RICE BLAST DISEASE PREDICTION USING INTEGRATED SMOTE WITH MULTILAYER PERCEPTRON

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ABSTRACT

Agriculture is the primary source of income for the major population of India. Agriculture generates 17% of the total GDP of India and India is the second-largest producer of rice and wheat. Rice (Oryza sativa) is a major food crop for many parts of India. India has the largest area under rice cultivation; hence rice is the important crop of the country. Rice is such a major cereal crop, which provides 20% of total energy and leads as the main food for more than 50% of the world's population. Rice production has been challenged by recent changes in crop production technologies, that also has impact on disease occurrence. Thus, crop management includes extensive use of fertilization, repeated flooding increases the disease problem, increased monoculture of rice helps in support of pathogens from one crop to another crop. The Rice crop in India has affected by many pathogens. Among 36 rice diseases, rice blast is the disease caused by Magnaporthe Oryae, is the major destructive disease of paddy crop. This disease having significant threat to the production of paddy crops all over the country. Rice blast continues to be a cryptic problem in several rice-growing regions (tropical and temporal) where the pathogen spreads exponentially and is difficult to manage by the farmers and thus reduces yield of paddy crop in the field.

In India, rice blast is a major concern due to favourable weather conditions during the crop season. Climate plays major role in the disease appearance, multiplication, and spread of the fungus. Along with climatic factors, the varieties of seeds also influence the occurrence of rice blasts, primarily the climate factors have a strong influence on the occurrence of blast disease even though a sufficient amount of nutrients are present in the plant. Thus, rice blast disease will occur and develop when certain weather conditions continue for the given period. Forecasting models that make predictions of possible blast disease occurrence may give important information to the producers of rice to manage the disease. Therefore, this project implements the rice blast disease prediction using data balancing technique based multilayer perceptron.

Keywords: Rice blast disease, Integrated smote, Multilayer perception.

1. INTRODUCTION

Agriculture is vital to the Indian economy and is second in rice productions. Rice is cropped in literally every state including Tamil Nadu, West Bengal, Punjab, Uttar Pradesh, Assam, and Bihar, to name a few. The agricultural industry contributes roughly 19.9% of the overall gross domestic output. In India, rice is one of the most widely consumed grains. Diseases impair the development and quality of rice plants, lowering the profitability of the cultivation. Different illnesses can affect specific rice crops, making it difficult for farmers to identify them due to their limited expertise gathered through experience. Automatic data processing expert is used for this accuracy and early detection of plant diseases diagnosis. As a result, the development of a healthy and prosperous crop is possible. In agriculture, computer vision technology has been used to estimate crop yields, diagnose crop nutritional deficiencies, estimate crop geometric sizes, and recognise weeds for decades. Image processing, pattern recognitions, SVMs (support vector machines), and hyperspectral detections have been used in computer vision to diagnose diseased crops or plants . Cluster analysis was utilised to distinguish healthy tomatoes from diseased in multispectral remotely sensed images of tomato farms.

SVMs extracted form and textural aspects of rice bacterial leaf blasts and leaf, sheath blights. The study used GAs (Genetic Algorithms) in combination SVMs with to categorise rice brown spots, bacterial blights, and leaf blasts and thus recognize sick leaves in plants. RGB (Red Green Blue) values of afflicted parts followed by application of NBs (Naive Bayes) in classifications. Tomato's mosaic disease and wheat leaf rusts were identified utilising infrared thermal imaging where crop's temperature information was retrieved. Though many existing algorithms detect crop diseases with decent accuracies, they are heavily dependent on manual feature extractions making the generalizations of these extractions difficult. Furthermore, certain approaches need the use of specialised equipment, which is not always easily available to users. All of these flaws make it difficult to use these technologies to diagnose agricultural diseases.

Filtering, wrappers, and embedding approaches are the three types of feature selection strategies. Filter approaches look at the data's inherent traits, and feature selection is independent of the classifier. As part of the selection process, wrapper models require improving a predictor. Although they produce superior results, filter approaches are often less computationally costly than wrappers. The embedded technique incorporates the selection procedure within the classifier's learning process. There are obstacles in identifying effective features by algorithms due to noises or redundancy or irrelevant information present in the data added to their higher dimensionalities. This makes selection of efficient feature selection techniques challenging. Feature selection's performances are reliant on their success learning of data. Instability of feature selection methods were reviewed in the overview of feature selection strategies. Multiple selection strategies including filters, wrappers, and embedding techniques were examined in terms of feature selections. Feature selections using wrappers or ensembles employ their own learning processes but may not perform well with other classifiers. Filter-based approaches have less computational complexity than embedded and wrapper-based techniques. Wrapper-based approaches have a considerable risk of overfitting due to their complexity. Filter based techniques generate stabilized sets of features which resist data over fits. More generic strategies for feature selections are ensembles. A commonly employed filter technique that analyzes intrinsic properties of inputs without classifiers on mind is used for feature selections in this work called Neutrosophic logic. The maps generated by NCMs are neutral between true and false and useful filters for selection of features where lesser number of characteristics characterise the complete data. Many filters and wrappers including MCFSs (multi-cluster feature selections), Relieff, LSs (Laplacian Scores), Inf-FSs (infinite feature selections), ILFSs (infinite latent feature selections), local learning-based CFSs (clustering feature selections), and GAs are compared with this works suggested neutrosophic logic-based feature selections. These algorithms are intended to rank and choose relevant traits as feature subsets according to relevance or significance to applications. The focus of this research is on the hybrid feature selection method.

To circumvent disadvantages of crop disease diagnostic methods DLTs (Deep learning techniques) could be used. DLTs have become popular in recent years for image categorizations, object identifications, and content suggestions. In fact, DLTs have been employed by researchers to identify illnesses in a variety of crops. To identify diseased wheat crops, researchers first used CNNs (convolution neural networks), Faster R-CNNs (Faster Recurrent CNNs) on sugar beet's leave imagers. Data Over fits occurs while using MLTs (Machine Learning Techniques) based on single prediction models whereas ensemble learn using series of algorithms and integrate feasible predictions thus addressing this issue. Ensemble learning has been used to predict illness diagnosis, soybean production, protein binding hot spots, and wheat grain yield since the introduction of computer technology. Since, ensembles have been established as a strategy in earlier researches, they were used in this work to improve accuracy of sickness detections. To summarise, DLTs have the potential to identify diseases in a wide range of crops with higher accuracies. Existing researches on

use of DLTs to trace rice ailments concentrate on limited number of diseases amongst identified diseases in Rice crops which include rice leaf blasts, fake smuts, neck blasts, sheath blights, bacterial stripes, and brown spots. However, existing methods do not perform well on high dimensional datasets where errors mainly stem from their feature selection processes impacting classifier's performances.

2. LITERATURE SURVEY

Varsha, M., B. Poornima, et al. [1] proposed study is to predict the severity of rice blast disease using the linear SVM model. Prediction of rice blast disease severity is divided into four classes: 0, 1, 2, and 3. Data imbalance is the most challenging problem in multi-class classification. This study has efficiently handled imbalanced data using k-means SMOTE and SMOTE oversampling techniques to balance training and testing data. Finally, cross-location and cross-year models are developed using a linear support vector machine and predict the severity of rice blast disease to the classes 0, 1, 2, 3, respectively. Cross-year and cross-location models are cross-validated using five-fold cross-validation.

Sriwanna, Kittakorn, et al. [2] proposed ensemble features ranking method have a higher classification performance than the other methods. The ranking of the final features for all classifiers reveals that average visibility, amount of rainfall, hours of sun, maximum wind speed, and days of rain are the five most effective weather features for rice blast disease prediction. Moreover, various classification models achieve satisfactory performance, especially those that are combined with feature selection.

O. V. Putra, N. Triangulum, et al. [3] proposed a method based on transfer learning to tackle such issues. Our method contains several steps. In the first step, the rice leaf is preprocessed. Second, due to data imbalance, balanced class weighting was employed. Third, to improve the network performance, three layers of convolution were added to the transfer learning model. The parameters in fully connected layers were optimized using bandit-based approach. In the last step, the leaf was classified into nine categories. They compare our method with the state-of-the-art (SOTA) works. Our model reaches the top in terms of accuracy with 98 % compared to the other SOTA.

Jiang, Zhencun, et al. [4] improve the Visual Geometry Group Network-16(VGG16) model based on the idea of multi-task learning and then use the pre-training model on ImageNet for transfer learning and alternating learning. The accuracy of such model is 97.22% for rice leaf diseases and 98.75% for wheat leaf diseases. Through comparative experiments, it is proved that the effects of this method are better than single-task model, reuse-model method in transfer learning, resnet50 model and densenet121 model. The experimental results show that the improved VGG16 model and multi-task transfer learning method proposed in this article can recognize rice leaf diseases and wheat leaf diseases at the same time, which provides a reliable method for recognizing leaf diseases of many plants.

Bhatia, Anshul, et al. [5] implemented Extreme Learning Machine (ELM) algorithm for plant disease prediction based on a dataset collected in real time scenario namely Tomato Powdery Mildew Disease (TPMD) dataset. Since, the collected TPMD dataset was imbalanced thus; various resampling techniques namely Importance Sampling (IMPS), Synthetic Minority Over-sampling Technique (SMOTE), Random under Sampling (RUS), and Random over Sampling (ROS) have been used here for balancing the dataset before using it in the specified prediction model. ELM models have been developed for each of the balanced TPMD datasets obtained from these resampling techniques as well as for the imbalanced TPMD dataset.

Ma, H.; Huang, W.; et al. [6] proposed approach incorporating both growth and environmental parameters of different crop periods could distinguish wheat powdery mildew and aphids at the regional scale. The bi-temporal growth indices and environmental factors-based SMOTE-BPNN, BPNN, and SVM models all had an overall accuracy high than 80%. Meanwhile, the SMOTE-BPNN method had the highest G-means among the three methods. These results revealed that the combination of bi-temporal crop growth and environmental parameters is essential for improving the accuracy of the crop disease and pest discriminating models. The combination of SMOTE and BPNN could effectively improve the discrimination accuracy of the minor disease or pest.

Gao, Qijuan, et al. [7] ensemble method combines different balanced data algorithms including Borderline SMOTE (BSMOTE), Adaptive Synthetic Sampling (ADSYN), SMOTE-Tomek, and SMOTE-ENN with the XGBoost model separately. The performances of the SMOTE-ENN-XGBoost model, which combined over-sampling and under-sampling algorithms with XGBoost, achieved higher predictive accuracy than the other balanced algorithms with XGBoost models. Thus, SMOTE-ENN-XGBoost provides a theoretical basis for developing evaluation criteria for identifying orphan genes in unbalanced and biological datasets.

Nettleton, D.F., Katsantonis, D., et al. [8] proposed four models for predicting rice blast disease, two operational process-based models (Yoshino and Water Accounting Rice Model (WARM)) and two approaches based on machine learning algorithms (M5Rules and Recurrent Neural Networks (RNN)), the former inducing a rule-based model and the latter building a neural network. In situ telemetry is important to obtain quality in-field data for predictive models and this was a key aspect of the RICE-GUARD project on which this study is based. According to the authors, this is the first-time process-based and machine learning modelling approaches for supporting plant disease management are compared.

Luo, Yh., et al. [9] new method for rice blast grading based on sensitive bands was proposed. Then, the method of system clustering method, BP neural network and probabilistic neural network were used to establish the rice blast classification prediction model, respectively. Comparing the three models, the classification effect based on probabilistic neural network is the best. In the training samples, the logarithmic spectral classification accuracy is 97.8%. In the test samples, the logarithmic spectral classification accuracy is 75.5%.

Samudra, Ami Anggraini, et al. [10] aimed to develop a web-based system to predict the potential probability of blast disease occurrence by combining weather variable and cultural practices factor. ANN method was used to analyze the influence of weather variables on the occurrence of blast disease and to analyze the influence of cultural practices on the occurrence of blast disease executed by decision tree method. Results of this research indicate that proper cultural practices may inhibit the development of blast disease although weather variables support the development of the disease. As conclusion, a web-based system has been developed and can be used to predict the potential probability of blast occurrence.

Das, Ankur, et al. [11] extracts different types of features from the disease portions (i.e., images) of the plants and identifies the most valuable features that can distinguish the disease types. To identify the most valuable features, initially, a weighted graph is constructed with extracted features as nodes and similarity between every pair of features as the weight of the corresponding edge. Based on the weights assigned to the edges, importance of each node of the graph is calculated. Finally, a graph-based clustering algorithm namely, Infomap clustering algorithm is applied on the graph to partition it into a set of connected subgraphs.

Daniya, T., and S. Vigneshwari, et al. [12] notable ML and image processing concepts in detecting and classifying the plant diseases are discussed. Probabilistic Neural Network (PNN), Genetic Algorithms (GA), k-Nearest Neighbor Classifier (KNN) and Support Vector Machine (SVM) are the various classification techniques used in various applications in the agricultural research. Different input data yields varied quality of an outcome and so selecting a classification method is a critical task. Biological research, agriculture, etc. are the disparate fields where the plant leaf disease classifications are applied.
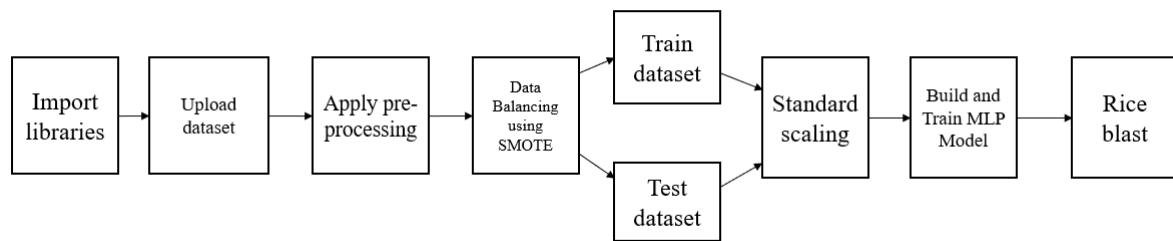
3. PROPOSED SYSTEM

Fig. 1: Block diagram of proposed system.

3.1 Pre-processing

Data Preprocessing in Machine learning

Data pre-processing is a process of preparing the raw data and making it suitable for a machine learning model. It is the first and crucial step while creating a machine learning model.

When creating a machine learning project, it is not always a case that we come across the clean and formatted data. And while doing any operation with data, it is mandatory to clean it and put in a formatted way. So, for this, we use data pre-processing task.

Why do we need Data Pre-processing?

A real-world data generally contains noises, missing values, and maybe in an unusable format which cannot be directly used for machine learning models. Data pre-processing is required tasks for cleaning the data and making it suitable for a machine learning model which also increases the accuracy and efficiency of a machine learning model.

- Getting the dataset
- Importing libraries
- Importing datasets
- Finding Missing Data
- Encoding Categorical Data
- Splitting dataset into training and test set
- Feature scaling

Splitting the Dataset into the Training set and Test set

In machine learning data pre-processing, we divide our dataset into a training set and test set. This is one of the crucial steps of data pre-processing as by doing this, we can enhance the performance of our machine learning model.

Suppose if we have given training to our machine learning model by a dataset and we test it by a completely different dataset. Then, it will create difficulties for our model to understand the correlations between the models.

If we train our model very well and its training accuracy is also very high, but we provide a new dataset to it, then it will decrease the performance. So we always try to make a machine learning model which performs well with the training set and also with the test dataset. Here, we can define these datasets as:
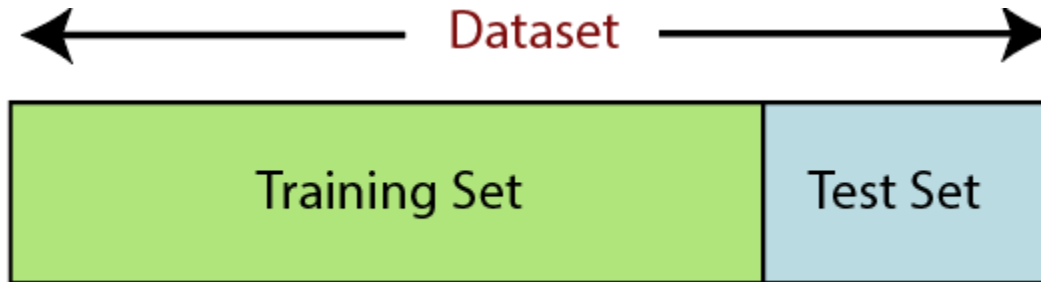
Training Set: A subset of dataset to train the machine learning model, and we already know the output.

Test set: A subset of dataset to test the machine learning model, and by using the test set, model predicts the output.

3.2 Feature Extraction

Extracting features that are effective for classification from raw representations, is the key to successfully applying machine learning for PPI sites prediction. In recent years, researchers carried out a series of studies on extracting and encoding features from protein sequences. Such efforts typically fuse physicochemical properties, sequence information, evolutionary information, structural information, functional annotation, as well as others, in order to obtain a rich and comprehensive set of protein features. Murakami et al. extracted characteristic information based on position-specific scoring matrix (PSSM) and predicted accessibility (PA). Dhole et al. conducted feature extraction by integrating PSSM, averaged cumulative hydropathy (ACH) and predicted relative solvent accessibility (PRSA). Zhang et al. applied various feature extraction methods including 3D-1D scores, conservation score, and protein sequence coding. Chou used the pseudo-amino acid composition (PseAAC) method to encode protein sequences and classify the interaction data of three types of proteins. Dong et al. combined the sequence spectrum and solvent accessible surface area to identify residues on the interaction interface and achieved good results. Xie et al.fused amino acid encoding, PSSM, position specific frequency matrix (PSFM), composition-transition-distribution (CTD), and five structure features to encode protein sequences. Chen et al. combined PseAAC, autocorrelation descriptor (AD), conjoint triad (CT), and local descriptor (LD) features, to predict PPI. Zeng et al. used the n-gram frequency method to obtain three features from protein sequences. The features were then combined in a weighting scheme to make full use of the sequence information. Göktepe et al. fused weighted skip-sequential conjoint triads, PSSM, Bi-Gram representation, AAC and PseAAC to extract information features from protein sequences, and achieved good results. GcForest-PPI adopted PseAAC, autocorrelation descriptor (Auto), multivariate mutual information (MMI), CTD, amino acid composition PSSM (AAC-PSSM) and dipeptide composition PSSM (DPC-PSSM) to extract features for prediction. Furthermore, a variety of improved methods based on PseAAC have been applied to extract protein sequence information. For example, Nanni et al. [19] used a sequence-based algorithm combining the augmented Chou's pseudo amino acid composition based on the autocovariance

approach. Göktepe et al. proposed a method based on the weighted amino acid composition information and the correlation factors of the protein. Xu et al. incorporated two tiers of sequence pair coupling effects into the general form of PseAAC to improve the predictive ability of the model.

Biological information hidden in protein sequences needs to be identified and predicted by high-throughput, high-accuracy prediction algorithms. Therefore, the selection of classifiers is crucial in the prediction of PPI sites. Common classification algorithms include logistic regression (LR), support vector machine (SVM), neural network, Naïve Bayes (NB), conditional random field (CRF), decision tree (DT) and random forest (RF). Ofran and Rost applied a neural networks approach to predict PPI sites from sequence information. Neuvirth et al. used primo Bayes to identify potential action sites of protein structures in the monomer state. Yan et al. were the first to apply the SVM algorithm to the identification of PPI sites, and later developed a two-stage classifier combining SVM and NB to further improve the prediction. Murakami et al. used kernel density estimation to train a Bayes classifier to improve prediction performance. Dhole et al. predicted PPI sites through combining a neural network and regularized LR for training. Wei et al. and Wang et al. identified PPI sites through the RF classifier. Wei et al. applied integrated SVM and weighted RF for the prediction of PPI sites. Zeng et al. used a text convolutional neural network to extract features from protein sequence and applied the deep neural network to predict PPI sites.

Although the existing machine learning based methods have achieved good results in the prediction of PPI sites, there are still many problems to be addressed. First, the extreme class imbalance between positive and negative samples may negatively affect prediction results and hinder the predictive ability of traditional machine learning algorithms. Second, on the one hand, a single feature extraction method cannot comprehensively represent the sequence information. On the other hand, fusing multiple features in order to enrich sequence information, although beneficial, does introduce redundancy and noise to the features. Finally, we find that existing classifiers for PPI sites prediction, such as RF, NB, and LR, can still be improved upon.

3.3 SMOTE Algorithm

Borderline SMOTE is an improved oversampling algorithm based on SMOTE, which uses only a few class samples on the border to combine new samples, thus improving the sample category distribution. Borderline SMOTE samples are divided into three categories: Safe, Danger and Noise. Finally, only a few Danger samples were oversampled. The algorithm steps are as follows:

(1) For every sample in a few classes xi, compute the nearest m samples from the entire dataset. The number of other categories in the most recent samples m is denoted by m′.
(2) Classify the samples xi:If m′=m, the surrounding samples of xiare all samples of different categories, which are denoted as noise data. Such data will have adverse effects on the generation effect; thus, it is considered not to use these samples in the generation.

3.4 Multilayer Perceptron (MLP)

The multilayer perceptron is a traditional and classic ANN model. The structure is composed of the input layer, hidden layer and output layer. Typically, the MLP model consists of a backpropagation algorithm for error adjustment, also called BPNN which was established by Rumelhart et al. in 1986. The layers of nodes whose input and output are seen only by other nodes are termed hidden layers. The connection weights are computed utilizing a learning algorithm. In this study, a single hidden layer was conducted with an optimized perceptron element. The Levenberg Marquardt gradient search method is used with the batch update. In total, there were 1000 epochs, with a learning rate of 0.001 and an early stopping callback to prevent overfitting.

4. RESULT AND DISCUSSION

confusion_matrix
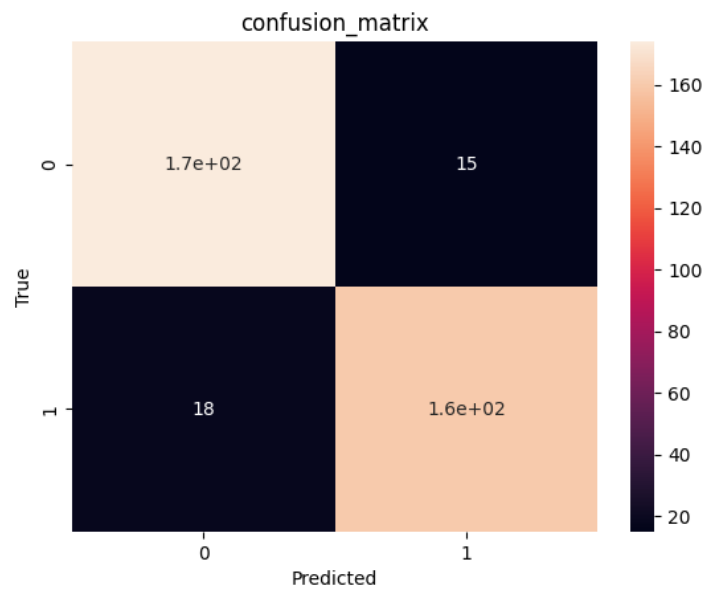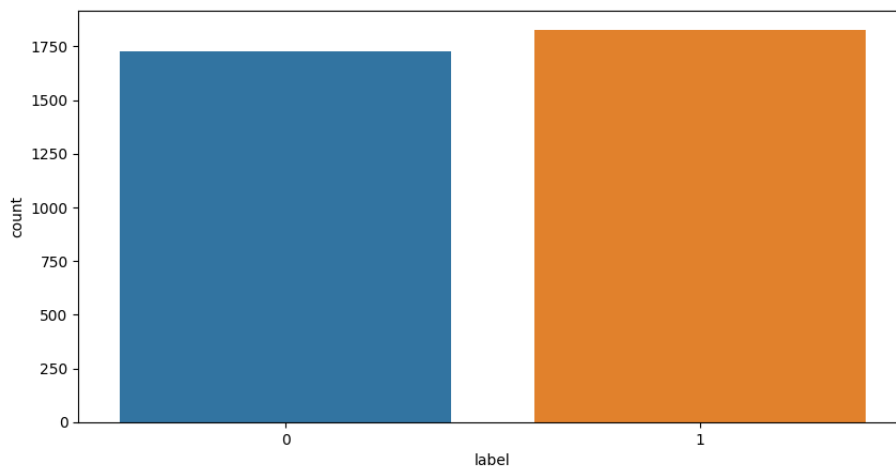
	precision	recall	f1-score	support
0	0.91	0.92	0.91	189
1	0.91	0.90	0.91	178
accuracy			0.91	367
macro avg	0.91	0.91	0.91	367
weighted avg	0.91	0.91	0.91	367

5. CONCLUSION AND FUTURE SCOPE

For the majority of Indians, agriculture is their main source of revenue. India is the world's second-largest producer of wheat and rice, and agriculture contributes 17% of the country's overall GDP. A significant food product for many regions of India is rice (oryza sativa). Rice is an essential crop in India because it was grown there on the largest scale. Providing 20% of all energy and serving as the primary food source for more than 50% of the world's people, rice is a significant cereal crop. Recent advancements in crop production technology had put a strain on rice output and had an effect on disease occurrence as well Thus, intensive fertilization is a key component of crop management, while repetitive flooding exacerbates the disease issue and expanded rice monoculture aids in the spread of pathogens from one crop to another. Numerous pathogens had harmed India's rice harvest. The most destructive of the 36 rice illnesses was rice blast, which was brought on by Magnaporthe Oryae. The output of paddy crops throughout the nation was seriously threatened by this disease. Rice blast was still a perplexing issue in several rice-growing regions (tropical and temporal), where the pathogen spreads exponentially and was challenging for farmers to controlled, lowering paddy crop output in the field

Due to favourable weather during the crop season, rice blast in India was a major worry. The fungus that caused the illness manifests, multiplies, and spreads as a result of climate. Although the plant had enough nutrients, the climate factors had a significant impact on the frequency of rice blasts in addition to the climatic factors. This was true even though the plant had enough nutrients to support itself. As a result, the development of rice blast disease would occur and last as long as specific weather circumstances exist. In ordered to controlled the disease, rice producers may benefit from forecasting models that anticipate the potential occurrence of blast disease. Consequently, used a data balancing technique to implement the prediction of the rice blast disease

Future scope

The future course of this work can be performed with diverse mixtures of machine learning techniques to get better accuracy. Furthermore, new feature-selection methods can be developed to get a broader perception of the significant features to increase the performance of Rice Blast Disease.

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