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## RICE PLANT DISEASE IDENTIFICATION AND DETECTION TECHNOLOGY THROUGH CLASSIFICATION OF MICROORGANISMS USING FUZZY NEURAL NETWORK

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## Graphical abstract



### Abstract

This paper describes a method of using sound signal processing system to efficiently detect and identify the three common microorganisms that cause diseases in the rice farmland of the Philippines: (1) Xanthomonas oryzae, (2) Thanatephorus cucumeris and (3) Magnaporthe oryzae. Sound signals from samples of rice leaves infected by the above mentioned bacteria were recorded using a designed anechoic chamber through an electret condenser microphone and were processed via spectral subtraction to eliminate the effects of noise. Mel Frequency Cepstral Coefficient was used to extract the needed features of each input for the ANFIS learning algorithm. The Fuzzy neural network was applied to train the system based on 450 recorded sound data where 80% were used for training and 20% for testing. A program was also developed that will generate a report in PDF format showing the diagnosis and curing methods for the infected sample to prevent its further infestation. Test results showed recognition accuracy of the bacteria, Xanthomonas oryzae, Magnaporthe oryzae, and Thanatephorus cucumeris, of 93.33%, 100% and 96.67% repectively.

Keywords: Rice plant diseases, sound signal processing, fuzzy neural network

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## **1.0 INTRODUCTION**

Rice is the world's most important food crop; it is grown and consumed across the globe. For most agricultural country, rice is a food and an economic commodity where it is both a major expenditure item and a source of income for many of its households. Rice is one of our Philippines' major products, taking up more 4 million hectares of land. It remains the main food of more than 90 million Filipinos and provides about 60-65 percent in the smallest household income [1].

The challenge to increase rice production is not an easy task due to various agronomical factors which affect yield loss. According to International Rice Research Institute (IRRI) [2], farmers lose a significant amount of their crop yield about 37% due to pests and diseases, and this could still increase depending of the type of disease.

Diseases are considered major constraints in rice production [3]. Furthermore, rice diseases are mainly caused by fungi, bacteria or viruses, and are capable of being transmitted from infected to healthy plants under favourable environmental conditions. In the Philippines, there are three most common microorganisms that cause diseases in the rice plant: (1) Xanthomonas oryzae, (2) Thanatephorus cucumeris and (3) Magnaporthe oryzae.

The traditional way of identifying rice plant diseases is through the identification of visible structures produced by the pathogens but this method is confusing and prone to error, and thus unreliable. Also, these pathogens can be examined through culturing in laboratories which take a considerable amount of time. A study by Matsuhashi, et al. (1998) provided another method by capturing the sound waves produced by bacterial cells [4]. According to the study, certain microbes such as Bacillus subtilis emit sounds with a distinct frequency. Through the identification of the distinct frequency of a certain microbe, one can quickly determine if a rice plant is carrying a disease.

Application of the microphone technology would allow sounds made by bacteria to be analyzed. The potential of a microphone system to easily detect and identify bacterial and fungal contamination is thus considered for experimental evaluation to prevent the growing predicament that the food sector faces.

The motivation of this study is to provide a more accurate and systematic analysis regarding the health conditions of rice plant by sound signal processing utilizing Fuzzy Neural Network as the training model. It offers an early detection and identification of rice plant disease, eliminate time consuming traditional method, and facilitate the farmers to acquire higher crop productivity.

## 2.0 METHODOLOGY

The composition of the system is made of four sections namely the sound recording, signal processing, training system, and result. Figure 1 below shows the main block diagram of the system.



Figure 1 Main block diagram

#### 2.1 Sound Recording

The sound recording block is responsible for obtaining the sonic response of the three microorganisms (Xanthomonas oryzae, Thanatephorus cucumeris and Magnaporthe oryzae) using an anechoic chamber with an electret condenser microphone inside, ranging 20 Hz up to 120 KHz of frequency response and an audio frequency generator.



Figure 2 (a) Actual photo of the anechoic chamber (b) Inside of the anechoic chamber

The dimensions of anechoic chamber are as follows: 15 inches in length, 15 inches in width and 15 inches in height. For the materials used in this module box, plywood is used to achieve its durability. The chamber is lined with ferrite tiles on all sides with pyramid shaped foamed ferrite. It does help to make sound waves less, and are a good solution for sound absorption.

Computation for Reverberation Time:

$$RT = \frac{0.049 xV}{-\sin(1-a)}$$
(1)

Where,

$$S = 6 * side_{in}^{2}$$

$$S = 6 * [15in - 2(0.5in) - 2(3in)]^{2} = 384 sq. in = 2.6667 sq. ft.$$

$$A = 0.80$$

$$RT = \frac{0.049 \times 0.2963}{-(2.6667)\ln(1 - 0.8)} = 3.3828 \text{ milliseconds}$$

Samples of Xanthomonas oryzae, Thanatephorus cucumeris and Magnaporthe oryzae microorganisms of different concentration were inoculated onto separate agar plates in a 90x15mm polystyrene Petri dish. These samples were collected from the laboratory of the International Rice Research Institute at Los Banos, Laguna, Philippines. A total of 450 samples of varying concentration (150 samples of Xanthomonas oryzae, 150 samples Magnaporthe oryzae, and 150 samples of Thanatephorus cucumeris) were collected, from which 80% were used for the training and 20% for the testing.

The sonic response of the microbes, triggered by an artificial sound using an audio frequency generator with pure sine wave signal having a frequency range of 20 to 120kHz, were recorded by an electret condenser microphone (48V, 10mA phantom power, 47 mm length, and a frequency range of 20Hz-120kHz). Figure 3 shows the image of sample rice plants with disease manifestations of the three microorganisms



Figure 3 (a) Blast lesions on rice leaf (b) Leaf blast spindle shape manifestation (c) Sheath blight disease on leaf sheath

### 2.2 Signal Processing

The signal processing section covers the sound enhancement and feature extraction. In sound enhancement, noise reduction will be performed using spectral subtraction. In feature extraction, Mel Frequency Cepstral Coefficient (MFCC) will be the algorithm to extract the characteristics and give unique pattern for each input.

The spectral subtraction is based on the theory that the enhanced speech can be acquired by subtracting the estimated spectral factors from the continuum of the input noisy signal. This is further subdivided into parts and is shown in Figure 4.

Assuming n(s) is the noise signal, c(s) is clean speech signal and u(s) unclean noisy speech and it can be written as,

$$u(s) = c(s) + n(s) \text{ for } 0 \le s \le S - 1$$
(2)

Where s is the time index, S is a number of samples. Generally speech enhancement is calculate enhanced speech c(s) from given u(s) with the guess that n(s) is uncorrelated with c(s). Input signal u(s) is segmented into Z segments of the same time-span. The subsequent equation frequency domain is changed from time domain as,

Uz(w) = Cz(w) + Nz(w), for  $0 \le z \le Z$  (3) Where Z is the segment key and Uz (w), Cz (w), Nz (w) are the Fourier magnitude taken from equation (1).If an estimate of noise continuum NNz can be obtained, then the speech CCz can be get from Uz

$$CCz(w) = Uz(w) - \alpha NNz(w)$$
<sup>(4)</sup>

In noise spectrum, the noisy speech signal is estimated in the input signal. Voice activity detector is used to find the quiet position in single channel speech enhancement. Here noise is imagined to be short, so that noise from quiet frames can be used to remove noise from speech frames. The parameter a determines the degree of noise subtracted from the noisy signal. For full noise subtraction, a=1 and for over-subtraction a>1 [5].



Figure 4 Block diagram of spectral subtraction

Ambient noise and sound with microbes undergo spectral subtraction in which the output is a clean sound that comes only from the microbes, without any hint of sound from the environment or surrounding. The process follows feature extraction.

In order to increase the accuracy of the recognition, the best features that represent the acoustic signal must be obtained. To obtain the best parametric representation of the input signal, Mel Frequency Cepstral Coefficient is used, and its block diagram is shown in Figure 5. MFCC consists of performing inverse Discrete Fourier Transform on the logarithm of the magnitude of the output of the Mel Filter Bank section.

Finite Impulse Response (FIR) was obtained using Equation (5)

$$H(z) = 1 - \alpha z^{-1}, 0.9 \le \alpha \le 1.0 \tag{5}$$



Figure 5 Block diagram of mel frequency cepstral coefficient

Equation (6) and (7) shows the discrete time domain representation of Hamming window function and Discrete Fourier Transform.

$$h[n] = \begin{cases} 0.54 - 0.46\cos(2\pi n/N), & 0 \le n \le N \\ 0, & otherwise \end{cases}$$
(6)

$$X(k) = \sum_{n=0}^{N-1} x(n) e^{-j2\pi k n/N}, 0 \le k \le N-1$$
 (7)

The spectral magnitude of the speech signal can be obtained by using equation (8).

$$|X(k)| = \sqrt{(Re(X(k)))^2 + (Im(X(k)))^2}$$
 (8)

Equation (9) shows how to calculate Mel(f), used to convert linear scale frequency into Mel scale frequency.

$$Mel(f) = 2595 \log_{10}(1 + \frac{f}{700})$$
 (9)

The speech signal input of the system is processed in overlapping frames of 100 signal values each at a sampling frequency of 10 kHz over 10ms of speech per frame. The feature vectors are then derived from each frame through different processes such as pre emphasis, Windowing, MFCC analysis and computation.

#### 2.3 Training System

For the training system section, the recorded sound serves as the input. The input is processed in this section and the system is trained using the fuzzy neural network architecture to improve the accuracy of the program. Specifically, the Architecture of Adaptive Neuro-Fuzzy Inference System (ANFIS) which is shown in Figure 6 is used.

The database for the network must be comprised of sufficient data examples. For disease identification, a total of 450 sound recording samples were used. For the system, there are three inputs which correspond to the recorded sonic response of the three microbes of interest and an output which is the index. An index result of 1 represents Xanthomonas oryzae detection, 2 for Magnaporthe oryzae and 3 for Thanatephorus cucumeris. There are seven membership functions for each input therefore the system has a total of 343 rules.



Figure 6 Architecture of Adaptive Neuro-Fuzzy Inference System (ANFIS)

For the system training, the ANFIS toolbox in MATLAB is used. After 389 epochs, the training had stopped at it had reached a mean error equal to 1.1458e-13 which is below the acceptable 0.1 mean error.

#### 2.4 Result

The result section will generate a PDF report based on the analysis of the system and will consist the following:

For Disease Identification:

- Disease Identified
- Local names of the disease
- Symptoms
- When it occurs
- Where it occurs
- Cure of rice plant in different stages



Figure 7 Generated PDF recommendations for magnaporthe oryzae

## **3.0 SOFTWARE DESIGN**

## 3.1 Rice disease identification using Fuzzy Neural Network Implemented in MATLAB Software

The process of rice disease identification is detailed as follows: First, the frequency of the microbes in the leaves of the rice plant will serve as the input of the system. Frequent movement of microbes will be collected using an electret microphone observed in an anechoic chamber. The sound recording will be processed using MATLAB software and will undergo several stages to achieve accurate result. Based on the result, the program will generate a report in PDF format.

The MATLAB will serve as the Integrated Development Environment (IDE) for signal processing. This process includes recording system, sound enhancement, feature extraction, database and fuzzy neural network.

The neural network increases the accuracy of the sound processing system. Neural networks and Fuzzy logic have some common features such as distributed representation of knowledge, model-free estimation, ability to handle data with uncertainty and imprecision etc. Fuzzy logic has tolerance for imprecision of data, while neural networks have tolerance for noise.

## 4.0 EXPERIMENTS AND RESULTS

### 4.1 Result of Database Collection

The database consists of the microorganisms namely: Xanthomonas oryzae, Magnaporthe oryzae and Thanatephorus cucumeris acquired from the laboratory of IRRI. Using the anechoic chamber, the frequency of 9 different concentrations of microorganisms (50 trials of first concentration of Magnaporthe oryzae with 50000 spores per 50 milliliters, 50 trials of second concentration of Magnaporthe oryzae with 100000 spores per 50 milliliters, 50 trials of third concentration of Magnaporthe oryzae with 150000 spores per 50 milliliters, 50 trials of first concentration of Thanatephorus cucumeris with 50000 spores per 50 milliliters, 50 trials of second concentration of Thanatephorus cucumeris with 100000 spores per 50 milliliters, 50 trials of third concentration of Thanatephorus cucumeris with 150000 spores per 50 milliliters, 50 trials of first concentration of Xanthomonas oryzae 109 series fold of cells by 10 milliliters, 50 trials of second concentration of Xanthomonas oryzae 108 series fold of cells by 10 milliliters, 50 trials of third concentration of Xanthomonas oryzae 107 series fold of cells by 10 milliliters) were recorded and fed to the program as input. Variability in numbers of the sound per trial is due to the availability of the microorganisms that is available in the laboratory. Each sound undergoes two sound processing techniques: sound enhancement and feature extraction. All the features of the processed images are saved as a Matlab Workspace (.mat) and as an excel document (.xlsx) for backup.

The plots of Xanthomanas Oryzae, Thanatephorus Cucumeris, and Magnaporthe Oryzae in frequency domain are shown in the figure 8.

It can be seen from Figure 8, that the three microorganisms' frequency response are spread out to a broad spectrum from 20 to 120 kHz. For the three microorganisms, (a) Xanthomanas Oryzae, (b) Thanatephorus Cucumeris, and (c) Magnaporthe Oryzae, noticeable increase in power amplitude was noticed in specific frequencies as follow: For (a) 10,15,19,23,45,55,75,90 kHz (b) 3,8,14,17,45,54,78,88 kHz and (c) 2,6,12,17,38,44,77,91 kHz.



**Figure 8** (a) Power spectrum plot Xanthomanas Oryzae (b) Power spectrum plot of Thanatephorous Cucumeris (c) Power Spectrum plot of Magnaporthe Oryzae (d) Combination of Plots of Recorded Sound produced by the three microorganisms.

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### 4.2 Result of Disease Identification

The samples with inoculated diseases were obtained from experimental nurseries of IRRI. Thirty samples of each microorganism for disease identification testing were collected by the supervising scientist of IRRI. Each sample was given a special mark for identification by the supervising scientist. Samples of varying concentration of the microorganisms are then placed inside the acoustic chamber for the recording of the sonic response of each microbe. After 30 seconds the software included in the developed system will output a result, which identifies the detected disease. Figure 9 shows the result of the rice plant disease identification using the developed system and the manual visual inspection through electronic microscope by the supervising scientist.

The graph below shows the accuracy of the developed system against the manual electronic microscope ocular inspection made by the experts and scientist of IRRI. From the graph, the plant disease Xanthomonas Oryzae got the lowest recognition accuracy at 93.33%, while the Magnaporthe Oryzae got the highest recognition accuracy at 100%.

From observations, it was inferred that some of the errors might resulted from corrupted input samples as well as insufficient number of samples at different concentration in the database.





## 4.2 Disease Identification Training Data, Testing Data, Training Error

The training data set used for the fuzzy system contains an array of input and output. The input is the feature extracted from MFCC and is arranged as column vectors, while the output is placed in the last column vector. To best model the inputted training data in the fuzzy system, membership function parameters are adjusted. Figure 10 shows disease identification testing data plot. From the plot the data from the bottom represents the training error, while the ones of the top represent the checking error. The Adaptive Neuro-Fuzzy Inference System chooses the model parameters associated with the minimum checking error (just prior to this jump point).



Figure 10 Disease identification testing data plot

## **5.0 CONCLUSION**

The system had successfully recorded the sonic response of the bacteria, Xanthomonas oryzae, Magnaporthe oryzae, and Thanatephorus cucumeris by triggering it through an artificial sound produced by an audio frequency generator with frequency range from 20 to 120 kHz. It was found out that the three microorganisms' frequency response is spread out to a broad spectrum. Distinct power variation recorded frequencies was at (a) 10,15,19,23,45,55,75,90 kHz for Xanthomonas orvzae (b) 3,8,14,17,45,54,78,88 kHz Magnaporthe oryzae, and (c) 2,6,12,17,38,44,77,91 kHz Thanatephorus cucumeris. The disease identification testing of the system resulted to a recognition accuracy of the bacteria, Xanthomonas oryzae, Magnaporthe oryzae, and Thanatephorus cucumeris, which are 93.33%, 100% and 96.67% respectively.

With the given result, the system could therefore be further improved to increase the accuracy of disease identification through adding of more input microbe samples with a more varied concentration of spores per ml to the system's database.

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