

A survey of deep learning applications for disease identification and prediction in rice crop

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Introduction

- Rice is the primary food staple and a major source of income for 200 million families across developing countries, according to the Organization for Economic Co-operation and Development and the Food and Agriculture Organization of the United Nations (OECD 2022).
- By 2031, global rice production is expected to reach 584 Mt. On average, rice diseases account for up to 10% of yield loss, equaling a loss of 29 billion US dollars in monetary terms (Savary et al. 2000).
- Major rice leaf diseases in the world are: (Source: International Rice Research Institute)
Fungal diseases: leaf blast (LB), neck blast (NB), false smut (FS), sheath blight (SB), sheath rot (SR), brown spot (BS), narrow brown spot, seedling blight (RSEB)
Bacterial diseases: bacterial leaf blight (BLB), bacterial sheath rot (BSR), bacterial wilt (BW), bacterial stripe (streak) (BAS)
Viral disease: leaf tungro (LT)

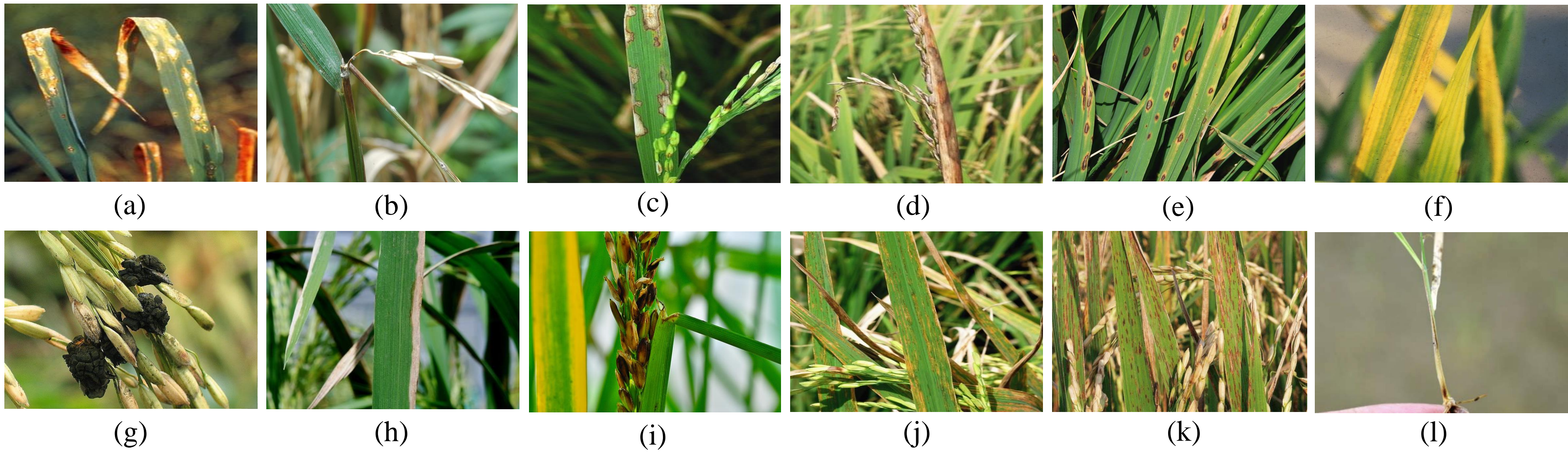


Figure 1. Pictures of rice diseases (a) LB, (b) NB, (c) SB, (d) SR, (e) BS, (f) LT, (g) FS, (h) BLB, (i) BSR, (j) BAS, (k) NBS, (l) RSEB (Source: <https://www.irri.org/>)

- Absence of large datasets and deep lesion feature often hinder machine learning models from achieving optimal results compared to deep learning models (Sujatha et al. 2021).
- Research trends show that application of deep learning (DL)-based rice disease identification and prediction started from 2017 (Lu et al. 2017) as per search results from IEEE Xplore, Web of Science, Science Direct, CAB direct, and Scopus (fig. 2). Keywords used: deep learning, rice disease, identification, classification and prediction.

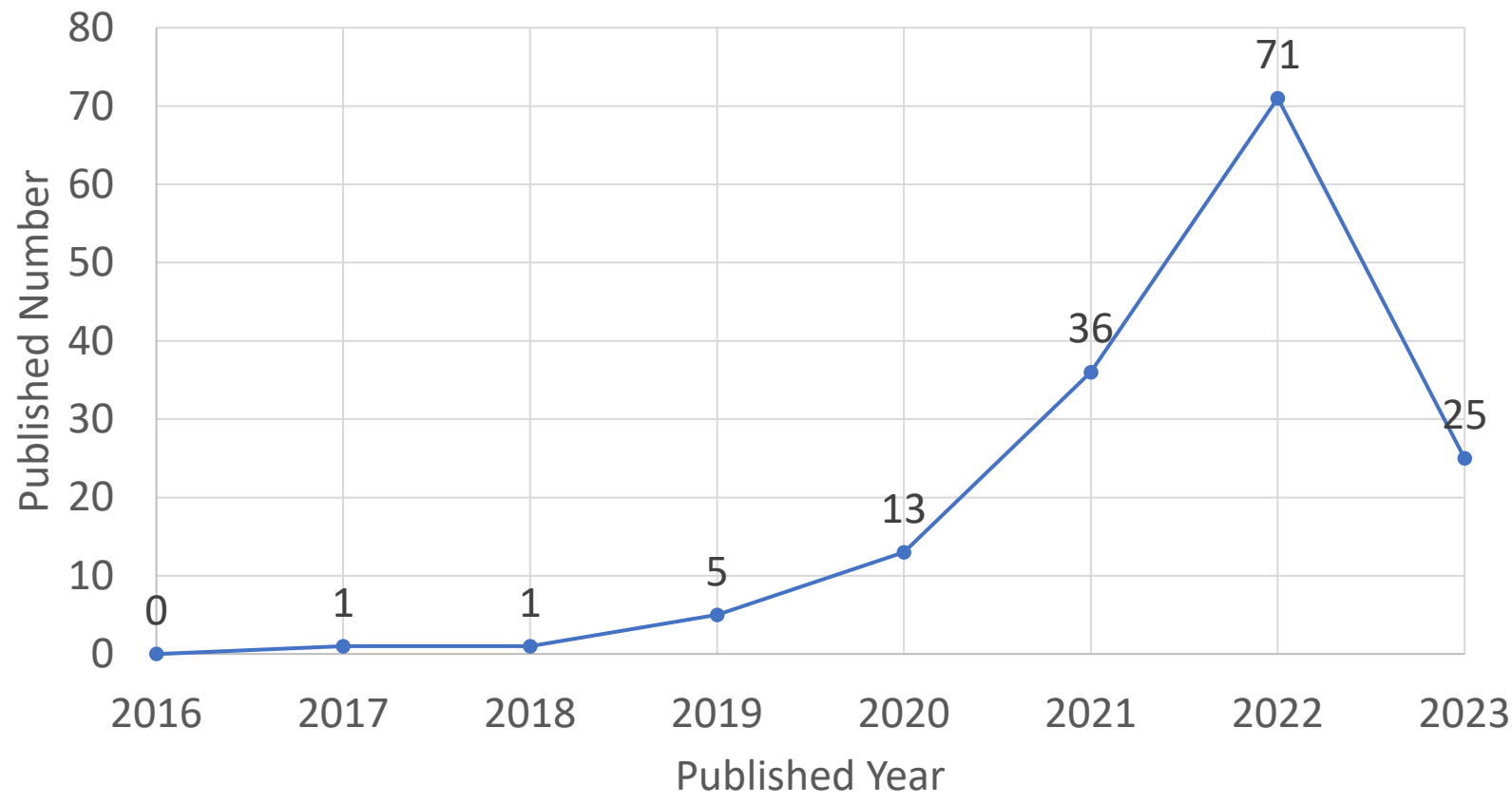


Figure 2. Research trends of DL applications for rice disease identification and prediction

Prediction

- About 85% of the farmers relied on their personal experience to predict and control rice diseases in Bangladesh (Mousumi et al. 2023).
- Recurrent Neural Network (RNN) was developed to address time-series data analysis models rather than deep feed-forward neural networks (Greff et al. 2017). However, RNN cannot retain gradient over time, so Long Short-Term Memory (LSTM) and Gated Recurrent Unit (GRU) networks were developed. The structures of RNN, LSTM, and GRU are shown in figure 3.

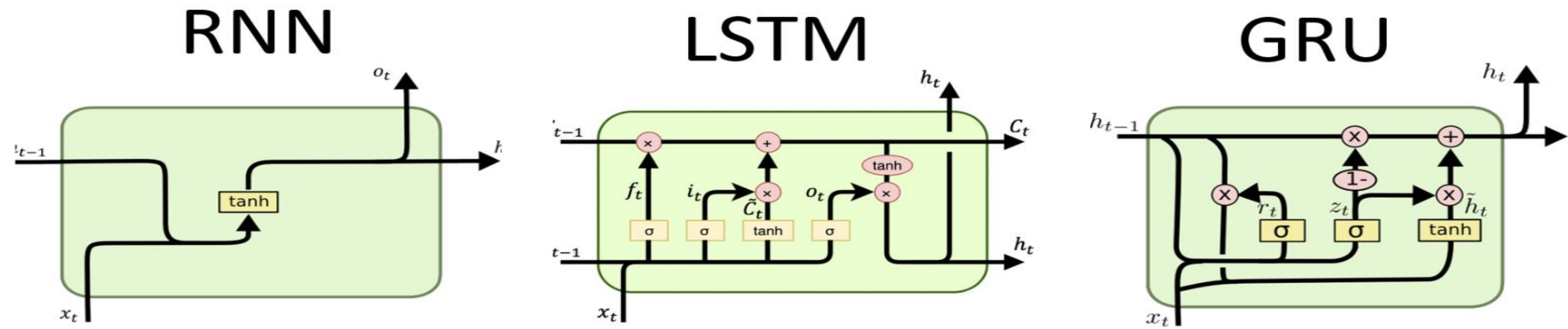


Figure 3. Structure of RNN, LSTM, GRU. (Source: <http://dprogrammer.org/rnn-lstm-gru>)

- Rice disease prediction models tend to yield higher accuracy when the climate conditions of the site are similar to the developed place of the model (Nettleton et al. 2019).
- Meteorological factors such as daily maximum, mean, and minimum temperature, average relative humidity, sunshine duration, disease score, precipitation, leaf wetness, zonal wind, and meridional wind are important inputs to train deep learning prediction models. A performance comparison of the DL-based prediction models is indicated in table 1.

Table 1. Comparison of rice disease prediction by deep learning models

Reference	Year	Input								Prediction	Model	Best prediction accuracy
		mean temperature	max temperature	min temperature	mean humidity	sunshine duration	past rice blast disease score	precipitation	leaf wetness			
Kim et al.	2018	x			x	x	x			rice blast	LSTM	Accuracy ^[a] = 79.4%
Nettleton et al.	2019		x	x	x				x	rice blast	LSTM	Area Under Curve ^[b] = 0.8
Ou et al.	2023	x	x	x	x			x		x rice blast	BlastGRU-TW	Accuracy = 87.3%

^[a] The accuracy is defined as the number of correctly classified data elements among the total number of test data elements

^[b] Area Under Curve = $\int_a^b (2E - 0.6x^3 - 0.0005x^2 + 0.0547x + 0.0017) \cdot dx$
where, a and b is the x-axis range (20th June to 7th July, translated into a numerical sequential index x = 1.18) to be evaluated

Identification

- Rice disease identification is laborious, time-consuming, and requires subject-matter training.
- Deep learning techniques offer the advantage of end-to-end learning, avoiding the need for complex hand-crafted features such as extraction required in traditional machine learning (O'Mahony et al. 2020).
- A performance comparison of the DL-based classification models is indicated in Table 2.

Table 2. Comparison of rice disease classification by deep learning models

Authors	Year	Modeling Techniques	Dataset Used	Framework	Diseases Studied	Best performing model and performance measure(s) used
Lu et al.	2017	CNN + Stochastic-pooling	500 images of rice diseases acquired from experimental fields in China.	N/A	RB, FS, BS, BD, HB, SR, BLB, SR, RSEB, BW	95%; N/A
Shrivastava et al.	2019	AlexNet + SVM	619 images of rice diseases acquired in laboratory settings	N/A	LB, BLB, SB	91.37%; N/A
Burhan et al.	2020	Image processing + VGG16, VGG 19, ResNet50, ResNet50v2, ResNet101v2	3,355 images of rice diseases acquired from Kaggle, and 200 images of rice diseases acquired from experimental fields in Pakistan	Keras	BS, LB, Hispa	Kaggle: ResNet50: 75.00%, Pakistan: ResNet101v2: 86.79%; N/A
Sethy et al.	2020	AlexNet, VGG16, VGG19, Densenet201, GoogleNet, Inceptionv3, Inceptionresnetv2, Resnet18, Resnet50, Resnet101 and XceptionNet with / without SVM	5,932 images of rice diseases acquired from experimental fields in India and from agricultural pest and insect pests picture database	MATLAB 2019a deep learning toolbox	BLB, LB, BS, LT	With SVM classifier: DenseNet201: 98.52%, Transfer Learning: DenseNet201: 79.92%; Accuracy = $\frac{(TP+TN)}{(TP+TN+FP+FN)}$ ^[a]
Rahman et al.	2020	VGG16, InceptionV3, MobileNetv2, NasNet Mobile, SqueezeNet v1.1, Simple CNN	1,426 images of rice diseases and pests acquired from experimental fields in Bangladesh	Keras with TensorFlow backend	FS, NB, SB, SR, BS, BLB	With fine tuning: VGG16: 97.12%, Two stage training: Simple CNN: 94.33%; 10-fold cross-validation accuracy along with standard deviation Overall Accuracy: VGG16: 93.11%; N/A Lighter model: DenseNet169: 77.79%; N/A
Shrivastava et al.	2021	(i) AlexNet; (ii) VGG16; (iii) ResNet152V2; (iv) InceptionV3; (v) InceptionRes NetV2; (vi) Xception; (vii) MobileNet; (viii) DenseNet169; (ix) NasNetMobile; (x) RasNetLarge	1,216 images of rice diseases acquired from experimental fields in India	Keras with TensorFlow backend	LB, BLB, BS, SB, SR, FS, healthy	
Deng et al.	2021	ResNet-50, DenseNet-121, SE-ResNet-50, ResNeXt-50, and ResNeSt-50	33,026 images of rice diseases acquired from experimental fields in China	PyTorch	LB, FS, NB, SB, BSR, BS	Ensemble model: 91%; Accuracy = $\frac{\sum_{i=1}^6 TP_i}{N}$ ^[b]
Wang et al.	2022	CNN + ResNet, MSSCNN, MSPCNN	826 images of rice diseases acquired from experimental fields in Taiwan	N/A	BLB, LB	MSSCNN: 92.64%; N/A
Dey et al.	2022	LeNet-5, ResNet-18,34,50, ResNeXt-50, DenseNet-121,169,201, Googlenet with Inception-v4, MSSCNN, MSPCNN	800 images of rice diseases acquired from experimental fields in Bangladesh, and 5,447 images of rice diseases acquired from Kaggle	TensorFlow	BS, LB, Hispa, NPK deficiency	VGG19: 91.8%; Accuracy = $\frac{(TP+TN)}{(TP+TN+FP+FN)}$
Patil and Kumar	2022	Rice Transformer	4,200 images of rice diseases acquired from experimental fields in India	Keras	LB, BS, BLB	Overall accuracy: 97.38%; N/A
Zhang et al.	2023	VGG16 combined with Inception V1	2,370 images of rice diseases acquired in laboratory settings on Kaggle	TensorFlow-gpu2.2 and Keras2.4.3	BS, LB, Hispa	97.10%; Accuracy = $\frac{1}{n_s} \sum_{i=1}^n \frac{n_{ii}}{n_i}$ ^[c]

[a] where, TP = true positive, TN = true negative, FP = false positive, FN = false negative

[b] where, N is the number of all test images, P is precision, i is the ith type of disease, and TP_i is the number of true positives

[c] where, n_s denotes the total number of sample categories, n_i the total number of i type samples and n_{ii} the number of i sample prediction results of type i.

Reference:



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