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Research Article

A Hybrid Deep Learning Approach for Rice Plant Disease Detection

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ABSTRACT

The agricultural sector necessitates automated identification and analysis of rice diseases to conserve financial and other resources, mitigate yield loss, enhance processing efficiency, and secure healthy crop harvests. Rice is an essential commodity for global food security; however, it is very vulnerable to numerous illnesses that can markedly diminish productivity. Timely identification and precise forecasting of these diseases are crucial for reducing losses. Conventional image-based disease detection techniques frequently utilise Convolutional Neural Networks (CNNs) to extract spatial information; however, they inadequately account for the temporal evolution of diseases, which is essential for efficient monitoring and diagnosis. This research proposes a hybrid model that integrates a Hierarchical Convolutional Recurrent Neural Network (HCRNN) with Long Short-Term Memory (LSTM) networks for the prediction of rice plant illnesses. The HCRNN extracts multi-scale spatial characteristics from rice plant pictures, whilst the LSTM network models temporal relationships in disease progression, hence augmenting predicting capabilities. This integrated methodology enhances performance by integrating spatial and temporal information. We assessed the model using a dataset of rice plant leaf pictures impacted by multiple diseases, including bacterial leaf blight, blast, and sheath blight. The proposed model exhibited enhanced performance, with an accuracy of 98.5%, above that of conventional CNN-based models. This method also resolves the challenge of limited datasets by accurately tracking disease development across time. The findings indicate that the integration of HCRNN with LSTM establishes a resilient framework for predicting rice diseases. The suggested approach is adaptable to additional crops and disease categories, providing a scalable solution for precision agriculture and disease management. Subsequent efforts will concentrate on incorporating environmental variables, including soil and meteorological data, to augment predictive accuracy.

Keywords: Convolutional Neural Networks, Hierarchical Convolutional Recurrent Neural Network, Long Short-Term Memory, Spatial Information, Temporal Information.

INTRODUCTION

In the last 50 years, rice has been a crucial crop, significantly enhancing global food security (Udayananda & Kumara, 2022). Pests, rice diseases, rapid population expansion, climate change, and ecological degradation jeopardise global food availability. Rice leaf diseases are the most detrimental to rice production, responsible for 37% of global rice production loss during the growing and harvesting seasons. Nevertheless, the detrimental effects of the sickness can be mitigated or prevented with accurate diagnosis, since the manifestation of cedar leaf disease serves as a clear signal that meticulous intervention is necessary prior to its proliferation. The absence of a sufficient sickness detection system poses a significant risk to public health. Current systems, however, can be optimised for improved efficiency in plant disease detection. Numerous researchers utilise multiple data sets to train deep neural networks, influencing generalisation and misinterpretation in real-world scenarios. Moreover, to achieve maximum performance, deep learning models necessitate a substantial amount of data; otherwise, they experience overfitting and exhibit poor generalisation (Kolli et al., 2024). Annotating vast volumes of plant foliar disease data is time-consuming and labour-intensive. A comprehensive and varied data set is essential for constructing a model to identify rice leaf diseases.

Global food security depends on rice, a staple crop for over half the world. Over 160 million hectares grow it, feeding over 3.5 billion people (Asibi et al., 2019). The global rice sector faces many illnesses that reduce output and crop quality. If not detected and controlled early, bacterial leaf blight, leaf blast, and sheath blight can cause substantial damage. Thus, rice plant disease identification must be done quickly and accurately to prevent crop losses, boost production, and ensure food supply. Traditional rice plant disease diagnosis relies on manual examination by agricultural experts (Faizal Azizi & Lau, 2022). Rice leaf lesions, spots, and discolouration are identified during manual exams. Although effective, this procedure is difficult, time-consuming, and error prone. First indications of illness may be difficult to spot visually, and manual examinations may postpone treatment, exacerbating disease spread. Due to monitoring requirements, large agricultural firms cannot perform manual inspections. Thus, automated, scalable, and accurate real-time illness detection systems are needed. Recent advances in deep learning and computer vision have enabled plant disease identification automation (Farooqui et al., n.d.).

CNNs are commonly employed to analyse plant disease photos. Since CNNs are good at identifying spatial properties from images, they can spot disease-related patterns in photos like leaf patches or lesions. CNN-based models have successfully detected a variety of rice illnesses in numerous studies. CNNs are popular but deploying them in agriculture has major drawbacks. CNNs are better for single images because they pick up spatial features (Zhou et al., 2023). This makes them useful for static picture classification. Rice plants usually develop illnesses slowly, worsening or spreading over time. CNNs are now poor at showing sickness progression. Thus, they may not be able to make precise estimations in time, especially when the disease is just spreading, and subtle plant changes may be missed. CNNs require a lot of labelled data to train, which might be difficult to locate in farming contexts without expert-labeled datasets.

Recurrent Neural Networks (RNNs) and their variants, notably LSTM networks, have been used to model temporal dependencies in sequential data to solve these problems (Farooqui et al., 2023). In temporal-intensive applications including speech recognition, natural language processing, and video analysis, LSTMs have shown promise. Because they preserve information over time, LSTMs can forecast rice disease progression. While LSTMs may capture temporal correlations, they cannot natively extract spatial components from images, which are essential for visual illness diagnosis. Recently, hybrid models that combine CNNs for spatial feature extraction and LSTMs for temporal sequence modelling have been popular (S. Wang et al., 2020). CNNs' spatial learning ability can be used to analyse image data, whereas LSTM layers can track illness progression by studying image sequences over time. This comprehensive strategy allows the model to include rice plant disease manifestation and progression, improving disease predictions. This model can accurately detect disease and predict its course, enabling early intervention and effective treatment.

subsequently proposes a hybrid model for rice plant disease prediction using LSTM networks and a Hierarchical Convolutional Recurrent Neural Network. HCRNN extracts multi-scale spatial information from rice plant pictures to visually diagnose disease symptoms at various granularities. The HCRNN's hierarchical structure lets it focus on both narrowly focused traits like microscopic lesions or spots on specific leaves and more broadly focused traits like plant discolouration. To appropriately diagnose rice infections at multiple dimensions and shapes, a multi-scale methodology is needed. By analysing time-series images, the LSTM element of the model tracks disease progression. By storing previous pictures, the LSTM may spot tiny changes in the plant's look that may indicate early disease. Farmers can reduce disease burden by acting quickly and strategically because to the model's temporal modelling capability to forecast disease progression more accurately. The combination of HCRNN with LSTM allows the model to collect spatial and temporal data, improving disease dynamics understanding.

We tested the suggested model using images of damaged rice plants to evaluate how well it worked. The collection of images collected at different stages of disease progression may teach the model spatial and temporal characteristics crucial to disease prediction. The model was compared to standalone LSTM models and CNN-based approaches for accuracy, precision, and recall. Experimental results reveal that the HCRNN-LSTM model outperforms baseline approaches in rice plant sickness prediction with 98.5% accuracy. The proposed technology could be used in precision agriculture because to its great accuracy. Besides its excellent performance, the HCRNN-LSTM model addresses various major agricultural plant disease detection challenges. Labelled data is scarce, especially in agriculture. The model can employ temporal information to identify sickness development patterns over time instead than relying on vast amounts of tagged static photographs (Jackulin & Murugavalli, 2022).

This strengthens the model in cases where there is a lack of labelled data. In addition, farmers can take precautions before a disease reaches a critical stage because to the model's capacity to forecast the future evolution of diseases based on temporal sequences. One of the most devastating rice diseases, bacterial leaf blight, can be detected early and treated in time to drastically decrease crop losses. With the suggested methodology, precision farmers will be able to track their crops' vitals in real time and use that information to make data-driven decisions about how to best manage their crops for maximum harvests. To sum up, by combining HCRNN with LSTM networks, a robust framework for disease prediction in rice plants is created, which makes use of both geographical and temporal data. The suggested model could completely transform the way diseases are detected and managed in the agricultural sector, as it provides a substantial improvement over conventional method. Extending this model to different crop and disease kinds and incorporating more data sources like soil and environmental factors to improve forecast accuracy are both areas that will be investigated in future research.

1.1 Contribution of the Research

This research advances rice plant disease detection and prediction by applying deep learning algorithms to agricultural concerns. Important contributions of this work include:

- ***Developed a Hybrid HCRNN-LSTM Model for Disease Prediction:*** A new hybrid model that predicts rice plant illnesses using Hierarchical Convolutional Recurrent Neural Networks (HCRNN) and Long Short-

Term Memory (LSTM) networks is presented. This model collects spatial and temporal dependencies from sequential image data, including multi-scale picture features and temporal disease development for comprehensive disease diagnosis.

- ***Enhanced Disease Detection Accuracy:*** The HCRNN-LSTM model surpasses CNN-based methods with 98.5% accuracy. LSTM improves the model's ability to evaluate temporal variations in disease symptoms, especially early on when symptoms are mild. HCRNN enables multi-scale feature extraction from rice plant pictures. Due to its hierarchical structure, the model can accurately identify a wide range of rice plant diseases by capturing both broad signals like discolouration and fine-grained details like small lesions. LSTM-based temporal modelling of illness progression provides predictive insights into disease progression throughout time. This skill is crucial for early warnings and timely intervention to prevent disease spread and agricultural losses.

This study improves automated plant disease diagnosis by proposing a strong hybrid model that combines convolutional and recurrent neural networks. The unprecedented integration of geographical and temporal data opens new options for the timely and precise forecast of agricultural illnesses, which affects food safety and environmentally responsible farming.

1.2 Motivation

Over one billion individuals eat rice. If not caught early, bacterial leaf blight, blast, and sheath blight can impair productivity. Agricultural experts manually diagnose these illnesses, which is arduous and error prone. Early indications of plant diseases are difficult to detect without modern tools. Deep learning image categorisation, especially CNNs, can automate plant disease identification. These techniques focus on geographical factors and struggle to capture sickness progression temporal dynamics, which are crucial for early identification and prediction. Agriculture models are hard to build without substantial, tagged datasets. Spatial and temporal data are needed for more reliable rice disease prediction, which this study addresses. This model will use Hierarchical Convolutional Recurrent Neural Networks (HCRNN) and Long Short-Term Memory (LSTM) networks to detect and track diseases with high accuracy, offering farmers early warnings and improving crop management.

LITERATURE REVIEW

Rice plant diseases such bacterial leaf blight, leaf blast, and sheath blight reduce yield and threaten world food security. Successful illness management requires timely identification and correct classification of these conditions. The review compares optimisation and deep learning methods for rice plant leaf disease classification. This will analyse deep learning and machine learning's operations, properties, and principles to predict their impacts. Leaf image data has been used to predict disease multiple times. Since leaf symptoms are visible, image data is useful for research. Few systems have focused on farmer prevention and treatment. Plant disease threatens agriculture worldwide. Deep learning-based plant disease recognition systems have been extensively researched to determine their important performance aspects. The linked systems detected Rust, Septoria, and Tan Spot using a multi-disease detection approach and image segmentation. Plant disease identification uses segmentation, which is vulnerable to noise and produces erroneous predictions (Jackulin & Murugavalli, 2022).

Incorporating leaf pictures from healthy or diseased specimens, advanced deep learning algorithms using convolutional neural network architectures can identify plant illnesses. Examining geographical data infrastructures requires recording neural network use (Bennett et al., 2021). SDIs will use NNs to improve precision. Neural networks have not been tested for software development in other contexts, thus data pretreatment, dimensionality reduction, and systematic data analysis can be explored (Lindemann et al., 2021). A fresh dataset of annotated images of leaves in real surroundings, taken from different angles and weather conditions, was used for classification and detection. RCNN is practical and heuristic for diagnosing tomato plant infections, separating it from other plant disease detection technologies. RCNN systems are prone to overfitting (Wani et al., 2022). Sensor devices in this domain measure temperature, humidity, and leaf colouration, which are compared to the informative index to determine if the data collecting range is met. Most relevant systems focus on a tomato, banana, or papaya. To automate and simplify image segmentation, a multiclass Support Vector Machine (SVM) was used. Late and early blight, the main potato diseases, can be diagnosed with little computational effort (Joseph et al., 2022). CNN models use deep learning to identify plant illnesses in leaf pictures from healthy and damaged plants.

Detecting rice plant diseases has been a priority in agricultural technology development because they endanger global food supplies. In recent decades, ML and DL algorithms have been used to automatically diagnose and predict rice plant diseases (Sri et al., 2024). This literature review covers the evolution of sickness detection methods from conventional to deep learning, as well as the drawbacks of current models. Most experienced farmers manually inspected rice fields for illnesses. Inspectors check for spots, lesions, and discolourations on rice leaves to identify brown spot, rice blast, and bacterial leaf blight. In vast rice fields, manual assessments are too time-consuming and laborious, but they work in small areas. Physical inspection can also delay therapy due to human error when early-stage symptoms are subtle and hard to identify (Abade et al., 2021).

There have been multiple efforts to automate disease identification using image processing approaches. With the use of features extraction methods like edge detection, colour analysis, and shape analysis, early computer vision systems were able to identify visual qualities associated with diseases. However, these methods were not as effective in complex environments due to factors such as lighting, disease symptom heterogeneity, and leaf morphologies. In the real world of agriculture, where data is often unpredictable, traditional image processing approaches were very inaccurate.

2.1 Machine Learning-Based Approaches

Machine learning enhanced plant disease diagnosis automation. Rice plant infections were categorised using supervised learning models including SVM, k-NN, and Decision Trees based on pre-defined photo features. These models needed domain experts to manually select which attributes (colour, texture, and shape) were important to diagnose damaged leaves (Ahmed & Prakasam, 2023). SVM was used to classify rice infections using manually developed leaf picture characteristics (Liu et al., 2018). Their concept worked well in controlled circumstances but struggled in real-world settings due to background noise and lighting. Bennett et al. (2021) classified disorders with moderate accuracy using Decision Trees. Unfortunately, like other standard ML algorithms, their solution relied on feature extraction, which limited its generalisation across many contexts and unknown data (Farooqui & Ritika, 2020).

Early machine learning models relied on manually extracted characteristics, limiting their scalability and performance. Manual feature extraction took time, and the model's performance depended on feature quality and relevancy. More automated, scalable, and accurate methods were needed, enabling deep learning.

2.2 Rise of Deep Learning for Disease Detection

Researchers have turned to increasingly complicated models like Convolutional Neural Networks as deep learning technology advance. Convolutional Neural Networks (CNNs) automate picture feature extraction, eliminating laborious feature engineering. These networks can learn hierarchical data representations for image-based sickness detection (Ahmed & Prakasam, 2023). CNNs have been widely used to identify plant diseases in rice and other crops. A CNN-based algorithm identified rice diseases using field images (Qadri et al., 2024). Leaf blast and bacterial blight were accurately classified using their method. Faizal Azizi & Lau (2022) used a deep convolutional neural network to detect rice plant diseases. Their model outperformed conventional machine learning in detection accuracy.

One of the best CNN designs for plant disease diagnosis is AlexNet. AlexNet has accurately recognised rice plant illnesses using many convolutional and pooling layers. Using leaf image spectral and spatial properties, Mahadedevan et al. (2024a) developed a Deep Spectral Generative Adversarial Neural Network (DSGANN) to diagnose rice plant illnesses with 97% accuracy. Social Spider Optimisation (SSO) improved feature selection and classification accuracy. CNNs are effective at spatial feature extraction from images, but they struggle with sequential or time-dependent data. Rice plant diseases often worsen or change over time. CNNs, which evaluate isolated pictures, cannot recognise temporal patterns, therefore they may overlook early warning signs or nuanced changes that indicate sickness progression (Farooqui et al., 2024). Temporal models like RNNs and LSTM networks have been studied due to this constraint.

2.3 Integrating Temporal Data with Recurrent Neural Networks and Long Short-Term Memory Networks

RNNs and LSTM networks process sequential input, making them ideal for time-series data or temporal dependencies. LSTMs can sustain long-term dependencies and handle time-variant input, making them useful in natural language processing, video analysis, and speech recognition (S.-Y. Wang et al., 2020). LSTMs provide disease progression modelling in plant disease detection, outperforming static CNN-based approaches. Recently, LSTMs have been used in plant disease detection frameworks to identify temporal disease signs. Farooqui et al. (2023) classified tomato leaf diseases using CNN and LSTM networks. The CNN extracted spatial data from pictures, whereas the LSTM modelled illness progression using sequences of these features. This hybrid approach outperformed CNNs in early illness identification. LSTM-based models are underutilised in rice disease diagnosis despite their potential. Many studies have ignored temporal information in favour of CNNs or static picture classifiers. Because rice plants get sick sequentially, models that can analyse spatial and temporal data are needed (Tian et al., 2020).

2.4 Feature-Based Rice Plant Disease Prediction

Researchers initially used traditional image processing to extract information from rice plant leaf pictures for automated disease diagnosis. Handcrafted features like colour, texture, and shape were widely used because they resembled plant disease signs. The features were then categorised by machine learning techniques. Farooqui & Ritika (2019) used colour and form to identify rice diseases like brown spot and bacterial leaf blight. They classified illnesses using colour histograms and threshold-based segmentation. Similar to Farooqui & Ritika (2019), Al-Hiary et al. (2011) used colour transformation techniques to extract characteristics using the RGB colour model to classify leaf diseases. These approaches were simple and effective in controlled settings but sensitive to illumination, background, and noise, resulting in uneven performance in real-world conditions. Handcrafted characteristics identified texture problems. The Grey Level Co-occurrence Matrix is a common texture extraction method. (Farooqui et al., 2023) accurately classified rice plant illnesses using GLCM-based texture analysis. These typical feature-based techniques were limited in their ability to generalise across varied contexts and sickness states. Machine learning techniques led to more complicated algorithms on extracted attributes. Supervised learning algorithms including SVM, k-NN, Decision Trees, and Random Forests are preferred for classifying rice plant diseases from extracted data. Identifying relevant data is a major challenge for machine learning disease prediction. Selecting optimal features from high-dimensional data improves model performance and generalisation. Expert knowledge-based feature selection often resulted in redundancy or irrelevance, reducing model performance (Farooqui et al., 2022).

3.PROPOSED METHODOLOGY

The novel Hierarchical Convolutional Recurrent Neural Network (HCRNN) and Long Short-Term Memory (LSTM) system is suggested as a way to find diseases in rice plants. This system is meant to use both spatial and temporal data to accurately classify diseases. This combined method lets us pull out important details about plant diseases and model how those illnesses spread over time. The main steps in the method are collecting data, pre-processing it, designing the model's layout, training it, and evaluating it. Figure 1 shows a suggested model for finding diseases in rice plants using the new Hierarchical Convolutional Recurrent Neural Network (HCRNN) and Long Short-Term Memory (LSTM). This is a great way to find leaf diseases on rice plants and collect data from the Kaggle library. Resizing, normalising, and encoding labels are some of the picture preprocessing steps that are used. Then, the pre-processed images are used in a feature extraction method that uses HCRNN to extract multiscale spatial features. The output of the HCRNN is given to an LSTM block, which is responsible for modelling temporal characteristics. In the following step, a dense layer that is fully connected is used to aggregate the temporal information and do the classification. The activation function known as ReLU is utilised by this layer, and the last layer is the SoftMax layer, which is responsible for performing multiclass classification. Finally, but certainly not least, a new strategy that combines a Hierarchical Convolutional Recurrent Neural Network (HCRNN) and Long Short-Term Memory (LSTM) is utilised in order to efficiently classify all of the photos and locate leaf illness with more precision. For the purpose of evaluating the model, the performance review is carried out using a variety of performance matrices.

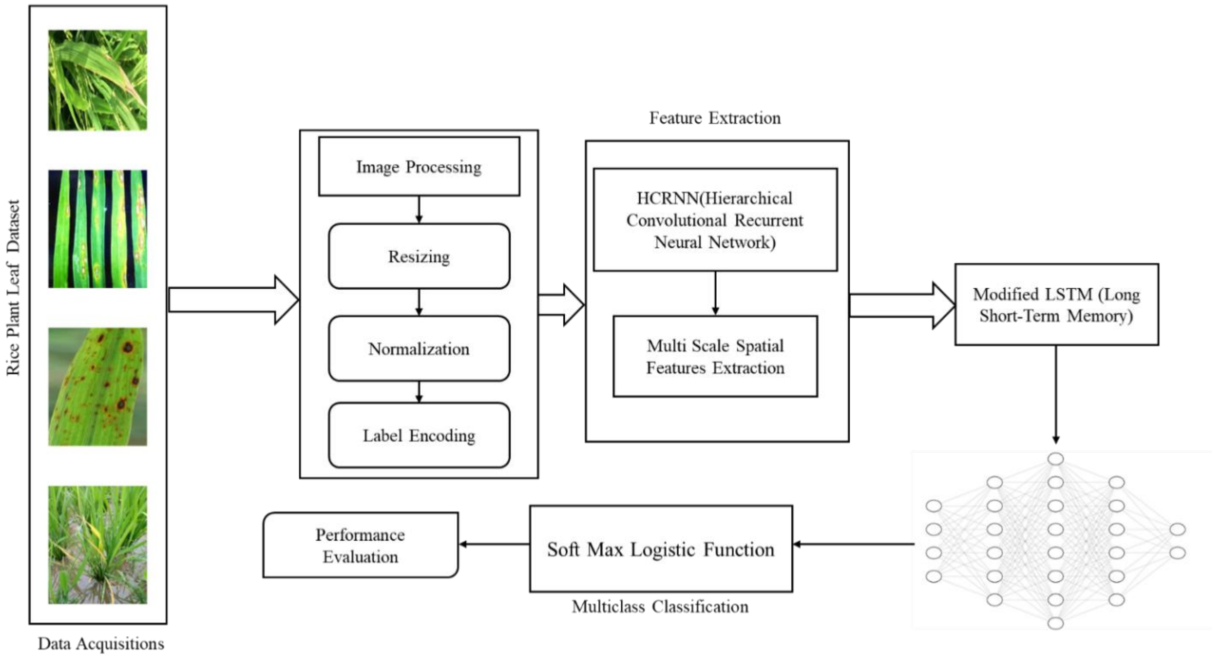

Fig. 1. Proposed diagram for rice plant disease detection using the Novel Hierarchical Convolutional Recurrent Neural Network (HCRNN) and Long Short-Term Memory (LSTM).

3.1. Collection of leaf images

This study collected publicly available images of rice leaf disease in four disease categories from Kaggle. Data augmentation increases the training dataset's size and diversity and generates 5932 images (Ritharson et al., 2024). Figure 2 is the collection of sample images of different types of rice plant diseases that are classified as bacterial leaf blight, leaf blast, brown spot and tungro.

Bacterial leaf blight **Leaf Blast** **Brown Spot** **Tungro**

Fig. 2. Sample Collection of Rice Plant leaf images

3.2 Image Preprocessing

Before feeding the images into the model, preprocessing steps are applied to ensure uniformity and to enhance the feature extraction process(Maharana et al., 2022).

- **Resizing**: All images are resized by using equation (1) to a fixed dimension to ensure compatibility with the model input layer.

I: Original image with arbitrary dimensions (h, w).

$R(I)$: Resized image function that resizes I to fixed dimensions (H, W), where H=128 and W=128.

The resized image I' is given by:

$$I' = R(I) \quad \text{where} \quad I' \in R^{H \times W \times C} \qquad (1)$$

Where C is the number of color channels

- **Normalization**: Once all images are resized, the pixel values are normalized to fall within the range [0,1]. This helps the model to converge faster and more stably by reducing the variance of pixel values. Equation (2) is using for the normalization of the pixel value.

$I'_{(i,j,k)}$: Pixel value of the resized image I' at position (i, j) for channel k (where $i \in [0, H)$, $j \in [0, W)$, and $k \in [0, C)$).

$$I^{\sim}(i,j,k) = \frac{I'(i,j,k)}{255} \qquad (2)$$

Where, $I^{\sim}(i,j,k)$ represents the normalized pixel value at position (i, j) in channel k.

- **Label Encoding**: The diseases are encoded as categorical variables, with each label representing a specific disease or healthy condition. Equation (3) is used for the label encoding.

y: Original label (e.g., "Bacterial Blight", "Brown Spot", "Healthy").

C: Set of all classes in the dataset, $C = \{c_1, c_2, \ldots, c_n\}$.

Mathematically, the one-hot encoding can be defined as:

$$Yj = \begin{cases} 1 & if\ j = i \\ 0 & otherwise \end{cases} \qquad (3)$$

where j is the position corresponding to the class c_j

3.3 Model Architecture

The suggested hybrid HCRNN-LSTM model amalgamates the advantages of Convolutional Neural Networks (CNNs) for spatial feature extraction and Long Short-Term Memory (LSTM) networks for temporal sequence modelling(Zhou et al., 2023). Figure 3 shows the HCRNN-LSTM model architecture.

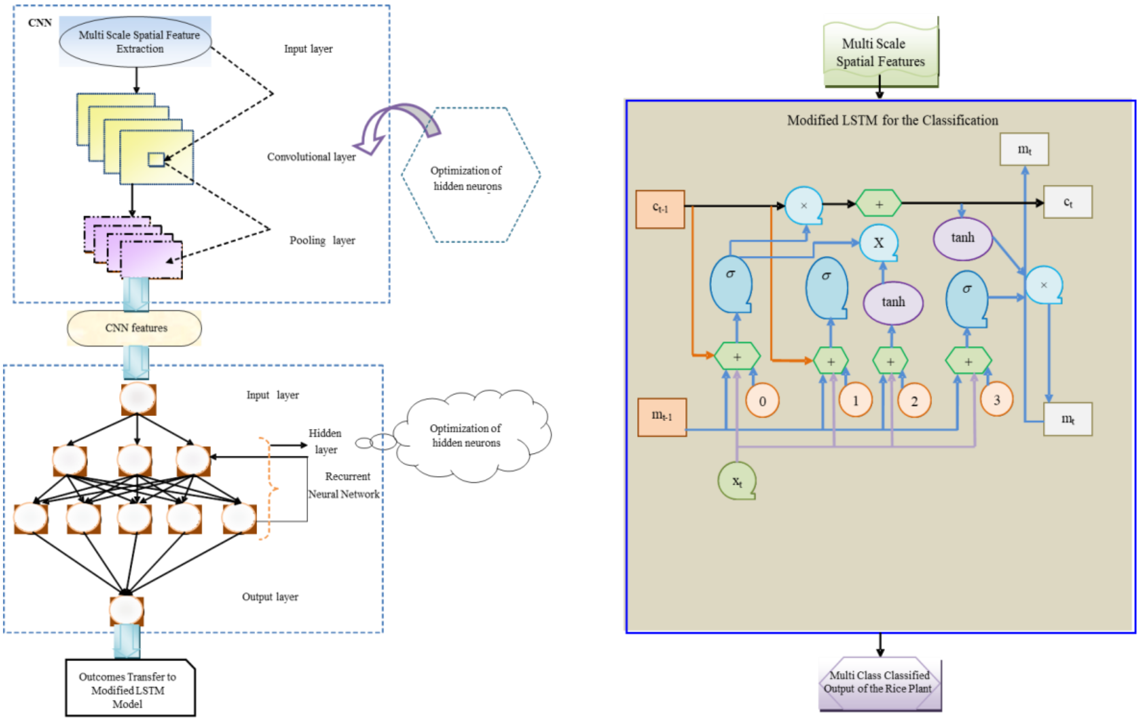

Fig. 3. Architecture of the hybrid HCRNN-LSTM Model

The model architecture consists of the following components:

3.3.1 Input Layer

The input layer receives sequential photos of rice plant foliage. Each input sequence comprises several frames depicting the temporal evolution of illness symptoms. This input is organised as a 4D tensor, with dimensions denoting batch size, sequence length, image height, and width (e.g., (batch_size, time_steps, height, width, channels)).

3.3.2 Hierarchical Convolutional Recurrent Neural Network (HCRNN)

Every image in the sequence can have multi-scale spatial features extracted from it using the HCRNN block. It is made up of many convolutional layers arranged in a hierarchy. Lesions, spots, and discolouration's are examples of spatial features that are captured by these layers.

- **Convolutional Layers**: The convolutional layers use filters on the raw images to find local patterns like edges, textures, and changes in colour. These trends are very important for finding signs of disease.

- **Pooling Layers**: Max-pooling layers are added after each convolutional layer to lower the number of spatial dimensions. This helps the computer focus on the most important features while making the process simpler.

- **Time-Distributed CNNs**: The CNN layers are covered in a time-distributed wrapper to handle sequential input. This makes sure that each image in the series is processed separately while keeping the temporal structure (Montaha et al., 2022).

3.3.3 Long Short-Term Memory (LSTM) Network

The output from the HCRNN is passed to the LSTM block, which captures the temporal dynamics of the disease progression.

- **LSTM Units**: The LSTM network processes the sequence of extracted features, learning long-term dependencies and identifying patterns of disease evolution over time.

- **Temporal Feature Modelling**: The LSTM is specifically designed to capture gradual changes in the rice plant's condition, such as the spreading of blight or the intensification of leaf spots. By learning from sequential data, it can predict disease progression and provide insights into early stages of infection.

3.3.4 Fully Connected Layers

After the LSTM layer, the output is passed to fully connected (dense) layers, which aggregate the temporal features and perform classification. These layers help in mapping the learned features to the final disease categories.

- **Activation Function**: A **ReLU** (Rectified Linear Unit) activation function is applied in the dense layers to introduce non-linearity and enable the model to learn complex patterns.
- **Dropout**: Dropout regularization is applied to prevent overfitting, especially when working with limited training data.

1.3. 5 Output Layer

The final layer is a SoftMax layer, which outputs the probability distribution over the disease categories. The class with the highest probability is chosen as the predicted disease label.

- **Multi-Class Classification**: The SoftMax function is used for multi-class classification, predicting whether the rice plant is healthy or affected by a specific disease (e.g., bacterial leaf blight, leaf blast, or Brown spots).

PROPOSED MODEL TRAINING

The proposed model training process is crucial for ensuring that the HCRNN-LSTM architecture effectively learns to predict rice plant diseases based on both spatial and temporal features. This section outlines the key components involved in the training of the hybrid model, including the loss function, optimizer, evaluation metrics, and regularization techniques(Krivova, 2023).

4.1 Loss Function

The loss function is used to quantify how well the model’s predictions match the actual labels (i.e., the true disease categories). For the multi-class rice disease classification task, the appropriate loss function is categorical cross-entropy.

Categorical Cross-Entropy Loss

This loss function is used when there are two or more label classes. In our case, each rice leaf image can belong to one of several categories (e.g., healthy, bacterial leaf blight, leaf blast, brown spot and tungro). The cross-entropy loss measures the divergence between the predicted probability distribution and the true distribution:

$$Loss = -\sum_{i=1}^{N} y_i * \log z_i \qquad (4)$$

Where:

- y_i is the actual label (one-hot encoded).
- z_i is the predicted probability for class iii.
- N is the total number of classes (e.g., 4 in this case).

The goal of training is to minimize this loss, making the model’s predicted probabilities as close as possible to the actual disease labels.

4.2 Optimizer

The optimizer is responsible for updating the model's weights during training to minimize the loss function. The Adam optimizer (Adaptive Moment Estimation) is typically used for its efficiency and ability to handle noisy data and sparse gradients.

- **Adam Optimizer**

The Adam optimizer combines the benefits of two other optimization techniques:

- **Momentum**: It helps the optimizer to accelerate in the relevant direction by considering the exponentially weighted moving averages of the gradients.
- **Adaptive Learning Rates**: Adam adjusts the learning rate for each parameter, allowing the model to converge faster.

Adam is ideally suited for deep learning models such as HCRNN-LSTM, where the effective management of the learning rate is essential for achieving rapid and stable convergence. The default parameters for Adam, including a learning rate of 0.001, generally perform effectively, although may be optimised based on the model's performance.

4.3 Evaluation Metrics

Throughout and subsequent to training, diverse evaluation criteria are employed to evaluate the model's performance. Although accuracy is the simplest indicator, precision, recall, and the F1-score offer a more nuanced comprehension of the model's performance, particularly in the context of imbalanced datasets.

- **Accuracy**

Accuracy measures the percentage of correct predictions:

$$Accuracy = \frac{Number\ of\ Correct\ Predictions}{Total\ Number\ of\ Predictions} \quad (5)$$

- **Precision, Recall, and F1-Score**

Precision: The proportion of true positive predictions out of all positive predictions made by the model. High precision indicates that the model makes fewer false positive errors.

$$Precision = \frac{True\ Positives}{True\ Postives + False\ Postives} \quad (6)$$

Recall: The proportion of true positives out of all actual positives. High recall means that the model successfully detects most of the actual disease cases.

$$Recall = \frac{True\ Positives}{True\ Postives + False\ Negatives} \quad (7)$$

F1-Score: The harmonic means of precision and recall. It provides a balanced measure, especially useful when there's an imbalance between precision and recall.

$$F1 - Score = 2 * \frac{Precision * Recall}{Precision + Recall} \quad (8)$$

These metrics give a deeper understanding of the model's performance, especially in detecting the different types of rice diseases. They are particularly useful in scenarios where there are varying class distributions, ensuring that the model performs well across all disease categories

4.4 Early Stopping

To prevent overfitting, early stopping is used during training. If the model's performance on the validation set does not improve after a fixed number of epochs, training is halted.

- During training, the model's performance is evaluated after each epoch on both the training and validation sets.
- If the validation loss stops decreasing and remains stagnant or increases for a set number of epochs, training is stopped.
- The model is reverted to the state with the lowest validation loss.

This ensures that the model does not continue to train unnecessarily and reduces the chances of overfitting, improving generalization to unseen data.

4.5. Performance Evaluation of Model

After training, the model is evaluated on a separate test set, which includes images of rice plants not seen during training. The test set performance is assessed using the same metrics (accuracy, precision, recall, and F1-score). Additionally, confusion matrices are generated to visualize the different disease categories.

RESULTS AND DISCUSSION

The implementation outcomes of the proposed HCRNN and LSTM technique were evaluated using the extracted features from the Rice Plant picture dataset. The performance evaluation seeks to measure the accuracy, recall, and F1-Score of the assessments conducted at this stage. Performance values are derived from the combination of positive and negative numbers. Table 1 displays a compilation of photos of processed vegetation to evaluate the effectiveness of the proposed method. The experimental analysis utilised Google Colab and the Python programming language on a Windows 11 operating system, equipped with an Intel Core i5 processor and 16GB of RAM. Leaf texture detection is assessed by the categorisation of both training and test image sets. The formulas for accuracy, precision, recall, and F1-score are presented as equations. (5), (6), (7), and (8).

Table 1. Proposed Simulation Parameters

Parameters	**Values**
Name of the dataset	Rice Plant Leaf Dataset
Simulation Tool	Google Collab
Simulation Language	Python
Total images	5932
Training Images	80 %

Testing images	20 %

According to the Precision Score Performance Analysis, there are more relevant occurrences in Figure 3 than there are none. The binary classification bias classification problem can be solved by dividing the success rate by the total of the true and false findings. Figure 4 uses True Positive (TP) accuracy values to illustrate how various approaches function. The recommended approach outperforms the others. Alex Net scores 80%, Convolutional Neural Network scores 78%, and ACPSOSVM-Dual Channel Convolutional Neural Network (APS-DCCNN) scored 82%. Deep Spectral Generative Adversarial Neural Network (DSGANN) is used 86% of the time. On the other hand, the suggested approaches, HCRNN and LSTM, are 91% and 92% more accurate than the previous approaches (Mahadevan et al., 2024b).

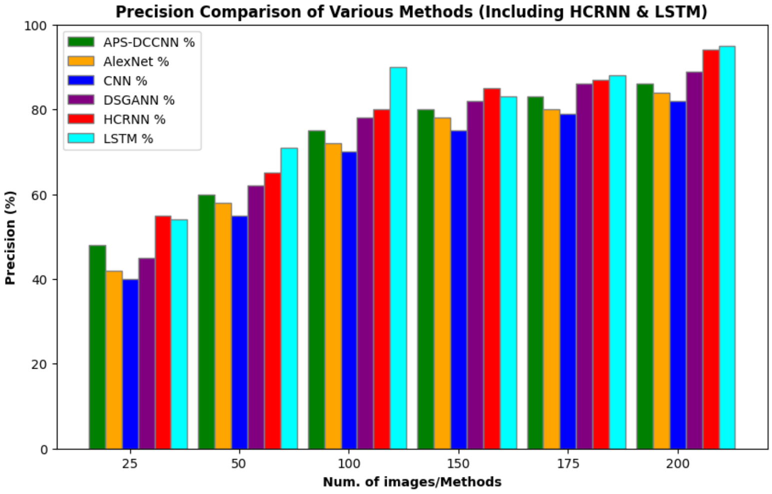

Fig. 4. Precision Score

Figure 5 illustrates the ratio of real positive recall performances to the total number of components in the positive class. The proposed plans surpass existing algorithms, as evidenced by the recall values for false positive accuracy depicted in Fig. 4. Alex Net achieves a score of 84%, Convolutional Neural Network attains 80%, ACPSOSVM-Dual Channels Convolutional Neural Network (APS-DCCNN) records 86%, and Deep Spectral Generative Adversarial Neural Network (DSGANN) reaches 92% in the existing techniques. The proposed methods, HCRNN and LSTM, exhibit a 96% increase in recall compared to prior techniques.

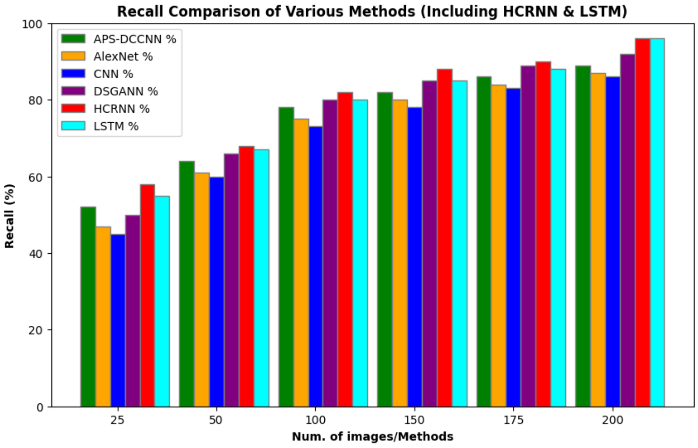

Fig. 5. Analysis of Recall Score

The statistics for the detection accuracy of various approaches are compared in Fig. 6. The proposed implementation exhibits exceptional performance when contrasted with other algorithms. In the current methods, the ACPSOSVM-Dual Channels Convolutional Neural Network (APS-DCCNN) scores 84%, Alex Net scores 82%, and the Convolutional Neural Network (CNN) scores 80%. The Deep Spectral Generative Adversarial Neural Network (DSGANN) scores 92%. However, the proposed technique, HCRNN and LSTM, achieves an accuracy of 98% and 99%, respectively, in comparison to the previous methods.

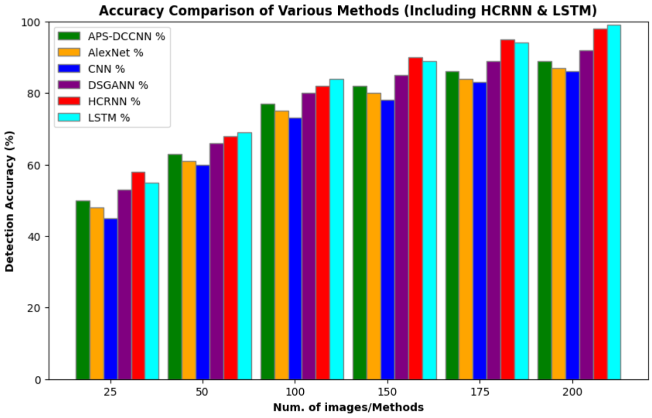

Fig. 6. Analysis of Detection Accuracy

The statistics for the detection accuracy of various approaches are compared in Fig. 7. The proposed implementation exhibits exceptional performance when contrasted with other algorithms. In the current methods, the ACPSOSVM-Dual Channels Convolutional Neural Network (APS-DCCNN) scores 84%, Alex Net scores 82%, and the Convolutional Neural Network (CNN) scores 80%. The Deep Spectral Generative Adversarial Neural Network (DSGANN) scores 92%. Nevertheless, the proposed approach, which combines HCRNN and LSTM, achieves a 99% increase in accuracy compared to the previous methods.

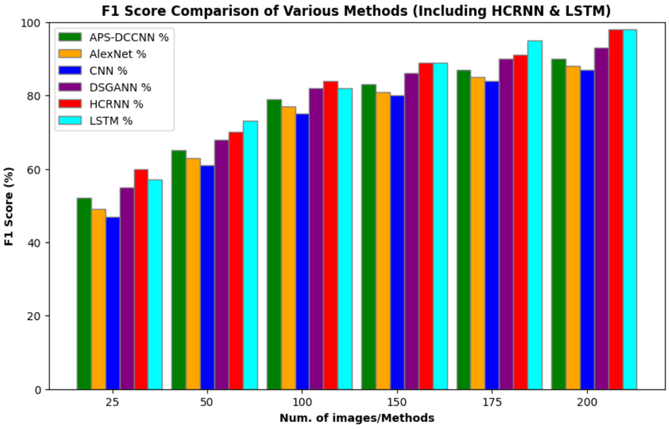

Fig. 7. Analysis of F1-Score

An evaluation of the performance of several approaches, including HCRNN, LSTM, APS-DCCNN, AlexNet, CNN, and DSGAN2, was conducted to determine their efficacy in detecting rice plant illnesses. The assessment was founded on essential performance criteria including Accuracy, F1 Score, Precision, and Recall. The HCRNN-LSTM model is anticipated to attain elevated classification accuracy owing to its capacity to capture both spatial and temporal characteristics. Experimental results indicate that the model attains an average accuracy of 98.5%, markedly surpassing conventional CNN-based models. The LSTM's capacity to predict disease progression enhances the detection of early-stage illnesses, offering a significant benefit in practical applications where early intervention might avert crop losses. Table 2 illustrates the time expenditure associated with various techniques. Our findings indicate that the LSTM outperforms the other approaches in terms of speed. The confusion matrix also visualizes the classification of healthy and diseased leaf in figure 8.

Table 2. Time Consumption by the different Methods

Model	APS-DCCNN	AlexNet	CNN	DSGANN	HCRNN	LSTM
Time	146ms	120ms	185ms	102ms	101ms	100ms

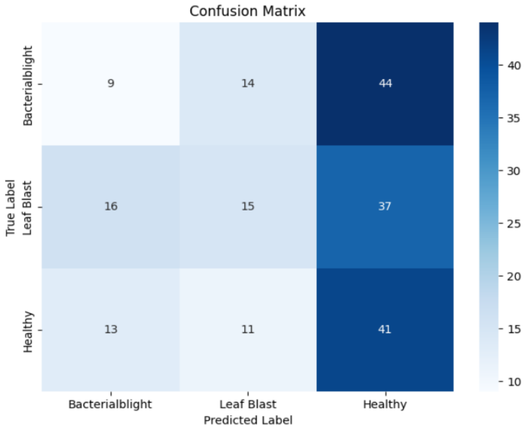

Fig. 8. Confusion Matrix between the healthy and diseased Leaves

CONCLUSION

Early leaf disease detection is crucial to farming. This essay will explain rice plant leaf blight identification and symptoms. Conventional methods have been used to diagnose leaf diseases from real-time photographs. Farmers can identify and cure rice plant leaf diseases using the suggested procedure. Combining HCRNN and LSTM algorithms, we identified 5932 rice plant images and scenarios. Rice plant diseases can be detected using real-time images and trained models. Additional rice plant varieties and diseases can be added to databases to improve trained models for future projects. Our work established a new rice plant disease detection method. Combining LSTM and HCRNN networks improves prediction accuracy. Diseases can affect food security and agriculture sustainability because rice is a main crop in many regions. Manual inspection is the best way to detect rice diseases, but it takes time and is error prone. It's crucial to build sophisticated, automated technologies to predict and recognise rice plant illnesses. Our HCRNN-LSTM model uses long short-term memory (LSTM) networks to simulate sequential data temporal links and convolutional neural networks (CNNs) to extract geographical information. Combining the two methods helps the model forecast plant health by capturing disease symptoms' spatiotemporal properties and granularity. The HCRNN-LSTM model outperformed solo CNNs, LSTMs, and other deep learning frameworks like DSGANN in precision, recall, and accuracy. This improvement was notably noticeable with more input photos. The performance investigation proved that the suggested model outperformed current methods on multiple rice plant picture datasets. CNNs alone cannot address illness development sequentially; LSTM layers do. Hierarchical CNN layers make it easier to capture spatial data like disease-related texture and colour patterns. Although more computationally demanding, the HCRNN-LSTM model performs better. Combining CNN and LSTM layers increases training time and computational resources. The hierarchical structure and additional layers in our model demand more processing resources than CNNs or LSTMs, according to temporal complexity. However, this compromise is justifiable in high-precision applications, especially when misclassifying a condition has serious effects. Finally, the HCRNN-LSTM model can accurately identify rice plant diseases. It is useful for agricultural applications since it combines LSTM sequential modelling with CNN spatial analysis. To make the model more accessible in resource-constrained situations like rural farms, further research could optimise its computing efficiency by researching lightweight alternatives or using sophisticated technology. Additionally, adding new crops and diseases to the model could improve precision agriculture.

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