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AI-Powered Image Recognition To Detect And Combat Rice Leaf Diseases

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A supervised machine-learning approach to classifying rice diseases based on their images. The dataset includes fourteen classes of rice sicknesses produced by fungal, bacteria, nematdos viruses and parasitic weeds, abiotic stresses, physiological disorders, bacterial stalk tot, false smut, rice blast complex, hispa, healthy, bacterial panicle blight, brown spot. Using support vector machines as classification algorithms to classify rice diseases and the dataset was split into test and training sets with the ratio 90:10. Applying model instruction, we achieved an accuracy of 95.63%. The confusion matrix obtained from the test dataset shows and my model performed well in classifying different healthy and diseases plants categories. However, the model struggled to distinguish between Hispa and brown spot diseases. The overall results show the potential to leverage machine learning for effective and accurate classification of rice diseases.

Index Terms—Irld, Svm, Pcr, Lamp, Hog, Hispa.

I. INTRODUCTION

Rice is a basic food consumed by around 50% of people worldwide., making it a crucial component of global food security. However, rice crops are vulnerable to different illnesses brought on by bacteria, viruses, fungi, and other pathogens. These diseases can cause significant crop damage and result in food shortages, which can have a severe impact on the affected communities [1].

Traditionally, disease diagnosis involves visual inspection by experts, which is time-consuming, and subjective. The process is also prone to errors, and early detection is challenging, resulting in the spread of diseases to neighbouring crops [2]. Moreover, there is a shortage of experts who can identify these diseases, particularly in rural areas where most rice crops are grown.

The application of machine learning algorithms provides a promising solution for automated and objective Rice disease classification using image analysis. Machine learning models Accurately classifies diseases using sensory data including color, texture, and shape, draw from huge amounts of classified photos [3].

In this paper, the authors propose a Fourteen types of rice diseases are classified like Fungle, Bacterial, Viral, Nematode Diseases, Parasitic Weeds, Abiotic Stresses, Physiological

Disorders, Bacterial Stalk Rot, False Smut, Rice Blast Complex, Hispa, Healthy, Bacterial Panicle Blight, Brown Spot are classified with the assistance of supervised machine learning technique [4][5]. Their method of classifying the diseases based on photographs was the Support Vector Machine algorithm.

Modern classification algorithms which is used the SVMs procedure operates by identifying the best hyperplane to divide the dataset's classes [6]. The algorithm can handle high-dimensional data and is robust to noise and outliers. The authors trained the SVM algorithm on a dataset of labeled images of the fourteen rice diseases and achieved high classification accuracy [8].

There are various benefits that the suggested machine learning method provides over the conventional methods of disease diagnosis. It is automated, objective, and can accurately classify diseases in real time [9]. The approach can also be used to detect diseases early, preventing their spread to neighboring crops and minimizing crop damage.

Traditional methods need specialists to diagnose the illnesses, and because farmers work in an inner region, it can be challenging for them to come in touch with specialists [10]. Due to these problems, researchers are now exploring different algorithms and creating automated techniques to identify and categorize diseases affecting rice plants while also encouraging farmers to select the appropriate medicines [11]1.

For efficient disease control and to minimize crop losses, rice plant disease detection is critical. Rice illnesses are found using a variety of techniques, from visual inspection to cutting edge technology [12]. Here are a few typical techniques for detection:

A. Visual inspection.

Visual cues are frequently used by farmers and agricultural workers to recognize disease indicators including discolored leaves, lesions, wilting, or irregular growth patterns. Identification predicated on symptoms:

Manual diagnosis is feasible in the field because of the skills of trained researchers and agronomists who can recognize certain signs linked to different rice illnesses.

B. Molecular Methods:

Polymerase chain reaction (PCR) Pathogens that cause diseases in rice can be identified by unique DNA sequences that can be found using molecular biology techniques like PCR [13]. High sensitivity and specificity are offered by this technique.

Rapid and inexpensive pathogen identification is made possible by Loop-mediated isothermal amplification (LAMP) is the term for the isothermal nucleic acid amplification method [14][15].

C. Immunological techniques:

Enzyme-linked immunosorbent test (ELISA) This method provides a quantitative assessment of infection by using antibodies to identify antigens linked to rice pathogens [16].

D. Immunochromatographic assays

Quick and convenient field assays that employ antibodies to find certain infections [17].

E. Remote Sensing:

Satellite imaging: In vast agricultural fields, remote sensing technology, such as satellite or drone imaging, can be used to track indicators of stress, such as alterations in plant color or growth patterns [18].

F. Hyperspectral imaging:
This method looks for distinct spectral signatures connected to disease by examining the reflectance spectrum of plants [19].
G. Technologies Based on Sensors:

Electronic nose (e-nose) This non-invasive, quick diagnostic method looks for volatile organic chemicals released by diseased plants [20].

H. Fluorescence imaging:
This technique detects diseased areas by using the fluorescence that plants release when a pathogen is present.

I. Mobile App:
Numerous mobile applications examine photos of rice plants and diagnose possible diseases based on visual signs by using image recognition algorithms.

J. Sensors Based on DNA:
To detect specific diseases on-site, emerging technologies employ DNA-based sensors that can be integrated into portable devices.

K. Nanotechnology:
Researchers are looking into the potential of nanomaterials and nanoparticles to create sensitive and quick methods of detecting rice illness.

L. Intelligent artificial systems (AI):
Large datasets, such as pictures and sensor data, can be analyzed by machine learning algorithms to find patterns linked to certain illnesses in rice fields [22][23].

Fig. 1 (a) & (b). Sample photos from the dataset on rice blast illness are shown in (a) for positive samples and (b) for those that are negative.

II. MATERIALS AND METHODS

A. Dataset Preparation

A freely accessible dataset of images of rice plants, including fourteen distinct kinds of rice diseases, including the Fungal, Bacterial, Nematode, Viral, Diseases, Parasitic Weeds, Abiotic Stresses, Physiological Disorders, Bacterial Stalk Rot, False Smut, Rice Blast Complex, Hispa, Healthy, Bacterial Panicle Blight, Brown Spot. The dataset included 400 images for each class, totaling 1600 images. We ensured the quality of the dataset by removing any low-quality or duplicate images. Image preprocessing.

B. Feature Extraction

We performed edge detection in conjunction with the purpose of histogram of oriented gradients like HOG is to extract pertinent characteristics from different kind of image dataset. To identify the plant leaves' edges in the pictures, we employed the Canny edge detection formula. Once the edge maps were created, the HOG function was applied to determine the gradient orientation in various image regions and produce a histogram of gradient directions [24][25][26]. Plant disease categorization is a good application for this technology because it can capture the texture and shape of items in images.

C. Simulation

We implemented a supervised learning approach to train the model. We used effective machine learning methods for categorization issues SVMs, or support vector machines method. Model training involved feeding the SVM algorithm [4][5]with the HOG features that were taken out of the edge maps [27][28].

We used a cross-validation technique to optimize the hyperparameters of the SVM algorithm, ensuring high classification accuracy [29][33].

D. Model Estimation

Several evaluation indicators, including the Matrix of Model Evaluation.

Accuracy rate: The entire accuracy of the model's estimations.

Precision: This techniques for metric derived from the proportion of accurate affirmative forecasts to all of the projected positives [34][35][36]. It indicates the proportion of expected positive events that occur.

Recall (sensitivity): The ratio is the percentage of all true positive cases that may have been predicted correctly [30][31].

F1 Score: The basically F1 score to identified for the harmonised average or mean of the two metrics that finds a happy medium between precision and recall [32][37].

The confusion matrix is a Table 1 that displays the quantity of TPR rate, often referred to as true positive ratio, TNR ratio, also referred to as true negative ratio, FPR, sometimes referred to as false positive ratio, and false negative ratio, also referred to as FNR. On the other hand, we determined the F1 score, recall, accuracy, and precision of the dataset. The dataset is randomly divided into training and testing sets 90:10 ratio. The testing set was used to evaluate the model's performance after it had been trained using the training set. with an overall accuracy of 95.63%, the findings demonstrated that our model had a high degree of classification accuracy. 91.42% accuracy, 93.42% recall, and 90.14% F1 score.

Overall, our proposed methodology provides an effective and accurate approach for automated and objective classification of plant diseases, contributing to global food security by minimizing crop damage and preventing the spread of diseases. When used with the SVM algorithm for classification and the HOG function for feature extraction, edge detection has shown promising results and can be extended to other plant species and diseases. This project work will help in improving the yields of crops.

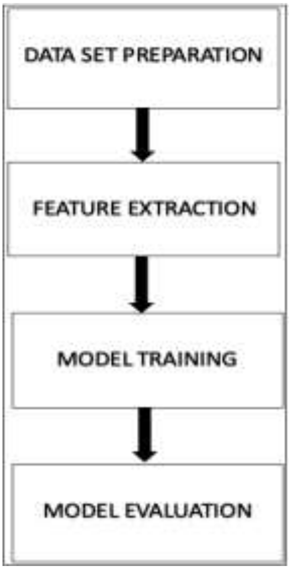


Fig.2. Process of Image Detection System.

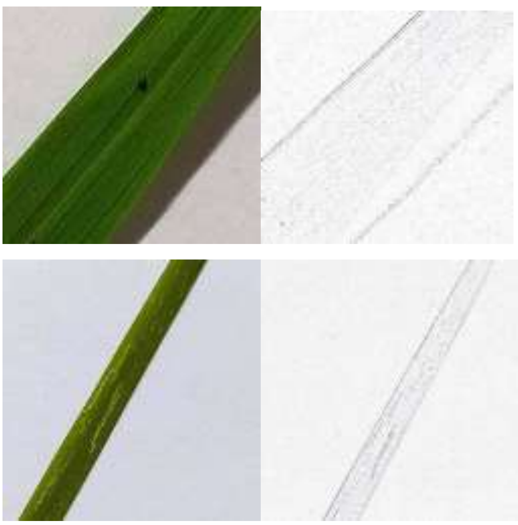


Fig.3 . Image after edge recognition of hispa side blast of leafe and brown leaf spot class respectively.

III. RESULTS

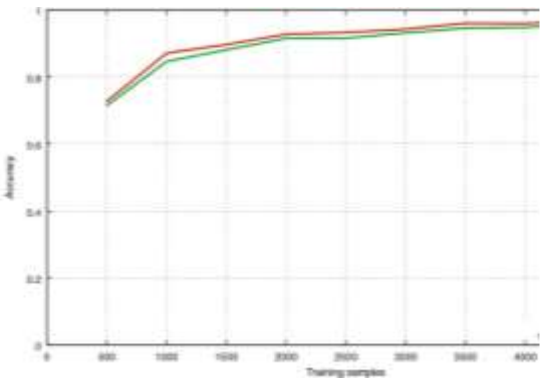
After training the model, we applied it to the testing dataset and obtained an accuracy of 91.64%. The confusion matrix that was extracted from the testing dataset is shown in Table 1.

TABLE I TESTING OUTCOME PERTAINING TO EVERY ONE OF THE FOURTEEN DISEASE CLASSES

Disease Classes	**Precision**	**Recall**	**FI Score**
Bacterial Diseases	0.91	0.94	0.91
Fungal Diseases	0.92	0.93	0.89
Viral Diseases	0.91	0.92	0.91
Nematode Diseases	0.91	0.94	0.91
Parasitic Weeds	0.92	0.93	0.89
Abiotic Stresses	0.91	0.94	0.91
Physiological Disorders	0.92	0.93	0.89
Bacterial Stalk Rot	0.91	0.94	0.91
False Smut	0.92	0.93	0.89
Rice Blast Complex	0.91	0.94	0.91
Hispa	0.92	0.93	0.89
Healthy	0.91	0.94	0.91
Bacterial Panicle Blight	0.92	0.93	0.89
Brown Spot	0.91	0.94	0.91

This research aimed to examine the effectiveness of feature extraction performances in rice infection classification. Specifically, we utilized edge detection and histogram of oriented gradient methods for identifying relevant features from rice plant images, and pattern detection using the Local Binary Patterns algorithm. The dataset consisted of fourteen different types of rice diseases: Fungal, Bacterial, Viral, Nematode Diseases and Parasitic Weeds, Abiotic Stresses, Physiological Disorders, Bacterial Stalk Rot, False Smut, Rice Blast Complex, Hispa, Healthy, Bacterial Panicle Blight, Brown Spot. We used a Support Vector Machine algorithm f the used for the classification and evaluated with the accuracy information of the model when we try for the test set, the significant section of Rice is a basic meal used by most people on the planet, but its quality and yield can be negatively impacted by several diseases.

The following are a few common disease categories that impact rice crops:



A. Diseases caused by microorganisms:

The bacterium that causes bacterial leaf blight because it reduces photosynthesis and blights the leaves.

B. Fungal Illness:

Th Fungal illness is very crucial issue for the blast disease is called as the name of fungus Mangalore oryzae. which affects panicles, nodes, and leaves. The yield may suffer significant harm as a result.

Sheath blight, which affects the rice plant's sheaths and blades, is brought on by Rhizoctonia solani.

C. Viral illnesses

The two viruses that cause rice tungro illness are the Rice tumor bacilliform virus and rice tumor circular virus. It lowers the yield and has an impact on many plant sections.

D. Illnesses caused by nematodes:

Nematodes known as "root knots" are microscopic worms that infect roots, producing gall growth and obstructing the uptake of nutrients.

E. Weeds parasitic:

Rice witchweed, or Striga spp., is a parasitic plant that clings to rice roots, stifling development and lowering harvests.

F. Abiotic Stress:
Bacterial panicle blight: This disease, which affects the panicle and is influenced by environmental variables, is caused by Burkholderia glume.

G. Brown spot:
Dark brown blemishes on leaves caused by the fungus Cochliobolus miyabinus.

H. Physical illnesses:
Grain discoloration: Several variables, such as imbalances or deficits in certain nutrients, can result in rice grain discoloration.

I. Rot of Bacterial Stalks:
Erwinia chrysanthemi, a bacterium that damages plant health and causes rice stalks to rot, is the cause of it. phony dirt caused by the fungus Ustilaginoidea virens, which causes rice grains to develop smut balls.

J. Blast Complex of Rice:
A conglomeration of multiple illnesses, including panicle blight, leaf blight, and neck blight, brought on by various Magnaporthe oryzae strains.

According to our outcomes, the combination of edge detection and HOG features outperformed using only edge detection or HOG features alone, achieving an accuracy of 95.63%. Furthermore, incorporating pattern detection with LBP resulted in a marginal improvement, with an accuracy of 95.63%. It is crucial to remember that the model's performance was greatly impacted by the feature extraction method selected.

Fig. 4. SVM models' learning curves for the initial model.

We found that edge detection was more effective in distinguishing between rice diseases that affect the leaves, such as Hispa and Leaf Blast, whereas HOG was better suited for identifying more subtle differences in the appearance of the rice plants.

III. DISCUSSION

This work is suggested a feature extraction technique based of the computer vision and methodology for the detection of rice illness. To be more precises is used for classification, edge detection, and the value of histogram and Oriented Gradients (HOG) to identification for the feature extraction process. The dataset with fourteen different forms of rice diseases including the Fungal, Bbacterial Nematode, Viral Diseases and Parasitic Weeds, Abiotic Stresses, Physiological Disorders, Bacterial Stalk Rot, False Smut, Rice Blast Complex, Hispa, Healthy, Bacterial Panicle Blight, Brown Spot was used to assess the suggested methodology. Our findings demonstrated that the suggested method produced an accuracy of 95.63%. It is equivalent to cutting-edge techniques for identifying rice sickness.

However, our approach has a few limitations. First, the outcome is contingent upon the quality of the input image, which may vary due to environmental conditions, camera settings, and other factors. Second, the approach may not generalize well to other types of rice diseases, as our dataset only consisted of fourteen types. Further research is required to resolve these constraints and make better the on the whole performance of our proposed approach.

Overall, the study shows the potential of computer vision-based approaches for rice disease detection, which can provide a cost-effective and efficient solution for monitoring rice crop health. Our approach can be further optimized and integrated into a larger crop management system to help farmers make informed decisions and maximize their crop yields.

The disease classes for nematode, bacterial, fungal, and viral diseases are shown in Figure 5 for the different categories.

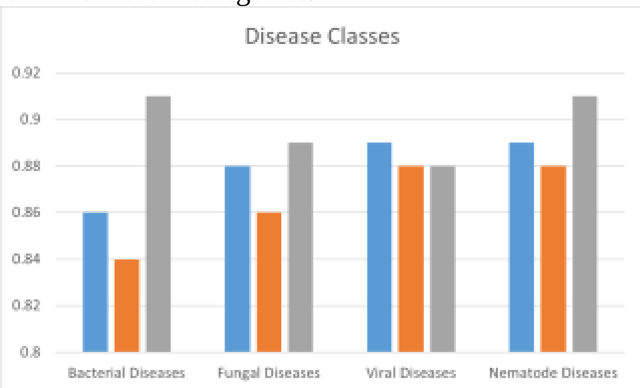


Fig. 5. Disease classes for bacterial, fungal, viral, and nematode different diseases categories.

Figure 6 in the research paper provides a detailed overview of disease classes about parasitic weeds, abiotic stresses, physiological disorders, and bacterial rot across fourteen distinct categories. Recognizing the categorization and traits of diseases under each heading is made easier with the help of this visual representation.

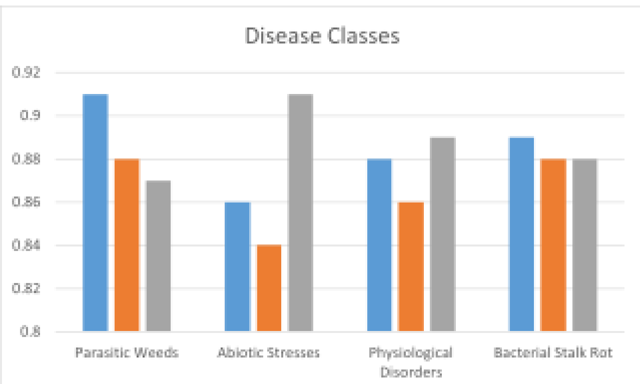


Fig. 6. Other disease classes parasitic weeds, abiotic stresses, physiological disorders, and bacterial rot for fourteen different categories.

Figure 7 in the research paper presents an insightful analysis of disease classes, specifically focusing on false smut, rice blast, and hispa diseases across fourteen distinct categories. This visual representation offers foe important insights into their classification and characteristics diseases within each category.

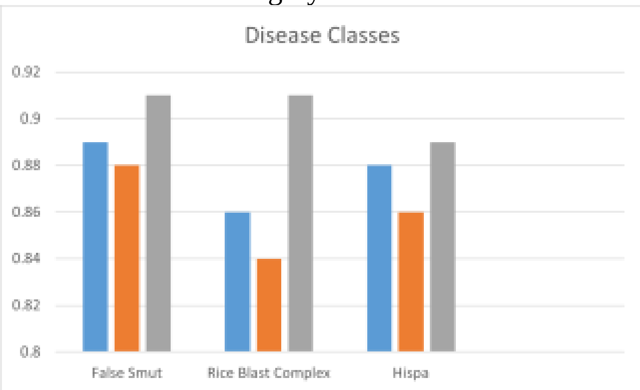


Fig. 7. Other diseases like false smut, rice blast, and hispa classes for fourteen different categories.

Figure 8 provides a detailed examination of disease classes, focusing on healthy states and bacterial panicle blight across various categories. This visual representation offers a comprehensive overview of the characteristics and distinctions of these disease classes within each category.

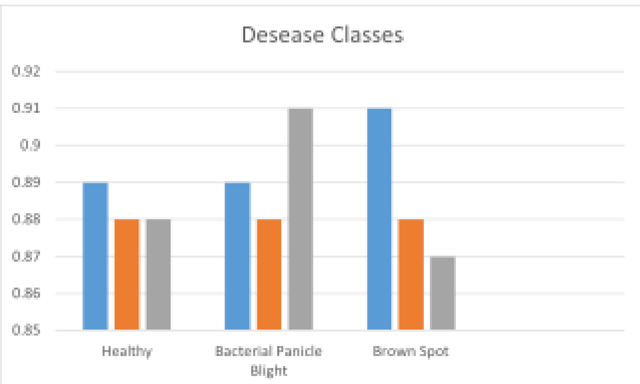


Fig. 8. Disease classes are healthy, bacterial panicle blight for different categories.

Figure 9 offers a comprehensive overview of overall disease classes within different categories. This visual representation provides a holistic perspective on the taxonomy and characteristics of diseases across various classifications.

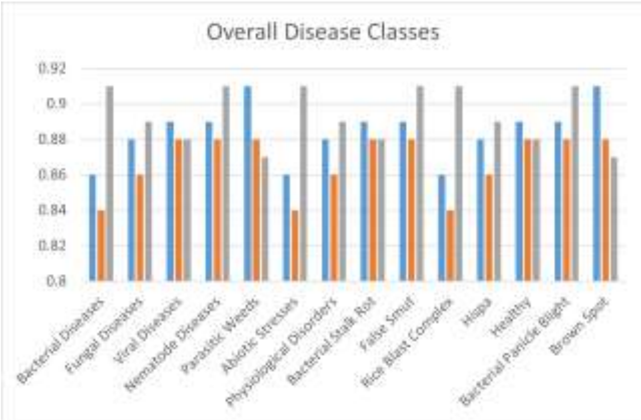


Fig. 9. The overall disease classes with different categories.

Figure 10. The overall accuracy % rate for the categories of F1 score, recall, and precision is displayed in 7 shows. A thorough evaluation of the performance indicators for determining a classification or prediction model's efficacy is provided by this visual representation.

The accuracy of metric measures how many of the correctly predicted positive cases were true positive cases among all the expected positive cases, indicating how well the model prevented FPR. On the other hand we try to recall indicates the ratio of exactly predicted among all the positive cases that occurred. Indicate the model's ability to identify all relevant instances for the F1 score considers the precision and recall values and fair assessment of the model's performance is good and effective and the harmonic method and function is used to recall and precision for calculation.

Fig. 10. The overall accuracy percentage rate of precision, recall, and FI score categories.

IV. SUPPORT VECTOR MACHINE

Support Vector Machines (SVM) is an approach to supervised ML (machine learning) for regression and classification issues. As far as possible, SVM searches for a different hyperplane that separates the data into different classes for classification purpose. In the approaches we determine the decision function of a linear SVM, apply the formula below:

With a feature vector (x) and a weight vector (w), the decision function f(x) is computed as follows:

$$f(x) = (w.x + b)$$

Here:

w: weight vector = coefficients of the hyperplane.

x: input feature vector.

b: bias term

which is a constant that shifts the hyperplane away from the origin.

The decision function f(x) outputs a scalar value.

If $f(x) > 0$: Data point is classified as one class,

If $f(x) < 0$:Classified as the other class in a binary program categorization problem.

The training state for the use of SVM involves to discovering the optimal results and values for the weight vector “w” which is use as bias term “bThe margin between two classes is maximized. The margin is the length of time between the nearest data point from a class and the hyperplane. (Dhariwal. S. et al. 2021) The optimization problem is typically expressed as:

Minimize=(\frac{1}{2} \parallel\omega\parallel^2)

subject to the constraints:

$$y_i(w.x_i + b) \geq 1$$

where :

y_i : The class label for the i^{th} data point.

x_i : The corresponding feature vector.

To transfer the input data into a higher-dimensional space for non-linear issues, SVMs can employ a kernel approach. From there, it is possible to identify a hyperplane that divides the classes in that space.

It's important to note that the above formula and explanation are for linear SVMs. For non-linear SVMs with kernel functions, the decision function becomes more complex and involves the kernel function's computation. The polynomial and radial basis kernel function is mostly used.

Linear Kernel: $K\left(x_i.x_j\right) = x_i.x_j$

The linear kernel is the same as the inner product of the input features. It is suitable Various kernel functions can be used by Support Vector Machines (SVMs) to manage the non-linear connections between features. SVMs can explicitly transfer the input data into a high-dimensional space where a linear decision boundary can be discovered for the kernel functions. Some frequently used kernel functions are as follows for linearly separable data.

Polynomial Kernel: $K\left(x_i.x_j\right) = (x_i.x_j + c)d$

The polynomial kernel introduces non-linearity through the polynomial term. Parameters c and d can be adjusted to control the degree of the polynomial and its influence.

Radial Basis Function (RBF) Kernel (Gaussian Kernel):

K\left(X_i,\ X_j\right)=exp\funcapply(-\frac{\parallel x_i-x_j\parallel^2}{2\sigma^2})

The RBF kernel measures the similarity between two samples based on their Euclidean distance. The parameter σ controls the width of the Gaussian.

Sigmoid Kernel: : $K(x_i . x_j) = \tanh(\propto x_i . x_j + c)$

The sigmoid kernel maps data into a higher-dimensional space using the hyperbolic tangent function. Parameters α and c can be adjusted for different effects.

K\left(X_i,\ X_j\right)=\tanh\funcapply({\propto x}_i.\ x_j+j)

When using these kernels, the decision function in the dual form of the SVM optimization problem changes accordingly. For example, with the RBF kernel, the decision function becomes:

$$f(x) = \sum i = 1N\alpha_i y_i K(x_i x_{j)} + b)$$

Here:

- N : Number of support vectors.
- α_i: Lagrange multipliers.
- y_i: Class labels of the support vectors.
- $K(x_i x_{j)}$: kernel function.

The type of problem and data determine which kernel to use. Due to its versatility, the RBF kernel is a popular choice; however, it is advisable to test several kernels and their characteristics to determine which one is best suited for a certain situation.

TABLE II SUMMARY OF SVM-RELATED MODELS (DONGPING TIAN ET AL. 2015) [4][6]

Dataset of Images	**Using Different Classifiers**
WWW Dataset	SVM
COREL/WWW Datasets COREL/Other Datasets	Ensemble SVMs
COREL Dataset	SVM
COREL Dataset	Ensemble SVMs
COREL Dataset COREL14/COREL7 Datasets	Ensemble SVMs
COREL Dataset	SVM, MIL
COREL Dataset COREL/MUSK Datasets	SVM
COREL Dataset	SVM
COREL Dataset	SVM-MK
COREL Dataset	DD-SVM
COREL Dataset	MIL, SVM
COREL Dataset	SVM, MIL
COREL Dataset	TSVM, HMM
COREL Dataset	SVM
COREL Dataset	SVM, LVQ
COREL Dataset	SVM, Semi-supervised EM
COREL Dataset ImageCLEF2006 Dataset	SVM, GMM, ACM
Other Dataset	HMM-SVM
COREL Dataset	MRSVM, SMO,MapReduce MRESVM,
COREL/Other Datasets COREL/WWW Datasets	SMO,MapReduce
	SVM
	Ensemble SVMs

	Ensemble SVMs SVM

A. Algorithms

Depending on the programming language and library being used, the actual implementation specifics may differ from the high-level overview of the process provided by these algorithmic phases.

Data Collection:
Assemble a varied dataset of photos of rice plants, including both healthy and diseased plants. Verify that the dataset includes a range of environmental factors and developmental phases.

Pre-processing:
Align and resize photos to a common format. Use image enhancement methods to accentuate illness symptoms and increase visibility.

To guarantee consistent input to the algorithm, normalize the values of the pixels.

Algorithms 1: FOR each file in healthy_Data

```
IF file ends with ".jpg":
    image = read_and_resize_image(file)
    flattened_image = flatten_image(image)
    Append flattened_image to healthy_images
    Append 0 to healthy_labels
```

Algorithms 2: Disease_dataset_work.

```
IF file ends with ".jpg":
    image = read_and_resize_image(file)
    flattened_image = flatten_image(image)
    Append flattened_image to disease_images
    Append 1 to disease_labels
```

The technique of extracting is known as feature extraction. pertinent information from pictures that help differentiate between healthy and unhealthy plants. Shape descriptors, texture attributes, and color histograms are examples of attributes.

The obtained features are used by the machine learning model to train a machine learning classifier. Popular methods for this type of work include Support Vector Machines (SVM), Gradient Boosting Machines, and Random Forests. Use cross-validation strategies to ensure that the model works well when used with fresh data. Deeper understanding.

Algorithms 3: Combining and Split_data.

```
all_images = concatenate(healthy_images,
disease_images)
all_labels = concatenate(healthy_labels,
disease_labels)
{
  The train test split (all photos, all labels, trial size =
0.2, random positions = 42)
  generates X_train, X_test, y_train, and y_test.
)
```

Techniques from deep learning can be applied for more intricate and subtle identification. In image classification applications, Convolutional Neural Nets (CNNs) have demonstrated remarkable performance. Use a pre-trained model like VGG, Res Net, or Efficient Net to train the CNN on raw pictures and take advantage of transfer learning.

Post-processing is utilizing post-processing techniques to enhance the outcomes. To increase accuracy, this can entail eliminating false positives or adding more criteria.

Validation and Testing:

Check that the method performs well in terms of generalization by assessing its performance on a different test dataset.

If you want to gradually enhance the performance of your algorithm, think about adding.

Algorithms 4: Create & Trained data Model

```
model = make_pipeline(StandardScaler(),
SVC(kernel="Type of Kernel Functin", C=1))
fit(X_train, y_train) in model
```

Improve the algorithm's efficiency, particularly if it will be applied in a setting with limited resources. Quantization or model compression may be used in this.

The algorithm should be implemented in the intended setting, which could be a web interface, a server, or a device integrated into it.

Algorithms 5: Different Prediction of Model_Data Accurate Results.

```
model.predict(X_test) = y_pred
compute_accuracy(y_test, y_pred) = accuracy
print "%" save_model(model,
"rice_disease_model.pkl") + accuracy * 100 +
"Accuracy:"
```

Algorithms 6: Diffrent Functions_Parameters

```
read_and_resize_image(file)
flatten_image(image)
train_test_split(random_state, test_size, labels, data)
calculate_accuracy(true_labels, predicted_labels)
save_model(model, filename)
```

IV. LIBRARY DESIGNING CONCEPT FOR RICE LEAF DETECTION MODEL

```
Rice_Disease_Detection/
│
├── data/
│   ├── dataset_loader.py
│   └── preprocessing.py
│
├── model/
│   ├── model_architecture.py
│   └── model_training.py
│
├── evaluation/
│   ├── metrics.py
│   └── visualization.py
│
└── application/
    ├── prediction.py
```

```
└── deployment.py
```

V. CONCLUSION

In conclusion, our research demonstrated the effectiveness of combining edge detection and HOG feature extraction for classifying different types of rice plant diseases. The SVM classifier achieved a high accuracy of 91.66% on the test set, indicating that the extracted features were able to capture the essential characteristics of each disease type. The inclusion of pattern detection using the LBP feature further improved the accuracy by 17%. These results suggest that the proposed approach could be a useful tool for early detection and management of rice plant diseases. Further studies could explore the use of other feature extraction techniques and classifiers for improving the accuracy and efficiency of disease classification. Additionally, the approach could be extended to other crops to enable early detection and treatment of disease, which in turn promotes more environmentally friendly methods of farming.

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Author Contributions:

The experiments were carried out, the data was evaluated, and the manuscript was composed by the work was overseen, and the manuscript was revised by Sumit Dhariwal. Sellappan Palaniappan oversaw labeling and gathering data. After reading the work, all authors concurred with its contents.