, $Z(x,y)$. In the filter window J , the four subsets are represented as,

$$\begin{cases} J_1(x, y) = \{Z(x, y + d); -D \leq d \leq D\} \\ J_2(x, y) = \{Z(x + d, y + d); -D \leq d \leq D\} \\ J_3(x, y) = \{Z(x + d, y); -D \leq d \leq D\} \\ J_4(x, y) = \{Z(x + d, y - d); -D \leq d \leq D\} \end{cases} \quad (1)$$

In the four sub-windows, the median gray value of the pixel is represented as,

$$\begin{cases} W_1(x, y) = med [m(x, y) \in J_1(i, j)] \\ W_2(x, y) = med [m(x, y) \in J_2(i, j)] \\ W_3(x, y) = med [m(x, y) \in J_3(i, j)] \\ W_4(x, y) = med [m(x, y) \in J_4(i, j)] \end{cases} \quad (2)$$

where, the median gray values are denoted as, $W_1(i,j)$, $W_2(i,j)$, $W_3(i,j)$ and $W_4(i,j)$. The output from the weighted multistage median filter is given as,

$$M(x, y) = med [M_{\min}(x, y), M_{\max}(x, y), Z(x, y)] \quad (3)$$

The multilevel median filter produces the following output,

$$M(x, y) = \sum_{i=1}^4 W_i(x, y) / 4 \quad (4)$$

The gray value of the pixel is determined by averaging the median value of four sub-windows. In the median filter, the large and the small window size worsen the noise reduction effect. The problem in the noise reduction is solved by including the two-dimensional filter mask. The image filtering is carried out in the four 1D filter windows by including the three 3D filter mask windows depending on the weighted multistage median filter. The possibility of retaining the detailed features and reducing the erroneously culling edge information while removing the noise is improved as the mask

shape and size are different for different image regions. The seven windows are represented as,

$$\begin{cases} J_1(x, y) = \{Z(x-i, y-j); -1 \leq i \leq 1; -1 \leq j \leq 1\} \\ J_2(x, y) = \{Z(x-i, y-j); -2 \leq i \leq 2; -2 \leq j \leq 2\} \\ J_3(x, y) = \{Z(x-i, y-j); -3 \leq i \leq 3; -3 \leq j \leq 3\} \\ J_4(x, y) = \{Z(x, y-i); -3 \leq i \leq 3\} \\ J_5(x, y) = \{Z(x-i, y); -3 \leq i \leq 3\} \\ J_6(x, y) = \{Z(x+i, y-i); -3 \leq i \leq 3\} \\ J_7(x, y) = \{Z(x-i, y-i); -3 \leq i \leq 3\} \end{cases} \quad (5)$$

The 2D mask filtering window of 3×3 is represented as, J_1 , 2D mask filtering window of 5×5 is represented as, J_2 , 2D mask filtering window of 7×7 is represented as, J_3 , and the value of J_4 - J_7 is same as equation (1). After the improvement, the basic steps followed are as follows, initially, the position of the pixel in the rice disease image is determined which is followed by the calculation of the variance in gray value of the window. While comparing the variance of the 2D window, if the threshold is higher than the 2D window then, the filtering window is the window having smallest variance. If the threshold is lower than the 2D window then, the filtering window is the 1D window with smallest variance. Finally, the median filtering process is used in the filtering window for preserving the details of the picture of the rice leaf.

Segmentation of Image Using Faster 2D-Otsu

In the segmentation process, the target rice leaves are separated from the background for improving the detection accuracy and removing the interferences. The conventional 2D Otsu algorithm removed the noise as it segments the image by considering the gray value and the mean of the neighborhood. A threshold, l and b is obtained by the original rice disease image, $p(m,n)$ and neighborhood mean image, $B(m,n)$. The discrete data is divided into two categories based on the threshold l . The variance between two classes are represented as,

$$l_r = c_0 c_1 (w_0 - w_1)^2 \quad (6)$$

where, the probability of the background and target class is denoted as, C_1 and C_0 , the mean of the background and target class is denoted as, w_1 and w_0 . The larger the variance, the larger is the l_r value between the classes. The discrete data is categorized into two types based on the threshold l . The mean of the two types represented by the occurrence probability of W_0 and W_2 , is given as, r_x . The variance of two data types is denoted as,

$$l_1 = \sum_{x=0}^I r_x (x - w_0)^2 \quad (7)$$

$$l_2 = \sum_{x=P+1}^{G-1} r_x (x - w_1)^2 \quad (8)$$

Within the two classes, the total variance is represented as,

$$l_c = c_0 l_1 + c_1 l_2 \quad (9)$$

The cohesiveness of the two data types in the data group is denoted as, l_c . The discriminant function determined using the intra-class variance ratio method is denoted as,

$$P = l_r / l_c \quad (10)$$

The optimal threshold is the corresponding gray value that satisfies the equation, $P^* = \text{argmax}\{P\}$.

Rice Disease Detection Using the Optimized KM and Faster R-CNN Fusion

The images of the diseased paddy plant are first obtained, and the image noise is eliminated using a combination of a 2D filtering mask and a weighted multi-level median filter (2DFM-AMMF). The denoised image is then segmented using a quicker 2D Otsu algorithm to recover the target leaf lesion from the image (Abbas F.H. Alharan et al. (2019)). The retrieved characteristics are then applied to the classification framework. The Sailfish Optimizer (S. Shadravan et al. (2019); K.K. Ghosh et al. (2020)), maximum and minimum distance algorithms, and the chaos theory were combined to create the SCM-KM method, which is used to optimize the K-Means clustering technique. The K-means output is input into the Faster R-CNN (G. Zhou et al. (2019)) to extract rice illness features and disease categorization.

For increasing convergence speed and resetting the bounding box size, the suggested SCM-KM method is combined with the Faster R-CNN algorithm. The parameter setting in KM clustering is solved using the SCM method. The following are the processes involved in fusing the SCM-KM and Faster R-CNN algorithms:

- i) The characteristics, such as the shape, color and texture of the disease is present in the original image beside that the large proportion of the characteristics is also present in the marker boxes. Both the segmented and the original color image of the data set

image is considered for making the network fully capable and preventing the influence of other areas.

- ii) The difference in target frame size in the left, right, and top corners of the target provides the input to the SCM-KM algorithm. The target data set's frame size is then subjected to cluster analysis.

The cluster centre is used as input in the standard Faster R-CNN algorithm, and the Faster R-CNN algorithm is trained using a new bounding box scale. The cluster center and category value H are given to the generate anchor function during the first candidate box creation. Finally, in order to produce cluster categories ($d=4$), the maximum and minimum distance technique is used. By combining the SCM-KM and the Faster R-CNN algorithms, the rice disease features are retrieved and classified.

Proposed SCM Algorithm for Optimizing k-means Clustering

The proposed SCM algorithm optimized the KM clustering for detecting rice disease. The KM clustering algorithm is used for the classification of the j samples into d categories. The drawbacks of the KM clustering algorithm are the impact on the random selection of H value on the computational complexity and accuracy, the fall of the algorithm in the local optimum. During the local search, the hunting behavior of the sailfish is used for improving the speed of convergence in the KM clustering method. Thus, the KM clustering algorithm is improved in terms of the global optimization search by the SCM-KM algorithm.

a) Sailfish Optimizer

Initially, the population of the sardine and sailfish are initialized. Consider the current position of the u^{th} member in the f -dimensional space at the h^{th} searching bout is represented as, $Y_{u,h} \in A(u=1,2,\dots,s)$, where, the number of sailfish is denoted as, S the number of variables are denoted as, f . The fitness function of the sailfish is given as,

$$X(Y) = X(Y_1, Y_2, \dots, Y_s) \quad (11)$$

The sardines are the small fishes hunted by the sailfish. The fitness value of the sardines is given as,

$$X(YS) = X(YS_1, YS_2, \dots, YS_k) \quad (12)$$

where, the number of sardines is given as, k , the objective function is represented as, X and the fitness of the sardine is denoted as, $X(YS)$. The injured sardine is considered as the best sardine, whereas the elite sailfish is considered as the best. The obtained fitness of the sailfish that is determined so far is the elite sailfish. During the group hunting, the lashing motion with the rostrum of the sailfish injures the sardines. At each iteration, the position of the injured sardine is saved (R. John Martin and S. Sujatha (2016)). The injured sardine is selected as the optimal solution for the sailfish's collaborative hunting. At the u^{th} iteration, the injured sardine's an elite sardine's position with the highest fitness is represented as, $V_{injured_Y}^u$ and $V_{elite_Y}^u$ respectively. If the termination condition is not satisfied then, the coefficient μ_u is calculated followed by updating the sailfish's position. At the u^{th} iteration, the coefficient μ_u is given as,

$$\mu_u = 2 \times rand(0,1) \times P_D - P_D \quad (13)$$

Where, the density of the prey in every iteration is given as, P_D . P_D is the important parameter for updating the sailfish's position. The new sailfish's position is updated as,

$$V_{new_Y}^u = V_{elite_Y}^u - \mu_u \times (rand(0,1) \times (V_{elite_Y}^u + V_{injured_Y}^u) - V_{old_Y}^u) \quad (14)$$

After updating the position of the sailfish, the attack power of the sailfish at each iteration is calculated as,

$$P_A = C \times (1 - (2 \times v \times \sigma)) \quad (15)$$

Where, the power attack value is decreased using the coefficients, σ and v . The random number v varies from 0 to 1. If the attack power is lesser than 0.5, the number of variables and the sardines required for updating the position is calculated as,

$$\omega = S_N \times P_A \quad (16)$$

$$\rho = f_u \times P_A \quad (17)$$

where, in each algorithm cycle, the number of sardines is given as, S_N and at u^{th} iteration, the number of variables is denoted as, f_u . Based on the value of the ω and ρ , a set of sardine is determined and the position of the sardine is updated as,

$$V_{new_YS}^u = v \times ((V_{elite_Y}^u + V_{old_YS}^u + P_A)) \quad (18)$$

If the attack power is greater than or equal to 0.5 then, the position of the sardine is directly updated based on the equation (18). In the sardine population, if there is a better solution then, the sailfish is replaced with the injured saline as,

$$V_y^u = V_{ys}^u \text{ if } X(YS_u) < X(Y_u) \quad (19)$$

Then, the hunted sardine is removed from the population which is followed by the updating of the best sardine and the sailfish.

b) Maximum and Minimum Distance Algorithm

For determining the cluster's center value H, the maximum and minimum distance technique is used. After determining the Euclidean distance, the closest neighbor concept is used to classify the sample points that belong to the center cluster. The object Rx is chosen as the first cluster's center from the sample points. The Euclidean distance between each point Rx is then computed. The point Rx that is further away from the distance, is the new cluster center. The Euclidean distance is calculated as,

$$E_d(R_x, R_y) = \sqrt{\sum_{d=1}^i (R_{xd} - R_{yd})^2} \quad (20)$$

Until there is no generation of the new cluster center, the calculation of the Euclidean distance is followed. Finally, the total cluster center H is determined.

c) Chaos Theory Optimization Cluster Center

The chaotic theory cluster KM is used for improving the ability of global search and avoiding the cluster center of the sailfish algorithm in falling near the local minimum point. The tent map is used by the chaotic sequence for improved ergodic uniformity and convergence speed. The expression for the tent mapping is given as,

$$m_{\tau+1} = \begin{cases} 2m_{\tau}, & 0 \leq m_{\tau} \leq \frac{1}{2} \\ 2(1-m_{\tau}), & \frac{1}{2} \leq m_{\tau} \leq 1 \end{cases} \quad (21)$$

By applying the Bernoulli shift, the tent map is represented as,

$$m_{\tau+1} = (2m_{\tau}) \bmod 1 \quad (22)$$

Depending on the local optimal solution that is locally searched, the tent chaotic is generated by the proposed SCM algorithm. The global optimal solution is obtained by jumping out of the local optimum with the help of a tent search. The cluster center is

represented as, $C_z(x=1.2\dots d)$ and F_{xm} is the distance between the cluster centers. The new chaotic search space is formed by finding the minimum value, Z_{\min}^y and maximum value, Z_{\max}^y in the current class $j+1$ of the y^{th} dimension.

Results and Discussion

The dataset considered for the SCM-KM+Faster R-CNN implementation is obtained from the Rice leaf disease dataset (Jitesh P. Shah et al. (2016)). The dataset consists of 120 instances. It has multivariate dataset characteristics and integer attribute characteristics. The performance metrics used for the analysis of the proposed SCM-KM+ Faster R-CNN method is sensitivity, accuracy and specificity.

Experimental Results

The appearance of the input image (diseased leaf) at various stages of detection of disease is being described below. The selected input image is being subjected to filtering using 2D filtering mask with the weighted multilevel median filter in first stage. At the second stage the filtered image is being segmented using 2D Otsu here the targeted leaf lesions are extracted. The third step is that the filtered image is being optimized through KM and faster R-CNN method. The resultant image is the output image where the disease identification process is completed and the type of infection is displayed in the image.

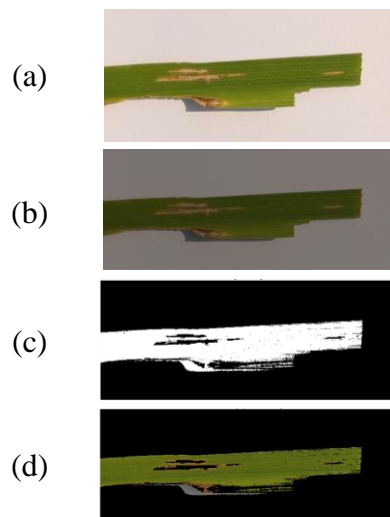


Figure 1 (a) Bacterial Leaf Blight input image (b) Bacterial Leaf Blight filtered image (c) Bacterial Leaf Blight segmented image (d) Bacterial Leaf Blight classified image

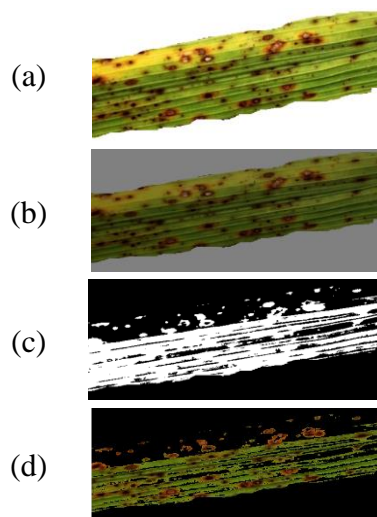


Figure 2 (a) Brown Spot input image (b) Brown Spot filtered image (c) Brown Spot segmented image (d) Brown Spot classified image

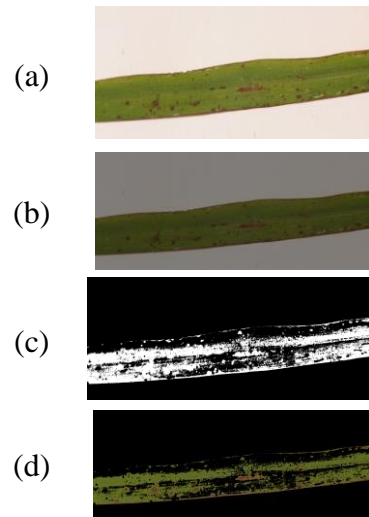


Figure 3 (a) Leaf Smut input image (b) Leaf Smut filtered image (c) Leaf Smut segmented image (d) Leaf Smut classified image

Comparative Methods

The proposed SCM-KM+ Faster R-CNN algorithm is compared with bench marking algorithms such as the Non-Parametric Approach (T. Coelli, S. Rahman and C. Thirtle (2005)), Deep learning (S. Bhattacharya et al. (2020)), CNN (S. Shindo et al. (2019)), and FCM-KM+ Faster R-CNN algorithm (B. Chilwal and P.K. Mishra (2020)). Different K fold levels ranging from 5 to 10 are applied to various existing methods viz., Non parametric approach (non-random method), Deep learning, CNN, and FCM-KM+ Faster R-CNN. The process was repeated for all the performance metrics proposed in the present study and the data obtained are analyzed mathematically and presented graphically.

Table 1 Comparative analysis of accuracy by varying K fold values

K fold value	Non-Parametric Approach	Deep learning	CNN	FCM-KM+ Faster R-CNN	SCM-KM + Faster R-CNN
5	76.1756	77.19	77.2666	78.5090	80.3600
6	76.2967	77.7617	78.1000	79.7821	82.4493
7	76.7806	77.9233	78.3901	79.9163	82.5042
8	76.8218	78.2126	79.8080	80.5936	82.5066
9	76.9500	78.2377	80.3956	80.9719	84.7566
10	78.8900	80.4100	80.4329	83.1669	84.8695

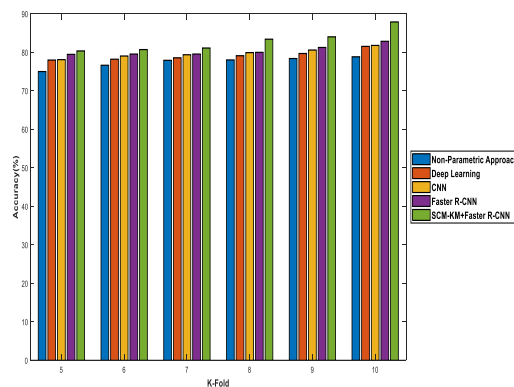


Figure 4 Comparative analysis of accuracy by varying K fold values

Table 2 Comparative analysis of sensitivity by varying K fold values

K fold value	Non-Parametric Approach	Deep learning	CNN	FCM-KM+ Faster R-CNN	SCM-KM+Faster R-CNN
5	72.7633	73.8222	74.5030	75.9876	78.17333
6	73.7080	75.3497	76.0119	77.6555	78.8800
7	74.0450	75.7908	76.9413	77.724	80.9407
8	74.6935	76.0647	77.2420	79.7573	81.3922
9	76.0043	76.4991	78.7899	80.6837	81.5033
10	76.6924	76.7791	79.7793	82.2762	83.5719

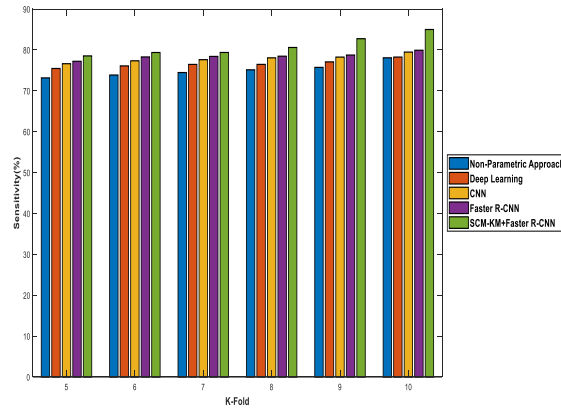


Figure 5 Comparative analysis of sensitivity by varying K fold values

Table 1, Table 2 and Table 3 shows the different levels of accuracy, sensitivity and specificity on each of the existing methods which exhibit at varying k fold levels as against the proposed method of SCM-KM+ Faster R-CNN method in rice disease prediction, and the respective graphical representations are presented adjacently with Figure 5, Figure 6 and Figure 7.

Table 3 Comparative analysis of specificity by varying K fold values

K fold value	Non-Parametric Approach	Deep learning	CNN	FCM-KM+ Faster R-CNN	SCM-KM+Faster R-CNN
5	83.5498	84.9777	85.8043	86.9950	88.3043
6	83.9963	85.3357	86.1287	87.0148	88.4992
7	84.9078	85.3541	86.1770	87.4099	88.7349
8	85.1807	85.4491	86.4052	87.4263	89.0881
9	85.4805	85.5533	86.5043	87.4520	90.3403
10	85.6892	86.3289	86.8430	90.0981	90.3713

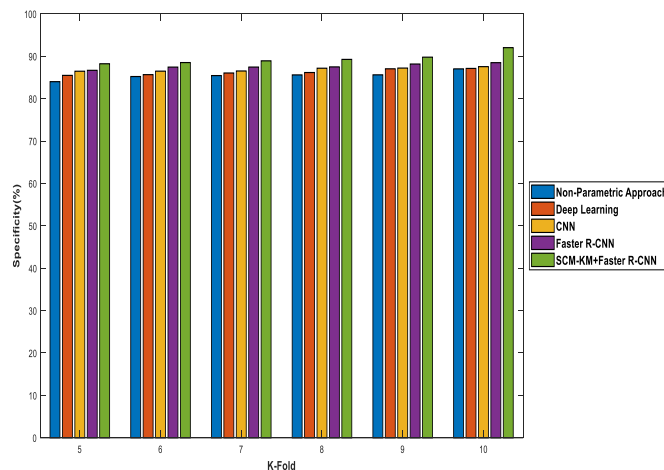


Figure 6 Comparative analysis of specificity by varying K fold values

Comparative Analysis Using Training Percentage

The performance metrics viz., sensitivity, accuracy, and specificity are selected as metrics by which the effectiveness of different methods in rice disease prediction is assessed. The study was conducted by altering the training percentage ranging from 40 - 90 for various existing methods viz., Non parametric approach (non-random method), Deep learning, CNN, and FCM-KM+ Faster R-CNN and the data was recorded. The same is compared with the data obtained for the proposed method of SCM-KM + Faster R-CNN. The process was repeated for all the performance metrics proposed in the present study and the data obtained are analyzed mathematically and presented graphically. Table4, Table5 and Table6 indicates the different levels of accuracy, sensitivity and specificity percentages in rice disease prediction on each of the existing methods exhibit at varying training percentage as against the proposed method of SCM-KM+ Faster R-CNN method.

Table 4 Comparative analysis using accuracy by varying training percentage

Train-ing%	Non Parametric Approach	Deep learning	CNN	FCM-KM+ Faster R-CNN	SCM-KM+Faster R-CNN
40	76.7250	82.4500	83.1764	92.7442	93.2773
50	79.5300	86.4730	89.2833	93.1243	93.6945
60	82.1466	86.9200	91.0442	93.3144	94.2646
70	84.6233	88.0200	91.7940	93.8845	94.8348
80	85.8600	89.6400	91.9840	94.4547	95.4049
90	88.2930	91.6167	93.6940	95.5950	96.5452

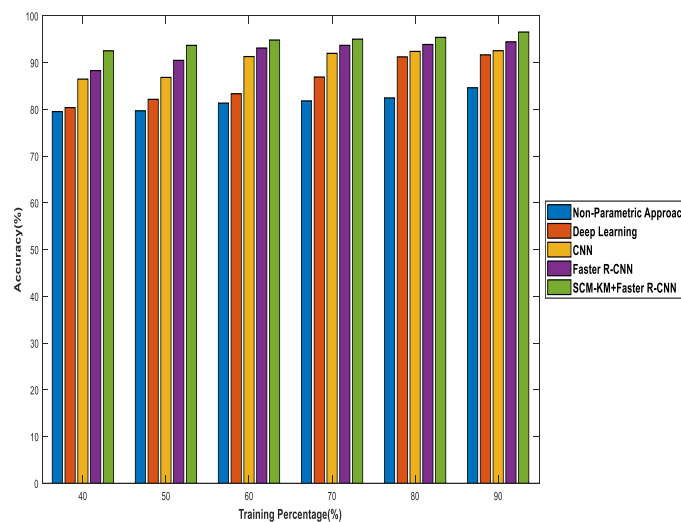


Figure 7 Comparative analysis using accuracy by varying training percentage

Table 5 Comparative analysis using sensitivity by varying training percentage

Train- ing%	Non Parametric Approach	Deep learning	CNN	FCM-KM+ Faster R-CNN	SCM-KM+Faster R-CNN
40	74.7286	80.3601	80.3894	90.1626	93.1000
50	78.2956	84.2868	87.8579	92.7200	93.6700
60	80.8969	85.1178	90.6469	93.2900	94.2400
70	81.7026	86.3146	91.7700	93.8600	94.8100
80	83.6868	87.9672	91.9600	94.4300	95.3800
90	85.2938	88.5271	93.6700	95.5700	96.5200

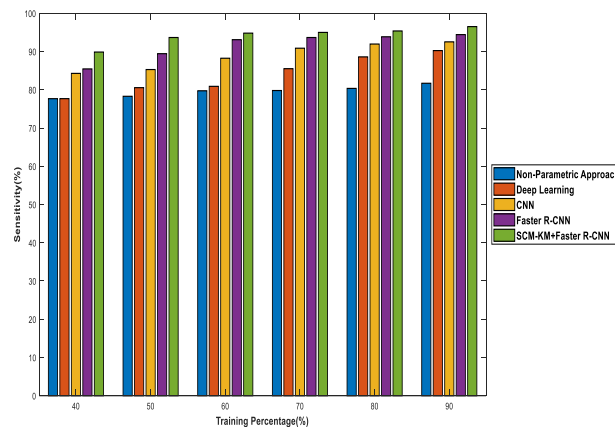


Figure 8 Comparative analysis using sensitivity by varying training percentage

Table 6 Comparative analysis using specificity by varying training percentage

Training %	Non Parametric Approach	Deep learning	CNN	FCM-KM+ Faster R-CNN	SCM-KM+Faster R-CNN
40	86.3838	87.7101	90.9471	93.696	94.4526
50	86.4015	89.2763	91.9258	94.0800	94.6560
60	88.1827	89.9633	92.3520	94.2720	95.2320
70	88.6493	91.5441	92.7360	94.8480	95.8080
80	88.7914	91.7760	92.9280	95.4240	96.3840
90	89.7700	91.9009	94.6560	96.5760	97.5360

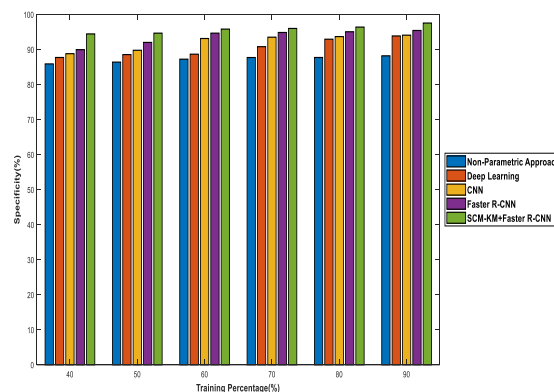


Figure 9 Comparative analysis using specificity by varying training percentage

Conclusion

In this study, the fusion of the SCM-KM and the Faster R-CNN approach has been used to detect rice diseases. For optimizing the KM clustering method, Chaos theory was integrated together with the maximum and minimum distance algorithm. The 2D Filtering Mask and Weighted Median Filter (2DFM-AMMF) eliminated the noises. A Faster 2D Otsu Method used to segment the target leaf lesion from the image. The SCM-KM method is used for detection of rice disease. The Rice diseases were characterized and classified by RPN and Faster R-CNN method. Comparative analysis of the SCM-KM+ Faster R-CNN method was performed using the metrics sensitivity, accuracy, and specificity. The SCM-KM+ Faster R-CNN method obtained a maximum sensitivity of 83.5719, maximum accuracy of 84.8695, and maximum specificity of 90.3713 for varied K-fold values and a maximum sensitivity of 96.52, maximum accuracy of 96.5453 and maximum specificity of 97.536 for varied training percentages. In this study, existing methods in the detection of rice disease were enhanced by implementing more advanced optimization algorithms and advanced classifiers. The SCM-KM+ Faster R-CNN was found superior to all the other existing methods.

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