Rice Plant Disease Classification and Comparative Analysis of SVM Hyperparameters

Rajvir Kaur, Avtar Singh
Dr. B. R. Ambedkar National Institute of Technology, Jalandhar
Corresponding author: Avtar Singh , Email: avtars@nitj.ac.in

Rice plant diseases are among the most critical problems that are being faced by farmers. The diseases affect the quality and quantity of the crop, which impacts the economy of countries like India, where agriculture is the primary occupation. Therefore, early and accurate identification of plant disease is crucial to get the maximum yield from the crop. Traditionally, identifying plant diseases by observing or testing them in the laboratory is time-consuming. Many researchers have worked on image-based machine learning (ML) approaches for the detection and classification of plant diseases. This paper presented an ML-based Support Vector Machine (SVM) kernel technique for detecting diseases in rice plants. Classification is done using SVM with different hyperparameters (SVM kernels and regularization parameters) for the early and critical assessment of rice plants. This paper concludes that the SVM model trained with the optimized parameters obtained the highest accuracy of 0.996, which is better than the previous techniques and reveals the novelty of the work.

Keywords: Rice Plant Diseases, Classification, Machine Learning, SVM Hyperparameters.

2023. In Vikram Dhiman & Pooja Dhand (eds.), *Emerging Trends in Engineering and Management*, 13–25. Computing & Intelligent Systems, SCRS, India.
https://doi.org/10.56155/978-81-955020-3-5-03

1 Introduction

Rice plant disease detection and classification in the early stage is one the most important steps in the cultivation of rice crop. Rice plant infection leads to crop failure, and that directly affects the economy, and 60% of the Indian economy depends on the agriculture sector [19]. Therefore, precision in rice disease identification is essential in order to prevent crop damage. Plant diseases have traditionally been identified either visually or through pathogen identification in the laboratory. The visual observations of the lesion are a biased subject and have a high chance of unsuccessful or wrong diagnosis. On the contrary, if the identification of pathogens is made in the lab, it becomes a tedious process as the pathogen culturing is a time-consuming process that may fail to deliver the results in a timely manner [33]. Both these processes strictly need expert supervision. Due to these constraints, scientists have decided to look at methods for accurately and automatically diagnosing plant diseases [28]. It supports farmer in making informed decisions about which pesticides to use.

There are several diseases associated with rice plant such as Rice Blast (RB), Bacterial Leaf Blight (BLB), Leaf Smut (LS), Leaf Scald, Sheath Rot, Sheath Blight (SB), Leaf Blast (LB), Brown Spot (BS) etc., that affect the production quality [29]. To address the issues, this paper focuses on the images of four common diseases of rice plant such as BLB, LB, LS, and BS. Numerous methods such as AlexNet model [28], Inception network [19], etc., are presented in previous studies to detect objects and related features.

In recent studies, rice diseases detection and classification have become a major area to be researched [1-2][7][9][29]. In [1], 3 classes of rice plant diseases (BLB, BS, and LS) are classified. 8 different classes are considered in [7] and [9]. Nowadays, the most significant and in-demand approach is based on ML algorithms [1-2]. There are various ML techniques being utilized for this purpose including K-nearest neighbor (K-NN) [2], SVM classifier [1], etc. Many studies involve deep learning methods due to their significant performance, especially in classifying images. Deep learning methods reduce the complex process of feature extraction in a way that it employs a neural network—a computer system supposed to function similarly to the human brain—containing multiple layers, each of which can extract one or more distinct features from the image [34]. Processing is frequently distributed in order to perform analysis in a timely manner. These techniques have proved to provide high performance in many kinds of problems such as image segmentation [3], image recognition [4], and speech recognition [5].

Deep CNN is used more often out of various other deep learning techniques, especially for image classification [6-7]. CNN architecture gives a connection between spatial details and the image's layers, which makes it a convenient method for image classification [8]. Various studies have been done on the implementation of CNN for multiple tasks. In [7], 95.48% of classification accuracy has been reported to classify ten categories of rice plant diseases. Another study [9] used the deep CNN technique to de-noise images and further SVM classifier to classify rice diseases and classification accuracy of 87.50% has been reported. Researchers have used different techniques to classify different classes of rice plant diseases and achieved classification accuracies for each of the models.

In [28], rice field images are captured for disease symptoms in leaves and stems. 619 images of rice plant diseases are used in four categories (RB, BLB, SB, and Healthy Leaves). As a feature extractor, a pre-trained deep CNN, and as a classifier, SVM are used. The accuracy achieved by [28] is 0.913. In [1], centroid feeding-based K-means clustering is used to facilitate accurate feature extraction, for disease segmentation from a leaf image. After applying SVM on the dataset to classify three classes of rice diseases (BLB, LS, BS), an accuracy of 0.733 over test dataset has been achieved. [9] focuses on paddy crop diseases (blast, BS, BLB, SB, false smut, root knot nematode, and white tip nematode), in which, 50 denoised images are trained with the deep CNN and SVM classifiers, and their features are used for pattern matching; remained 200 images are used for testing. Model is compared to previous other approaches that combined k-means and fuzzy logic classifiers and KNN and SVM classifiers. It was discovered that the model achieved an improved accuracy of 0.875.

In [7], 10 different classes of rice plant diseases are considered. CNNs using a dataset of 500 images captured from a rice field are trained to identify 10 common rice diseases. The model achieved an accuracy of 0.954 using strategy of 10-fold cross-validation.

In [36], a system is developed to classify three classes of rice plant diseases including BS and LB. Bayes' and SVM Classifiers used the radial allocation of the shade from the center spot as features for classification to the boundary. The system is evaluated with 1000 images (test spot) of rice leaves diseases, yielding accuracies of 0.795 and 0.681 for Bayes' and SVM Classifier-based systems, respectively.

Although there exist other classifiers such as decision tree, Naïve Bayes, etc., SVM provides a good solution to classify problems that have achieved great attention and proven to provide results while working with data with high dimensionality attributes [10]. The performance of SVM relies majorly on kernel selection and its parameters which has a direct effect on the ML performance [11]. Since there are various parameters [12, 13], regularization parameter (*i.e., C*) is the most crucial parameter that has a significant impact on classification performance [14]. *C* is used to find a balance between minimizing errors and increasing classification margin [15]. Support vectors count, testing errors, training errors, and even the value of *C* can be changed to control SVM margin [16]. The manual optimization process will be time-consuming. In order to obtain optimal results, parameters are tuned using different techniques of parameter optimization such as Grid Search [17], and Genetic algorithm [17]. In this paper, feature extraction has been done using Inception v3 architecture [18] which is deep Convolutional neural network (CNN) model [19]. This technique helps the model to demonstrate the difference between all of the characteristics of images for further understanding and interpretation [20]. Also, a Grid search with cross-validation has been used to adjust the parameters of SVM. This research proposed a classification system in which the model classifies the disease from the image of rice plants.

The objective of this paper is to address the data classification problem using an SVM classifier to achieve high accuracy. For this purpose, the SVM classifier is used with the optimized hyperparameters. The considered hyperparameters include kernels such as linear, polynomial, Radial Basis Function (RBF), sigmoid, and the regularization parameter (*C*). Degree for polynomial kernel function is also considered. The proposed model satisfies all the conditions of the global requirement to provide the most accurate system to predict different kinds of rice plant diseases.

The contribution of this paper includes the use of recently popular and successful methodologies such as Inception v3, Grid Search, and SVM kernels to provide the optimal solution for agriculture problems. The experimental assessment shows that the linear and the polynomial kernel function are identified as the absolute methods.

The remainder of this paper is divided into the following sections. Methods are discussed in Section 2. Results are described in Section 3. Section 4 includes the discussion and future directions to expand this research.

2 Methods

This work is implemented using Python 3.9.7 with libraries Pandas 1.3.4, Numpy 1.20.3, Sklearn (SciKit-Learn) 1.0.2, and Seaborn 0.11.2. The first step includes the data collection process, and rest of the steps include classification phase with result analysis.

2.1 Dataset

This study employs a rice plant classification dataset provided by UCI and available with Kaggle [21-22]. There are around 899 images of rice plant leaves in these collections. Images of diseased rice plant leaves are included. There are 40 images of BLB (**Figure 1**), 40 images of LS (**Figure 2**), 40 images of BS (**Figure 3**), and 779 images of LB (**Figure 4**) in this dataset (**Table 1**).

Table 1. Distribution detail of samples from datasets

Dataset	Number of samples taken	Diseases
Dataset 1	120	BLB (40 images) BS (40 images) LS (40 images)
Dataset 2	799	LB (799 images)

Fig. 1: BLB

Fig. 2. LS

Fig. 3: BS

Fig. 4: LB

2.2 Inception v3 based Feature Extraction

The Inception v3 architecture [18] is employed in this paper for feature extraction. Google developed Inception in collaboration with various other researchers. Convolutions, max pooling, concats, dropouts, fully connected layers, and average pooling are the building components of Inception v3 and hence, make it a 48 layers deep network [35]. Each image is thoroughly processed at different layers of the architecture [32]. Feature extraction aids the model in distinguishing between all of the features of images and comprehending them for subsequent interpretation. For each image, Inception v3 is used to compute a feature vector. It releases an improved data table with more columns called as image descriptors. Inception v3 here takes four categories of images as input and as output, is providing numeric data in the form of feature vector. These feature vectors are recorded as a csv file and then passed to SVM, which classifies our data of four different categories of diseases based on pre-trained knowledge. A total of 2054 features are extracted from each of the images. They are category names, image name, size of the image resolutions that is width and height of the image.

After the numeric data is collected, the next step involves data pre-processing. For the purpose of preparing and transforming the collected data into a suitable form, the data pre-processing technique is used. It plays an important role while building an ML model. This process involves three stages: a) removing irrelevant data values, b) dividing data into attributes and labels, and c) splitting the data into training and testing sets. Model selection package of SK-learn python library has been used for splitting purpose. Training-testing partition of (70-30) % has been taken for analysis. The training and testing datasets are prepared by random selection (**Table 2**).

2.3 Support Vector Machine classifier

The classifier SVM is a frequently used ML algorithm for classification and prediction. SVM is a data separation method that moves data from one-dimensionality to a high-dimensionality environment using a hyperplane. If the data points in the input area are not linearly differentiable, the SVM translates the data to the high-dimensional space using nonlinear transformation. SVM is a kind of supervised learning strategy used for data categorization and regression problems. Every sample in a set of training data with two distinct classes is identified and labeled as belonging to one of the classes. The sample data is mapped into hyperspace by SVM, which clearly divides the data into two categories.
Support vectors are a subgroup of the training set that helps to determine the decision boundary. The optimum separation of the hyperplane is obtained using support vectors, which may separate the points without errors while simultaneously increasing the distance between the closest point and the hyperplane.

Kernel functions are also used in the SVM to generate nonlinear classifiers that are effective [27]. Four SVM kernel functions that are used to obtain the best model includes which are given in equations below:

- Linear:

$$Q(r_1, r_2) = r_1 \cdot r_2 \qquad (1)$$

- Polynomial:

$$Q(r_1, r_2) = (r_1 \cdot r_2 + 1)D \qquad (2)$$

- RBF:

$$Q(r_i, r_j) = exp\left(-\gamma \|r_i - r_j\|^2\right) \qquad (3)$$

- Sigmoid:

$$Q(r, s) = tanh(\alpha r^T s + u) \qquad (4)$$

where α, γ, D, u are kernel parameters and r_1, r_2, r, s, r_i, r_j are vectors.
Another hyperparameter which is taken in this paper is regularization parameter (C). In typical SVM, C is used as the penalty parameter of the error term to limit the tolerance of systematic outliers. A higher C value allows for fewer outliers in the opponent classification.

2.4 Hyperparameter tuning using Grid Search

The performance of any model is greatly influenced by hyperparameter values. To find the most suitable values for a model, Grid Search is used. It is a function that performs hyperparameter tuning and gives optimal values for a particular model. Grid Search comes in handy as it automates the hyperparameter tuning process and reduces the time complexity as trying out all possible values for hyperparameters manually to know the best ones would rather take a large amount of time as well as resources.

GridSearchCV function is in model selection package of SK-learn (or Scikit-learn) library. This function loops through predefined hyperparameters to provide help to the model (estimator) to get fit to the training set, and finally, the best hyperparameters are selected out of listed ones.

As stated above, a list of predetermined hyperparameter values is used, which is passed to the GridSearchCV function. This is accomplished by establishing a dictionary and populating it with all possible hyperparameter values. The hyperparameters of the SVM model are considered in this paper includes C, kernels and degree (polynomial kernel function).

Grid Search evaluates the model using the Cross-Validation method for each possible combination of the dictionary values. As an outcome of utilizing this function, the accuracy for each combination of hyperparameters can be retrieved, and the optimal one can be chosen.

To come up with the finest possible combination parameter using the grid search method, it is believed that the parameter range is to be taken as wider as possible. Therefore, the experiment was carried out for four kernels named linear, RBF, polynomial, and sigmoid, where the range of C is taken from 0.001 to 10,000. The experiment includes range of degree from 1 to 5 for polynomial kernel while for gamma default value is considered. The strategy of 5-fold cross-validation has been conducted. The SVM algorithm uses the kernel trick to transform the data points and construct a suitable decision boundary. Kernels make it easier to deal with data of high dimensions in a very efficient manner.

Grid Search will provide the best estimator (model) out of all provided hyperparameters. Based on the best values of GridSearchCV, the accuracy of each SVM kernel function has been evaluated. Support Vector Classifier (SVC) is imported from the sklearn python library. The classification process is divided into two steps for each of the kernel functions and the C value set: (1) fit the classifier to the training set and (2) make predictions on the test set. To analyse the effect of different SVM kernels, the training-testing set is sent to each of the kernel functions along with the optimal value of C. Further, the accuracy for each model with C value (including degree value for polynomial kernel) is calculated (**Figure 5**).

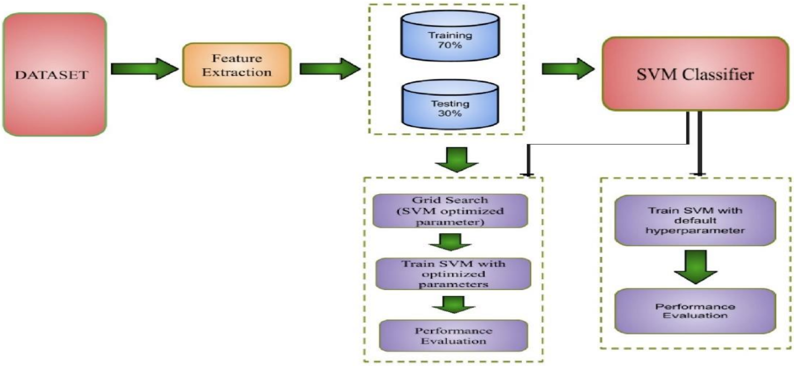


Fig. 5: Architecture explaining the working of the classification model

2.5 Performance Evaluation Metrics

Five evaluation metrics that are used in this paper are as follows:

- Accuracy ($A1$)- It is used for the representation of the correctly classified data instances out of the number of data instances in total.

$$A1 = \frac{True\ Positive + True\ Negative}{True\ Positive + True\ Negative + False\ Positive + False\ Negative}$$

(5)

- Precision ($P1$)- It states the percentage of all positive predictions that are genuinely positive out of all positive predictions.

$$P1 = \frac{True\ Positive}{True\ Positive + False\ Positive}$$

(6)

- Recall ($R1$)- It represents the percentage of predicted positives out of total positives.

$$R1 = \frac{True\ Positive}{True\ Positive + False\ Negative}$$

(7)

- F1-score ($F1$)- It is signifying the harmonic mean of both recall and precision.

$$F1 = \frac{2}{\frac{1}{P1} + \frac{1}{R1}} = \frac{2 * (P1 * R1)}{(P1 + R1)}$$

(8)

- Confusion Matrix – It is mainly a table that represents the classifier's performance. (**Fig. 6**).

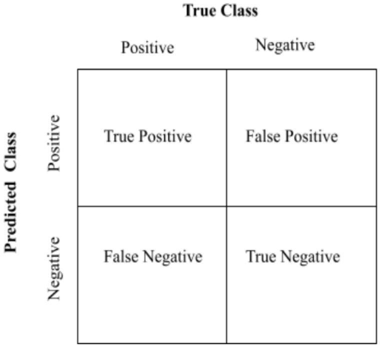


Fig. 6: Confusion Matrix.

3 Results

In this research, the SVM is used for classification, which is applied to train the model to detect the presence of different sorts of diseases in the images after extracting features from inception v3. The dataset includes training and testing sets prepared by the random selection (**Table 2**)

Table 2. Data Distribution

Total number of feature vectors extracted from each image	Number of feature vectors after pre-processing	Total Number of samples	Training set (Class, instances)	Testing set (Class, instances)
2054	2048	899	(629, 2048)	(270,2048)

3.1 SVM classification using default hyperparameters

In the first scenario, the implementation of SVM with default hyperparameters is done. Default hyperparameters mean where the kernel function by default is RBF, the value of C is 1.0 and default value for degree for polynomial kernel function is 3. As mentioned, the dataset is divided into training and testing data with (70-30) % split, and then using accuracy, precision, recall, and F1-score, model performance is evaluated. The obtained experimental results include testing accuracy of 0.988, precision is 0.985, recall as 0.988 and F1-score as 0.988 (**Table 3).**

Table 3. Results using default hyperparameters for (70-30) %

Performance metrics	Result
Accuracy	0.988
Precision	0.985
Recall	0.988
F1-score	0.988

3.2 SVM and Grid Search classification Results

In the second scenario, the combination of Grid Search with SVM kernel functions is applied. Here, Grid Search is implemented on the training set to obtain the optimal parameter *C* out of the passed list of values. The optimized value for *C* is 10 when applied to the training-testing set. This means that if the value of *C* is decreased or increased from 10 to any other value from the provided list of possible values, it will not be an optimized result. The optimized value of degree for polynomial kernel is obtained as 1. These values are further used to create a model which is to be implemented in the testing phase. The results obtained show that linear and polynomial kernels performed better as compared to other kernels. The investigated results show that linear and polynomial kernels obtained 0.996 testing accuracy, which achieves the highest values among others. Precision, recall and F1- score for both kernels are measured as 0.997, 0.996 and 0.996 respectively. Other kernel functions' performance is depicted in (**Table 4**).

SVM kernel Function at C=10	Accuracy	Precision	Recall	F1-score
Linear kernel	**0.996**	**0.997**	**0.996**	**0.996**
RBF kernel	0.992	0.993	0.993	0.992
Polynomial kernel	**0.996**	**0.997**	**0.996**	**0.996**
Sigmoid kernel	0.977	0.979	0.978	0.978

Table 4. Accuracy metric value at (70-30) %

The difference between the results obtained by the model with default hyperparameters and the models with optimized hyperparameters depicts that the optimized model executes better than the other one. (**Table 5**).

Table 5. Comparison of both the models

SVM with default hyperparameters	SVM with optimized hyperparameters	Improvement
0.988	**0.996**	**0.008**
0.985	**0.997**	**0.012**
0.988	**0.996**	**0.008**
0.988	**0.996**	**0.008**

Confusion matrices for all set of models achieved are shown in (**Fig 7-11**) and these confusion matrices are based on testing data. The whole test set contains different proportion of instances (**Table 6).**

Table 6. Instance Distribution for test set

Disease	Distribution among test set
BLB	14
BS	14
LS	7
LB	235
Total instances	**270**

Fig. 7 shows that for the SVM model with default hyperparameters, LB and BS diseases have not been misclassified with any other disease. On the other hand, BLB and LS are misclassified by 1 and 2 values of other diseases respectively.

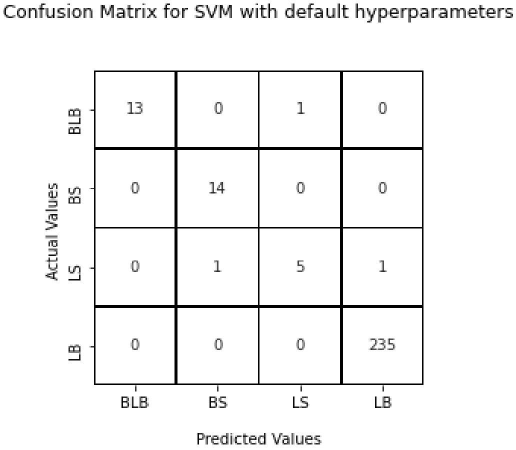
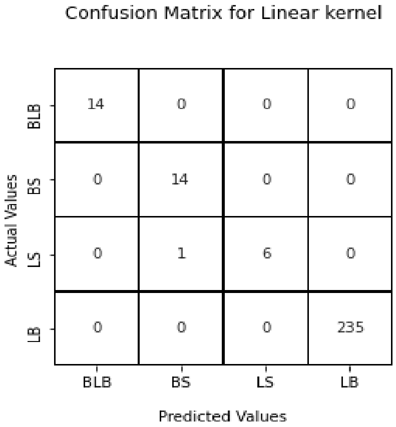


Fig 7: SVM model with default hyperparameters

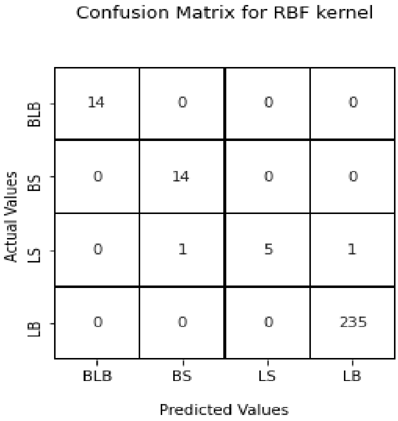
Similarly, for the models with linear kernel (**Fig. 8)** and polynomial kernel (**Fig. 10**), BLB, BS and LB are classified accurately whereas one instance of LS is misclassified as BS. For RBF -based model, three diseases named BLB, BS and LB are not misclassified with others but one of the instances of LS is misclassified as BS and one is misclassified as LB (**Fig. 9**). The confusion matrix shows that the model with sigmoid kernel, only BLB is the disease which is classified correctly while one instance of BS is misclassified with BLB and two more instances are misclassified as LS. Also, LS is misclassified as BS for once and two of the instances of LB are misclassified-one as BLB and other as BS (**Fig. 11**).



Confusion Matrix for Linear kernel

Actual Values \ Predicted Values	BLB	BS	LS	LB
BLB	14	0	0	0
BS	0	14	0	0
LS	0	1	6	0
LB	0	0	0	235

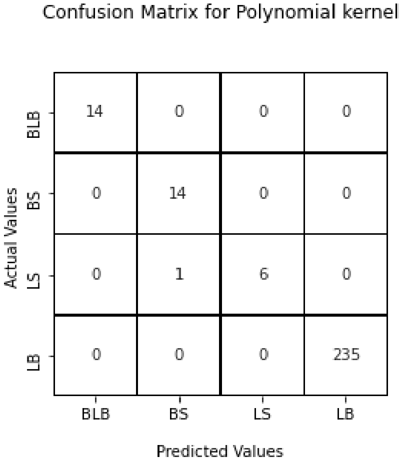
Fig. 8: SVM model with linear kernel.



Confusion Matrix for RBF kernel

Actual Values \ Predicted Values	BLB	BS	LS	LB
BLB	14	0	0	0
BS	0	14	0	0
LS	0	1	5	1
LB	0	0	0	235

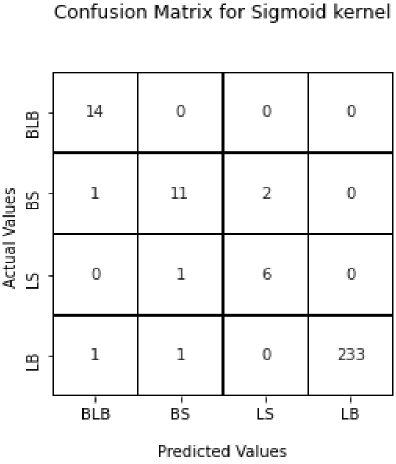
Fig. 9: SVM model with RBF kernel.



Confusion Matrix for Polynomial kernel

Actual Values \ Predicted Values	BLB	BS	LS	LB
BLB	14	0	0	0
BS	0	14	0	0
LS	0	1	6	0
LB	0	0	0	235

Fig. 10: SVM model with polynomial kernel.



Confusion Matrix for Sigmoid kernel

Actual Values \ Predicted Values	BLB	BS	LS	LB
BLB	14	0	0	0
BS	1	11	2	0
LS	0	1	6	0
LB	1	1	0	233

Fig. 11: SVM model with sigmoid kernel.

After comparing results in both cases, it is found that a combination of SVM with Grid Search can be helpful in providing an improved and accurate model**.** The findings show that all SVM models with optimized hyperparameters performed better than the SVM model with default hyperparameters.(Fig.12)

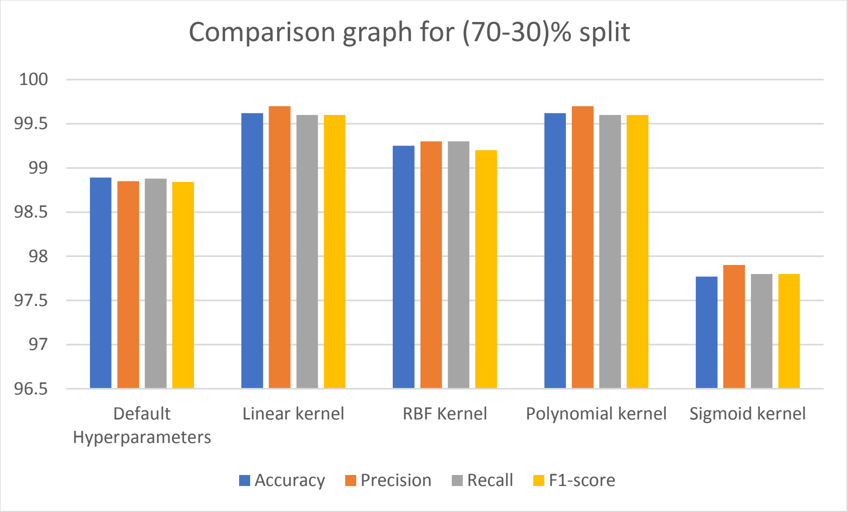


Fig. 12: Comparison graph between classification done by default hyperparameters and kernels with optimized parameters.

Table 7. Comparison between different models and average improvement.

Model	Accuracy Obtained	Difference between proposed model
[28]	0.913	0.083
[30]	0.994	0.002
[1]	0.733	0.263
[9]	0.875	0.121
[7]	0.971	0.025
[36]	0.795	0.201
Average Improvement from other models		11.58%

The paper concludes that the fusion of Inception v3, Grid Search, and SVM classifier with hyperparameters has obtained an average improvement of 11.86%, which is a significant enhancement and, therefore, reveals the novelty of the work (**Table 7).**

4 Discussion

Rice disease requires the use of proper techniques in order to produce a higher-quality crop. ML and deep learning can help a lot of researchers in this direction. In this paper, an overview of SVM with default hyperparameters and its different kernel methods with optimized parameters have been implemented and compared. The findings show that the SVM classifier works effectively using the default hyperparameters, but the combination of SVM kernels and tuned parameters improves model performance. Optimizing SVM parameters with the help of Grid Search is a powerful function to obtain significant accuracy. The experimental results show that the linear kernel and polynomial kernel function (with optimized value of degree), along with the optimized value of *C*-parameter of the SVM classifier, perform better than the models such as SVM with default hyperparameters, RBF, and sigmoid kernel functions. In the future, the number of images and categories of rice plant diseases can be further increased. Also, more research is needed to explore the model's utility in real-world situations.

References

[1] Prajapati, H., Shah, J. and Dabhi, V. (2017). Detection and classification of rice plant diseases. Intelligent Decision Technologies, 11(3):357-373.

[2] Suresha, M., Shreekanth, K. and Thirumalesh, B. (2017). Recognition of diseases in paddy leaves using knn classifier. 2017 2nd International Conference for Convergence in Technology (I2CT).

[3] Shelhamer, E., Long, J. and Darrell, T. (2017). Fully Convolutional Networks for Semantic Segmentation. IEEE Transactions on Pattern Analysis and Machine Intelligence, 39(4):640-651.

[4] Litjens, G., Kooi, T., Bejnordi, B., Setio, A., Ciompi, F., Ghafoorian, M., van der Laak, J., van Ginneken, B. and Sánchez, C. (2017). A survey on deep learning in medical image analysis. Medical Image Analysis, 42:60-88.

[5] Abdel-Hamid, O., Mohamed, A., Jiang, H., Deng, L., Penn, G. and Yu, D. (2014). Convolutional Neural Networks for Speech Recognition. IEEE/ACM Transactions on Audio, Speech, and Language Processing, 22(10):1533-1545.

[6] Krizhevsky, A., Sutskever, I. and Hinton, G. (2017). ImageNet classification with deep convolutional neural networks. Communications of the ACM, 60(6):84-90.

[7] Lu, Y., Yi, S., Zeng, N., Liu, Y. and Zhang, Y. (2017). Identification of rice diseases using deep convolutional neural networks. Neurocomputing, 267:378-384.

[8] Arel, I., Rose, D. and Karnowski, T. (2010). Deep Machine Learning - A New Frontier in Artificial Intelligence Research [Research Frontier]. IEEE Computational Intelligence Magazine, 5(4):13-18.

[9] Rajmohan, R., Pajany, M., Rajesh, R., Raman, D.R., & Prabu, U. (2018). Smart paddy crop disease identification and management using deep convolution neural network and SVM classifier. International Journal of Pure and Applied Mathematics,118(15):255-264.

[10] Ding, S. and Chen, L. (2010). Intelligent Optimization Methods for High-Dimensional Data Classification for Support Vector Machines. Intelligent Information Management, 02(06):354-364.

[11] Sudheer, C., Maheswaran, R., Panigrahi, B. and Mathur, S. (2013). A hybrid SVM-PSO model for forecasting monthly streamflow. Neural Computing and Applications, 24(6):1381-1389.

[12] Friedrichs, F. and Igel, C. (2005). Evolutionary tuning of multiple SVM parameters. Neurocomputing, 64:107-117.

[13] Rossi, A. and Carvalho, A. (2008). Bio-inspired Optimization Techniques for SVM Parameter Tuning. 2008 10th Brazilian Symposium on Neural Networks.

[14] Srivastava, K. and Bhambhu, L. (2009). Data classification using Support vector Machine (SVM), a simplified approach. J of Theo. & Appl. Inf. Tech., vol 1, no. 5, pp. 1–7. 2009.

[15] Tharwat, A. (2019). Parameter investigation of support vector machine classifier with kernel functions. Knowledge and Information Systems, 61(3):1269-1302.

[16] Amari, S. and Wu, S. (1999). Improving support vector machine classifiers by modifying kernel functions. Neural Networks, 12(6):783-789.

[17] Syarif, I., Prugel-Bennett, A. and Wills, G. (2016). SVM Parameter Optimization using Grid Search and Genetic Algorithm to Improve Classification Performance. TELKOMNIKA (Telecommunication Computing Electronics and Control), 14(4):1502.

[18] Xiaoling Xia, Cui Xu and Bing Nan (2017). Inception-v3 for flower classification. 2017 2nd International Conference on Image, Vision and Computing (ICIVC).

[19] Gunjan Chugh, Aman Sharma, Prakash Choudhary, and Rushali Khanna (2020). Potato leaf disease detection using Inception v3. International Research Journal of Engineering and Technology (IRJET) e-ISSN: 2395-0056 Volume: 07 Issue: 11.

[20] Lee, S., Chan, C., Mayo, S. and Remagnino, P. (2017). How deep learning extracts and learns leaf features for plant classification. Pattern Recognition, 71:1-13.

[21] Kaggle.com (2022). Rice Leafs. [online] Available at: <https://www.kaggle.com/shayanriyaz/riceleafs>

[22] Archive.ics.uci.edu. (2022). Index of /ml/machine-learning-databases/00486. [online] Available at: <https://archive.ics.uci.edu/ml/machine-learning-databases/00486/>

[23] Bzdok, D., Altman, N. and Krzywinski, M. (2018). Statistics versus machine learning. Nature Methods, 15(4):233-234.

[24] Cerrolaza, J., Picazo, M., Humbert, L., Sato, Y., Rueckert, D., Ballester, M. and Linguraru, M. (2019). Computational anatomy for multi-organ analysis in medical imaging: A review. Medical Image Analysis, 56:44-67.

[25] Haniff, N., Abdul Karim, M., Osman, N., Saripan, M., Che Isa, I. and Ibahim, M. (2021). Stability and Reproducibility of Radiomic Features Based Various Segmentation Technique on MR Images of Hepatocellular Carcinoma (HCC). Diagnostics, 11(9):1573.

[26] Umadevi, S. and Marseline, K. (2017). A survey on data mining classification algorithms. 2017 International Conference on Signal Processing and Communication (ICSPC).

[27] Mahlein, A., Rumpf, T., Welke, P., Dehne, H., Plümer, L., Steiner, U. and Oerke, E. (2013). Development of spectral indices for detecting and identifying plant diseases. Remote Sensing of Environment, 128:21-30.

[28] Shrivastava, V., Pradhan, M., Minz, S. and Thakur, M. (2019). Rice plant disease classification using transfer learning of deep convolution neural network. ISPRS - International Archives of the Photogrammetry, Remote Sensing and Spatial Information Sciences, XLII-3/W6:631-635.

[29] Agrawal, M.M. and Agrawal, D.S. (2020). Rice plant diseases detection & classification using deep learning models: a systematic review. J. Crit. Rev, *7*(11):4376-4390.

[30] Dhar, P., Rahman, M. and Abedin, Z. (2022). Classification of Leaf Disease Using Global and local Features. International Journal of Information Technology and Computer Science, 14(1):43-57.

[31] Vanitha, V. (2019). Rice disease detection using deep learning. Int. J. Recent Technol. Eng. (IJRTE), 7, 534-542.

[32] Google Cloud (2022). Advanced Guide to Inception v3 | Cloud TPU | Google Cloud. [online] Available at: <https://cloud.google.com/tpu/docs/inception-v3-advanced>

[33] Plant Disease Diagnosis (2022). Plant Disease Diagnosis. [online] Available at: www.apsnet.org/edcenter/disimpactmngmnt/casestudies/Pages/PlantDiseaseDiagnosis.

[34] Doc.arcgis.com (2022). Using deep learning for feature extraction and classification—Imagery Workflows | Documentation. [online] Available at: <https://doc.arcgis.com/en/imagery/workflows/resources/using-deep-learning-for-feature-extraction.htm>

[35] Patil, A.B., Sharma, L., Aochar, N., Gaidhane, R., Sawarkar, V., Fulzele, P. and Mishra, G. (2020). A literature review on detection of plant diseases. European Journal of Molecular & Clinical Medicine, 7(07):2020.

[36] Phadikar, S. (2012). Classification of Rice Leaf Diseases Based on Morphological Changes. International Journal of Information and Electronics Engineering.