Journal of Data Acquisition and Processing
ISSN: 1004-9037
https://sjcjycl.cn/
DOI: 10.5281/zenodo.777138

OPTIMIZED SVM MODEL FOR MAIZE AND RICE LEAF DISEASE DETECTION

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Abstract

Crop disease is not only treated for Food Security(FS) globally. However, it also leads to tragic consequences for farmers whose livelihood depends on healthy crops and food production. Agricultural exports must take various procedures to prevent crop health and crop loss due to disease. Plant disease detection is a significant factor in crop loss prevention. Recently, mobile-based plant disease detection approaches are getting popularity among formers. Still, this application has some limitations in other plant disease detection (PDD) due to the poor performance of the adopted present PDD methods. This study has addressed these issues by considering only two PDD such as rice and maize disease. It introduces a fish swarm-optimized Support Vector Machine(FSOSVM) model to perform the PDD. The food hunting behaviour of the fish swarm optimizer(FSO) is used to fine-tune the SVM parameters to improve detection accuracy.

Keywords: *Data Mining,Crop disease, Fish swarm optimizer, Machine learning, leaf disease, SVM, Optimization, Classification.*

I. Introduction

The agricultural system[1] is not only threatened with food production for beings, but it also plays a significant role in environmental production. Food security(FS) is treated by factors such as plant disease[2], climate change[3], the decline in pollinators[4], and many more. Modern technology[5] provides various supports for the formers to produce quality food to meet the demand of billions of people. A crop monitoring system[6] helps to identify potentially risky areas from the crop field to improve disease management. The presents of crop disease on the plant leaves costs formers a lot of money. Reports say that nearly 50% of foods produced by small farmers lose healthy foods during farming yearly due to various reasons such as plant disease[7], pest attacks[8], climate changes, nutrition deficiency[9], and lack of available technical support for timely detection. Traditional methods[10] physically analyze changes in specific leaves' features such as colour, texture, shape, etc. As a result, it is not an effective method. Since it takes lots of time to analyze each crop region, it takes lots of expenses for the disease condition analysis. Crop diseases[11] are classified as infection and non-infection. Some Crop infection-causing agents are fungi, viruses, bacteria, nematodes, and parasitic plants. In this, infection-based diseases need to be treated sensibly and early.

Otherwise, it quickly spreads and makes significant crop loss. Rice and maize[12-14] are the two common crops for many rural farmers to make their income. However, these crop infections affect most rice and maize crops and create a major disaster. Maize requires lots of areas to grow, and it requires proper sunlight. So, this crop is growing well in an outdoor environment. Maize crops are commonly affected by grey leaf spots, tar spots, leaf blight, and southern rust, and maize common rust. Bacterial blight, marrow leave sports, bacterial leaf steak and tungro virus infection are the common rice crops disease.

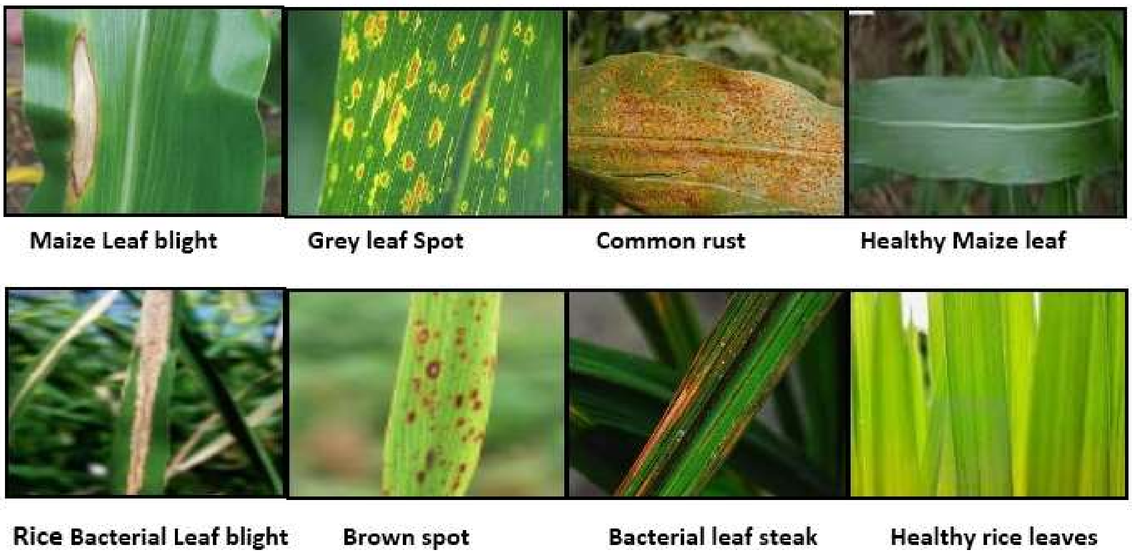


Figure 1: Rice and Maize leaf disease

Figure 1 shows some of the bacterial and fungal infection-based leaf diseases considered in this study. If these fungal or bacterial infections are left untreated, they spread to all other plants through air and wind water. Managing the disease early is vital to keep the maize healthy and protect the crop field from the disease. Crop disease detection is one of the compelling methods of food security. Researchers make various effects to make disease detection[15] to save crops' lives and reduce food loss. The traditional manual disease analysis methods are time-consuming and require more cost. So, this study's objective is to prevent the rice and maize crops from disease and also to control the spreading from one region to another. This has been achieved by introducing an efficient crop disease-optimized classification model for detecting Maize and Rice crop disease.

II. Related work

This study [16] analyzed different machine learning and deep learning models' performance while detecting plant leaf disease. It considers the best-performing three machine learning (ML) models and three deep learning(DL) models. Random forest(RF), Support vector machine(SVM), and Stochastic gradient descent(SGD) classifiers are considered the previously best-performing ML classifiers. VGG-16, VGG-19, and Inception-V3 are the three best-performing DL models. The analysis shows that the SVM model performs better (87%) than other ML models while detecting plant leaf disease, and the VGG-16 model obtained a maximum accuracy of 87.4%.

In this [17], the convolution neural network(CNN) model is utilized to detect leaf disease. It uses 54305 image data to train and test the detection performance of the CNN model. This dataset contains 38 classes. The performance analysis shows that the CNN model obtained a maximum of 95.8% accuracy in detecting 38 leaf diseases.

This research [18] prepares performance analysis of different ML models on plant leaf disease detection. It utilizes Naive Bayes (NB), K-nearest Neighbor(KNN), Decision tree (DT), RF, and SVM classifier. The analysis performed to choose a suitable model for maize leaf disease shows that the RF model obtained a better accuracy rate (79.23%) than other ML models.

This study [19] reviews different approaches to plant leaf disease detection problems. It investigates how the ML model is utilized to enhance the cycle of plant disease detection in the beginning phase to improve grain security and manageability of the agro-biological system.

This research [20] prepares an in-depth review of DL-based plant leaf disease detection approaches. It analysis the functionalities and performance of different DL and modified DL. Moreover, many visualization techniques or mapping methods are summarized to recognize the disease's symptoms. It identified that the DL-based models are suitable for various illumination condition image-based leaf disease detection approaches.

This study [21] proposes a prediction model for plant leaf detection using computer vision and the ML approach. Different ML models are utilized to classify disease. The evaluation has observed that while increasing the number of classes and images, the performances of the previous ML model are significantly decreased. This limitation is overcome using optimum ML.

This study [22] developed a Rice plant image-based leaf disease detection model. It mainly focuses on three commonly occurring rice crop diseases: leaf smut, bacterial leaf blight, and brown spot. It utilized different ML models to prepare performance analysis for the mentioned three rice disease detection. It proves that the NB method obtained a maximum of 97% classification accuracy.

In this [23], the RF classifier is utilized to identify healthy and non-healthy leave. The histogram of oriented gradient(HOG) method is used for feature extraction. It uses the ML model to train crop disease dataset using publicly available leaf disease dataset.

This work [24] inspects plant disease using two different ML models. But, it has under-fitting data issues. More investigation is required on pathological features-based features during the pathological analysis process. Optimal feature selection is one of the main changes in this study. It is responsible for reducing disease detection.

This work [25] fails to investigate the connection between the plant disease pathological features. Moreover, it is failed to investigate various asymmetric biological changes in the plant features associated with plant disease to seek other promising results.

In this [26], image data and processing steps are used to accurately predicts crop disease. But most of the classification models failed to handle the uncertainty. The model already has the pre-trained model. Additional time is required to predict the AD disease more accurately while taking the images.

This study [27] designed a feature selection method for hyperspectral image classification. In this, a new class separability measure called Surrogate Kernal and Hilbert Schmidt independence criteria (HSIC) is utilized to measure the feature importance of each feature. It aligns the empirical kernel map in the RKHS.

This study[28] improved the accurate target assignment of weapon target assignment problems in the air defence system by incorporating the improved artificial fish swarm optimizer(FSO). In this, individual visuals of artificial fish and genetic operations in particle swarm optimization (PSO) are incorporated to avoid local extremum traps.

This study[31] surveyed various data mining techniques,process and algorithms and the tools to implement the data mining algorithms.

This survey[32] analysied various Data Mining Techniques In Crop Diseases Identification and various types of crop diseases and prevention method for the diseases.

This study[33]reviewed SVM Algorithm for Crop Leaf Diseases Classification and its performance resulting better than other algorithms.

Finding a potential model to find crop disease is the major challenging factor in this field of research. This research considered above discusses research gaps to resolve the issues in the previous works. Hence the critical impartiality of this study is to improve plant disease prediction accuracy by determining the above problem definition.

III. Plant Leaf Disease Detection

This section discusses the functionalities of the proposed leaf disease detection methodologies in details. Figure 2 illustrates the various Stages of Plant leaf disease detection methodologies. It contains five stages.

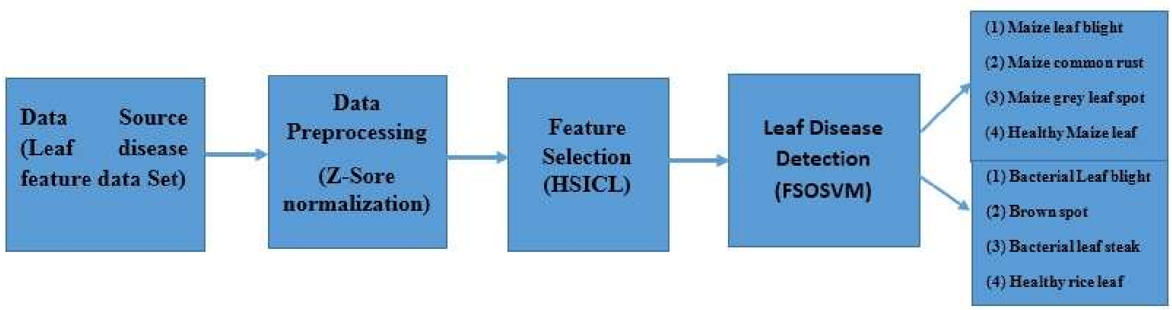


Figure 2: Stages of Plant leaf disease detection

A. Data source

The plant leaves disease detection system has been evaluated using the different agricultural Crop disease datasets. This study considers maize disease and rice leaf disease. It is utilized from kaggle.com data repository. This maize [29] and rice [30] leaf disease datasets are publicly available data source from the [29,30]. Table 1 contains the sample rice and maize crop leaf disease datasets. The performance evaluation uses some of the rice and maize leaf disease datasets for the following diseases, maize leaf blight(1046), maize common rust(1303), maize grey leaf spot (40), healthy maize leaf (1056), rice bacterial leaf blight (40), rice brown spot (40), the rice bacterial leaf steak (40), and rice leaf healthy (40).

Table 1: Sample leaf disease dataset for rice crop and maize

Paddy leaf disease dataset										
1	1.66E +04	6.96E +02	2.17E +00	1.82E +00	2.92E +01	1.45E +02	4.61E +02	9.58 E-01	4.24 E-01	7.84E +00
1	2.51E +04	7.33E +02	2.12E +00	1.23E +00	2.14E +01	1.79E +02	4.06E +02	9.67 E-01	4.86 E-01	8.37E +00
1	2.87E +04	7.41E +02	2.12E +00	1.08E +00	1.91E +01	1.91E +02	4.57E +02	9.62 E-01	3.84 E-01	8.90E +00
1	3.09E +04	7.94E +02	1.48E +00	1.43E +00	2.04E +01	1.98E +02	5.24E +02	9.57 E-01	4.78 E-01	8.15E +00
1	2.67E +04	7.41E +02	1.92E +00	1.27E +00	2.06E +01	1.84E +02	4.69E +02	9.62 E-01	4.70 E-01	7.99E +00
Maize leaf disease dataset										
1	7.10E +01	3.85E +01	1.88E +00	1.69E +00	2.09E +01	9.51E +00	5.19E +02	9.46 E-01	3.89 E-01	9.75E +00
1	6.50E +04	1.02E +03	1.00E +00	1.01E +00	1.60E +01	2.88E +02	6.81E +02	9.08 E-01	2.15 E-01	1.27E +01
1	5.49E +04	1.24E +03	1.00E +00	1.19E +00	2.78E +01	2.64E +02	5.90E +02	9.36 E-01	2.66 E-01	1.20E +01
1	4.86E +04	1.44E +03	1.00E +00	1.35E +00	4.28E +01	2.49E +02	1.01E +03	8.57 E-01	2.26 E-01	1.21E +01
1	3.68E +04	9.66E +02	1.00E +00	1.78E +00	2.54E +01	2.16E +02	4.32E +02	9.10 E-01	3.41 E-01	1.07E +01

The Maize dataset contains 160 data, and the rice data set comprises 3971 data. The two datasets are divided into training and testing samples in 75:25 ratios. Each record contains 10 features such as area, perimeter, aspectratio, rectangularity, circularity, equidiameter, contrast, correlation, inverse difference moments, and entropy. These feature are utilized to evaluate the performance of the proposed method.

B. Data Normalization

The Rice and Maize Crop disease-related feature values vary, such as high and low. The healthy leaf's feature value ranges completely differ from diseased leaf features. It may increase the burden of the classifier during the model training process. So, it is necessary to regularize the variations of the feature values. In this study, z-score normalization is utilized.

$$\left.\begin{aligned} Z_{score} &= \frac{a_i-\mu}{\sigma} \\ \sigma &= \sqrt{\frac{\sum(a_i-\mu)}{N}} \\ \mu &= \frac{\sum(a_i)}{N} \end{aligned}\right\} \quad (1)$$

In Eqn(1), the individual value of the feature, the mean of a feature vector, the total number of samples in a feature vector, and the standard deviation are denoted as a_i, μ, N and σ, respectively. The Eqn(1) normalizes the Crop disease-related input feature vector. It computes the input vector's mean and standard deviation to regularise the input feature vector's values. The normalized feature vector is utilized for dimensionality reduction.

C. Overfitting reduction

The Hilbert Schmidt Independence Criteria Lasso (HSICL) approach performs well on high and low-dimensional feature samples. So, the left disease classification framework utilizes the HSICL approach to select more significant features. The step-by-step flow of the HSICL-based feature optimization is given as follows,

$$HSICL: \min_{\alpha} \frac{1}{2} \sum_{NN,m=1}^{O} \alpha_{NN}\, \alpha_m HSICL(f_{NN}, f_m) - \sum_{NN=1}^{o} \alpha_{NN} HSIC\big(F_{NN,C}\big) + \lambda \|\alpha\|_1, \quad \alpha_1, \dots \dots, \alpha_n > 0 \quad (2)$$

$$HSICL: \min_{\alpha} \frac{1}{2} \left\| \bar{L} - \sum_{NN=1}^{O} \alpha_{NN}\ \bar{K}^{(NN)} \right\|_F^2 + \lambda \|\alpha\|_1, \alpha_1, \dots \dots, \alpha_n > 0 \quad (3)$$

Eqn(2) is framed and written as in eqn(3). It is used to compute the feature score for each feature. The computed importance score is utilized to select the top 5 significant feature subsets from Rice Paddy and maize leaf disease features. In this, $HSICL(f_{NN}, c) = tr(\bar{K}^{(NN)}\bar{L})$ is a kernel-based independence measure called the empirical HSICL. The $tr(.)$ method traces the observed HSICL values, and the notation λ is the regularization parameter. The $\overline{\mathrm{K}}^{(\mathrm{NN})} = \Gamma \mathrm{K}^{(\mathrm{NN})}\Gamma$ and $\bar{\mathrm{L}} = \Gamma \mathrm{L} \Gamma$ are input and output-centered Gram matrices of Rice Paddy and maize leaf disease-related features. $\mathrm{K}_{\mathrm{I,j}}^{(\mathrm{NN})} = K(u_{NN,i}, u_{NN,j})$ and $L_{i,j} = L(c_i, c_j)$ are Gram matrices, $K(u, u')$ and $L(c, c')$ are the two kernel functions. $\Gamma = \mathrm{I}_{\mathrm{o}} - \frac{1}{\mathrm{o}} 1_{\mathrm{o}} 1_{\mathrm{o}}^{\mathrm{T}}$ is the centering matrix, the 'I_{o}' is the o-dimensional identity matrix(number of leaf disease-related features). The 1_{o} is the m dimensional vector with all once, and $\|.\|_1$ is l_1-norm. The HSIC approach in the crop leaf disease detection system helps identify the minimal disease-defining features to train the SVM model. The HSICL is utilized in this study to reduce the over-fitting issue during the leaf disease classification. This study uses Gaussian Kernel, and the number of neighbours considered is 7. The total number of features used applied for the feature selection is 10 $(f_1, f_2, f_3, f_4, f_5, f_6, f_7, f_8, f_9, f_{10})$and the number of significant features selected by the HSICL is 7$(f_3, f_4, f_6, f_7, f_8, f_9, f_{10})$. The selected features are utilized for training the FSOSVM model.

D. FSOSVM classifier-based disease classification

i. Parameter fixing by Fish Swarm optimizer

The fish swarm optimizer(FSO) is utilized in this study to turn the parameters of the SVM kernel to improve the Crop (Rice and Maize) disease classification accuracy. It selects suitable parameter values while training the leaf disease features and tests. In this, the multi-objective behaviour of the fish swarm, such as random behaviour, target behaviour, teeming behaviour, and fish's following-based convergence, are utilized for parameters turning in SVM classification. The position of the input fish swarm is represented as Crop leaf (Rice and Maize) disease-related feature vector A,

$$A = (\alpha_{m1}, \alpha_{m2}, \alpha_{m3}, \ldots\ldots, \alpha_{mn}) \quad (4)$$

In Eqn(4), the A indicates the feature vector and the $\alpha_{m1}, \ldots\ldots, \alpha_{mn}$ are represents the different parameters of the Crop leaf (Rice and Maize) disease. The fitness function of the target (B) is denoted as A_m.

$$d_{mn} = \|a_n - a_m\| \quad (5)$$

In Eqn(5), the d_{mn} It computes distance among nth and mth parameter values. The target searching behaviour contains two conditions; in the first condition $if\ f(B_n) == f(A_m)$ then it is considered as convergence. So it takes value towards $A_m to\ A_n$, otherwise randomly choose the next state A_n.

$$\vec{A}_m = \begin{cases} if\ f(B_n) < f(A_m), & A_m + step\ a\frac{A_n - A_m}{d_{mn}} \\ else, & random\ search \end{cases} \quad (6)$$

Where $\vec{A}_m$ denotes the new state of the input parameter and the random interval value [0,1]. The Eqn(6) is used to perform convergence of input parameters based on the target behaviour of the fish swarm. In this phase, it takes fitness value for centroid (B_{cen}) of the target parameter or neighbour parameter value Nei_{iatr} And group factor of the target parameter value. Checking $if\ (\frac{f(B_{cen})}{Nei_{iatr}} < \partial a B_n)$ then it takes the centroid (cen) of parameter values; else, it remains in the target position value. The notation ∂ represents the group factor, and the range values assigned for the grouping factor belong to $\in (0,1)$. The fish selects the next position by their visual range. Likewise, the input parameter of the SVM classifier is updated in each iteration by choosing any of the local minima of a neighbour as a convergence value.

ii. Model training

The multiclass SVM classifier is suitable for mapping high-dimensional feature space. The classifier generates a line or hyperplane to separate different leaf disease classes. It optimizes different margins that are near together, which is referred to as a hyperplane or support vector. The classifier uses the 'one against all strategy' for multiclass problems. In this, each output is separated by estimating the posterior probability.

$$\hat{P}\left(\omega_j \middle| f_i(x)\right) = \frac{1}{1+\mathrm{ex}\ \left(\mathrm{A}_j f_j(x) + B_j\right)} \quad (7)$$

The sigmoidal function is represented in Eqn(7). It is used to estimate the probability between actual and predicted class objects. In this, the symbol ω_j Denotes the actual class of a feature and the $f_i(x)$ Denotes the predicted class of SVM classifier during the model training. The parameters A_j and B_j are estimated by minimizing the likelihood using the eqn(8).

$$-\sum_{k=1}^{n} t_k \log(p_k) + (1 + t_k)\log(1 - p_k) \quad (8)$$

In eqn(8), the p_k do the sigmoidal functions and the estimated probability t_k represent the target probability assigned.

This SVM model uses One for all approach based on the posterior probability. It estimated the probability separately for each class and computed the overall probabilities.

$$\widehat{P}\left(\omega_j \middle| (x)\right) = \frac{\exp\left(A_j f_j(x) + B_j\right)}{\sum_{j=1}^{c} \exp\left(A_j f_j(x) + B_j\right)} \quad (9)$$

In this study, multiple rice leaf and maize leaf diseases are used to train the SVM model. So, the multiclass softmax function represented in eqn(9) is used. The main steps of the classification approach are creating a feature vector and utilizing fixed parameters of sigmoidal and softmax functions. The Crop disease dataset contains multiclass, so it is essential to derive an unbiased dataset to train the SVM model. This study utilizes the random behaviour of Fish swarm optimization(FSO) to fix the parameters.

IV. Results and discussions

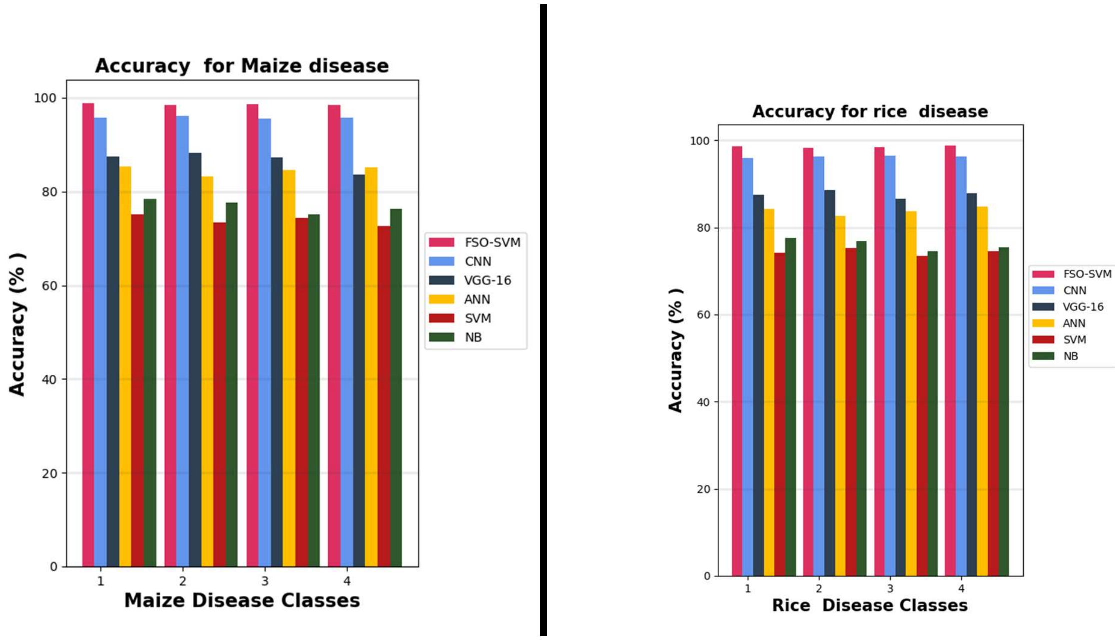
This section investigates the FSOSVM model's performance while classifying maize and rice leaf diseases. The model has been implemented in a python tensor-flow environment. It is an open-source library with many deep learning and machine learning packages. The parameters used by the FSOSVM model during the training and testing phase are dimensions (n_dim=2), population size (size_pop=100), maximum iteration (max_iter=100), Maximum try (max_try_num=100), Step (step=0.2), visual (visual = 0.1), the Kernal type (kernel =linear), degree (degree =3), and the q and delta value are q=0.98 and delta=0.3. Moreover, the system's excellence is determined by comparing the existing performance-wise best crop disease detection models using accuracy, recall, precision, and F-measure. SVM[24], ANN[24], Naïve Bayes[25], VGG-16[16], and CNN [17] models have been performing well in recent times for crop disease detection problems. Consequently, this study utilized these three models to compare the FSOSVM model's efficiency.

Table 2: Leaf disease detection performance of FSOSVM model

Maize leaf disease (classes)	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
Maize leaf blight (1)	98.9	97.5	98.7	98.7
Maize common rust (2)	98.5	99.1	98.3	97.2
Maize grey leaf spot (3)	98.6	97.4	94.2	95.3
Healthy (4)	98.4	98.3	99.1	98.1

Rice leaf disease (classes)	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
Bacterial Leaf blight (1)	98.7	98.4	98.5	98.5
Brown spot (2)	98.3	93.3	98.1	96.2
Bacterial leaf steak (3)	98.5	98.5	90.9	95.4
Healthy (4)	98.8	96.7	96.8	97.3

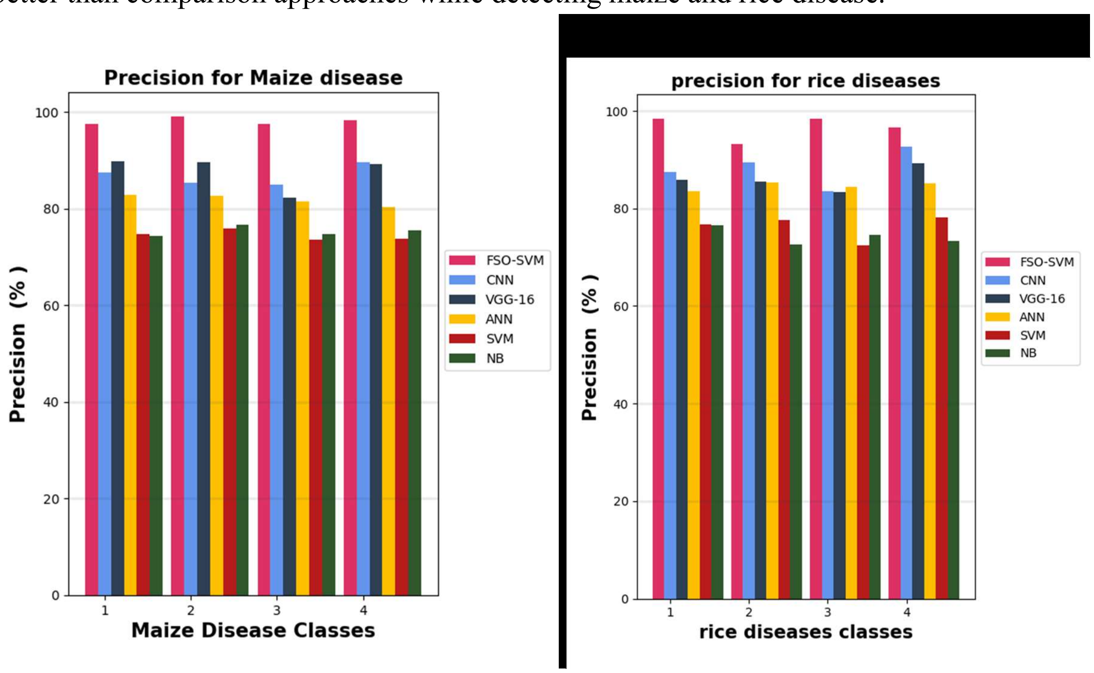
Table 2 contains the Leaf disease detection rate obtained by the FSOSVM model. The FSOSVM model got the maximum accuracy rate (98.8%) for healthy rice leaves and 98.9% obtained for maize Leaf blight disease.



a) ***b)***

Figure 3: Accuracy rate for maize and rice leaf disease detection

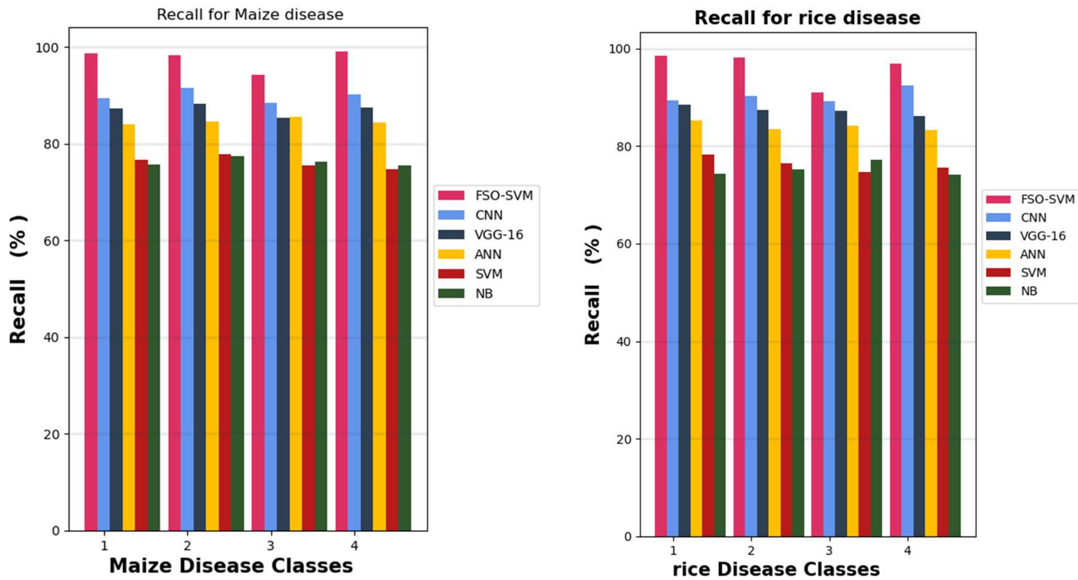
Figure 3 a) and b) shows the graphical representation of the accuracy rate obtained by FSOSVM, SVM, ANN, NB, VGG-16, and CNN models for detecting rice and maize crop leaf disease. It shows the FSOSVM model got a maximum accuracy rate of 98.8% for rice's healthy leaf and 98.9% for maize Leaf blight disease. It also depicts that the FSOSVM model performs better than comparison approaches while detecting maize and rice disease.



a) ***b)***

Figure 4: Precision rate for maize and rice leaf disease detection

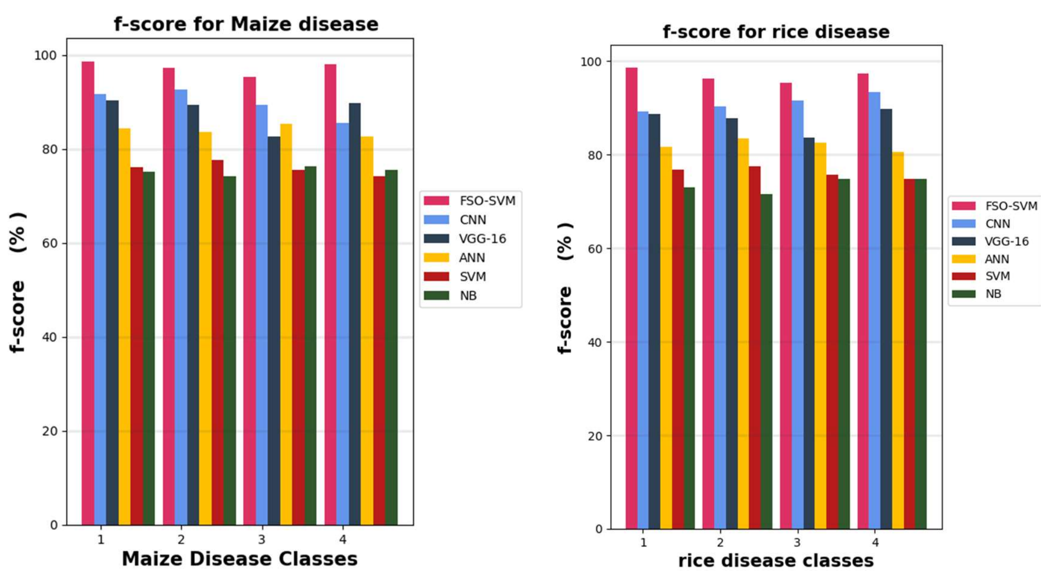
Figure 4 a) and b) shows the graphical representation of the Precision rate obtained by FSOSVM, SVM, ANN, NB, VGG-16, and CNN models for rice and maize leaf disease detection. The FSOSVM model got a maximum precision rate of 99.1% for Maize common rust and 98.5% for maize bacterial leaf steak disease.



a) ***b)***

Figure 5: Recall rate for maize and rice leaf disease detection

Figures 5 a) and b) show the graphical representation of the Recall rate obtained by FSOSVM, SVM, ANN, NB, VGG-16, and CNN models for detecting rice and maize crop leaf disease. The FSOSVM model got a maximum 98.5% accuracy rate for rice's bacterial leaf blight and brown spots. It obtained a 99.1% recall rate for healthy maize leaf detection.



a) ***b)***

Figure 6: F1-score rate for maize and rice leaf disease detection

Figures 6 a) and b) show the graphical representation of the F1-score rate obtained by FSOSVM, SVM, ANN, NB, VGG-16, and CNN models for detecting rice and maize crop leaf disease. The FSOSVM model got a maximum of 98.5% F1-score rate for raice leaf's bacterial leaf blight disease detection. It obtained a 98.7% f1-score rate for Maize leaf blight. Moreover, it also depicts that the FSOSVM model performs well than comparison approaches while detecting different maize and rice diseases.

The performance analysis discusses in this section shows that the Random behaviour of the FSO supports the SVM model in selecting suitable parameters for detecting four rice leaf diseases and four maize leaf diseases. Moreover, the HSICL approach helps the FSOSVM model to reduce the overfitting issues.

V. Conclusion

Thus, the results and analysis sections discuss the performance and efficiency of the FSOSVM on maize and rice leaf disease detection. The main impartial is to develop a model for plant leaf disease detection. It introduces a fish swarm-optimized Support Vector Machine(FSOSVM) model to improve the accuracy of plant leaf disease detection. Moreover, the study improved the performance of FSOSVM by reducing the overfitting issues with the help of HSIC. The resultant analysis of the previous section proves that the FSOSVM-based approach efficiently detects leaf disease than comparison approaches. It demonstrates that the Random behaviour of the FSO supports the SVM model in selecting suitable parameters for efficiently detecting four rice and four maize leaf diseases.The performance of the FSOSVM-based approach shows that the FSOSVM model performs well than present ML models. It has achieved a maximum of 98.3% and 98.9% accuracy rate in detecting rice and Maize leaf disease, respectively. So, the result concludes that the proposed FSOSVM method outperforms in detecting maize and rice leaf disease, and the research contribution successfully archives the research objective. Moreover, this study is limited to only two plant leaf diseases. So, future research is extended to develop a generalized machine-learning model for another leaf disease.

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