Hybrid DCNN-SVM Architecture for Optimizing Sugarcane Leaf Disease Classification

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Abstract— Sugarcane leaf diseases are major agricultural issues that lead to reduced production and economic losses. Early detection is crucial for controlling their spread. This study introduces a solution for identifying sugarcane leaf diseases using image processing and deep learning techniques. Preprocessing steps include normalization for pixel scale stabilization and Gaussian blur for noise reduction. Features are extracted using a pre-trained DenseNet201 model, and classification is performed using a Support Vector Machine (SVM) with an RBF kernel. The proposed hybrid DCNN-SVM architecture achieves a test accuracy of 96.74%, demonstrating effectiveness in disease classification. Comprehensive evaluations highlight the model's strengths and areas for improvement, providing a foundation for future research in plant disease detection.

Index Terms— DCNN, image classification, sugarcane disease, hybrid deep learning

I. INTRODUCTION

S UGARCANE (*Saccharum officinarum*), a plant that thrives in tropical regions, is a key source of raw material for sugar production [1]. The productivity of sugarcane is heavily dependent on leaf health, as diseases can significantly reduce yields and the quality of the sugar produced. Leaf diseases in sugarcane, often caused by fungal pathogens, are a major concern, with Fusarium being one of the most critical diseases globally [2]. This disease spreads rapidly and can lead to severe economic losses.

Early and accurate detection of sugarcane leaf diseases is essential for implementing timely and effective control measures. Traditional methods, which depend on visual inspections by plant disease experts, can be time-consuming

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Lukman Sunardi is a senior lecturer at Faculty of Engineering Science, Universitas Bina Insan, Lubuklingau 31626, Indonesia (email: <u>lukman sunardi@univbinainsan.ac.id</u>). and expensive. Therefore, there is an urgent need for an automated system that can classify sugarcane leaf diseases with high accuracy.

The accuracy of this system greatly relies on the quality of the input images. Proper preprocessing techniques can significantly enhance the performance of a model [3]–[5]. Various studies have utilized image processing techniques to extract relevant features while reducing noise. Researchers have explored methods such as dynamic adjustments of image size and shape, filtering, image conversion, contrast enhancement, and morphological operations [6]. Research by [7], highlighted the impact of wavelet transforms in enhancing model accuracy during image segmentation, facilitating more efficient feature extraction using algorithms like ant colony optimization. Additionally, background segmentation techniques have proven effective in reducing false positives and improving detection accuracy [8].

In recent years, deep learning-based approaches, particularly those using Convolutional Neural Networks (CNN) [9], have shown promising results in plant disease classification [10]–[13]. For instance, a hybrid deep learning model combining VGG-16 and MobileNet with stacking ensemble learning has been applied to sunflower leaf disease classification [14]. Another study focused on detecting bacterial spot diseases in peach plants, introducing a model combining Convolutional Auto-Encoder (CAE) and CNN, which significantly reduced training parameters while maintaining high detection accuracy [15]. Moreover, the MobiRes-Net architecture, a fusion of MobileNet and ResNet, has demonstrated substantial performance improvements in detecting olive leaf diseases [16]. In scenarios where feature extraction generates large volumes of data, techniques such as logistic regression in the fully connected (FC) layer have been employed to eliminate irrelevant features, as demonstrated in [17].

However, these models often require large amounts of high-quality training data, which can be challenging, particularly for rare or emerging diseases. To address these challenges, this research proposes a hybrid architecture combining a Deep Convolutional Neural Network (DCNN) for feature extraction and a Support Vector Machine (SVM) for final classification. The DCNN will be used to extract features from sugarcane leaf images processed with Gaussian blur, and these features will then serve as input for the SVM to classify the diseases.

The main objective of this study is to create an automatic

classification system that accurately identifies different diseases affecting sugarcane leaves. The key contributions of this research are as follows:

- 1) Application of Gaussian blur to enhance the quality of sugarcane leaf images before feature extraction.
- 2) Use of Deep Convolutional Neural Networks (DCNN) for feature extraction from the enhanced images.
- 3) Implementation of Support Vector Machine (SVM) for final classification based on the features obtained from the DCNN
- 4) Evaluation of the system's performance in terms of classification accuracy.

This paper is structured as follows: Section 2 presents the research methodology. Section 3 discusses the experimental results and provides analysis. Finally, Section 4 concludes the research.

II. PROPOSED METHOD

In this section, a concise description of the proposed method is provided, an explanation of the dataset used, preprocessing techniques (Gaussian blur), a detailed description of the DCNN-SVM model architecture, and an overall evaluation of the model. Figure 1 illustrates the proposed method for detecting sugarcane leaf diseases.

A. Dataset

The Sugarcane Leaf dataset is a publicly available collection of 6748 high-resolution JPEG images showcasing sugarcane leaves. [18]. Each image in the dataset is sized at 768×1024 pixels. The dataset is categorized into 11 classes, comprising nine disease categories, a category for healthy leaves, and a category for dry leaves. The disease category encompasses various common sugarcane leaf diseases, including smut, banded chlorosis, yellow leaf disease, pokkah boeng, mosaic, brown spots, grassy shoots, brown spots, brown rust, and set rot. To facilitate accessibility and identification of specific disease samples, each category is clearly labeled and organized into separate folders. Table I shows the distribution of different categories of sugarcane leaf diseases and healthy leaves in the dataset.

IMAGE DISTRIBUTION PER CATEGORIES							
Categories		Amount of Images					
	Yellow leaf disease	1194					
	Smut	316					
	Brown spot	1722					
	Pokkah boeng	297					
Diseases	Grassy shoot	346					
	Mosaic (viral disease)	663					
	Banded chlorosis	471					
	Sett rot	652					
	Brown rust	314					
Healthy leaves		430					
Dried leaves		343					
Total		6748					



Fig. 1. Proposed Method

B. Preprocessing

Preprocessing is an important step in processing image data before it is used in deep learning models [19], [20]. This process involves several techniques to improve image quality, reduce noise, and prepare data for model training. The three main techniques used in preprocessing are: resizing, normalization, and Gaussian blurring.

Images in a dataset often vary in size [21]. To ensure consistency and compatibility with the deep learning model architecture to be used, images must be resized to uniform dimensions. In this case, each image is resized to 224×224 pixels. This helps the model process images more efficiently and ensures that all images have the same dimensions.

The normalization technique is used to change the pixel values of an image so that they fall within a specified range [22]. In this case, the image is normalized by rescaling its pixel values to the range 0 to 1 by dividing each pixel value by 255 (the maximum value of a pixel in an 8-bit image). Normalization helps the model converge faster and improves training stability. Equation (1) shows the mathematical function of normalized pixels.

Normalized Pixel =
$$\frac{real \ pixel}{255}$$
 (1)

In order to improve the quality of the images, and reduce the noise to fine detail in images, Gaussian blur is used [23], [24]. This technique uses a Gaussian filter to create a soft blur effect that can help highlight important features in an image by blurring irrelevant details. Applying Gaussian blur can help models focus on more significant patterns for classification tasks. Equation (2) shows the function of the Gaussian filter.

$$G(x,y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2 + y^2}{2\sigma^2}}$$
(2)

Where, G(x,y) is the Gaussian value at coordinates (x,y), σ is a parameter that controls the sharpness of the Gaussian

curve, *x*, and *y* are the distances from the middle point of the filter to the pixel being processed. Figure 2 depicts the process of removing noise from the original input image.

C. DenseNet feature extraction

Feature extraction plays a crucial role in both machine learning and deep learning pipelines [25]. It is a pivotal process that significantly impacts the effectiveness and efficiency of these methodologies., especially when working with image data [26], [27]. In this research, we use the pretrained DenseNet201 model to extract features from images of sugarcane leaves.

DenseNet (Densely Connected Convolutional Networks) is a convolutional network architecture designed to have denser connections between its layers, this helps facilitate the flow of information and gradients throughout the network [28]. Huang et al proposed DenseNet. in 2017, where every layer is connected to all previous layers (dense connections), which has the property that each training image leads to a lot of back-propagation updates which in turn weaken certain gradients. This architecture solves the vanishing gradient problem which is common in deep networks, by facilitating a strong signal flow during backpropagation. DenseNet also demonstrates feature reuse, thanks to which the model is able to achieve state of the art accuracy by using lesser parameters compared ResNets. Figure 3 shows the process of extraction feature with DenseNet.

Using dense blocks as the key ingredient, DenseNet is able to facilitate direct connections between layers in deep neural networks. These connections contribute in suppressing vanishing gradients, promotes fast reuse of features and reduces number of parameters required for the model. In DenseNet, the output of each layer is appended to its previous layers resulting in better information flow through different layer & making network learning complex patterns and features.



Fig. 2. Noise removal with Gaussian smoothing

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Fig. 3. Feature extraction with DenseNet201

The variant utilized in this research is DenseNet201, which consists of 201 layers and has been pre-trained on the ImageNet dataset. This thorough pre-training enables DenseNet201 to effectively capture a broad spectrum of low- to high-level features. These features can then be transferred to other tasks, such as detecting sugarcane leaf diseases. The pre-trained nature of DenseNet201 eliminates the need for retraining the model using the sugarcane leaf extract detailed dataset. Instead, it can feature representations from the input images, which are subsequently used for classification.

TABLE II MODEL SUMMARY FOR FEATURE EXTRACTION

Layer (type)	Output shape	Param#
Input layer	(224x224x3)	0
Densenet201 (functional)	(7x27x1920)	18321984
Global Average Pooling	(1920)	0
Total params		18321984
Trainable params		0
Non-trainable params		18321984
Batch size		256

The process of feature extraction using DenseNet201 can be explained in several steps (Table II): (1) Input images: Sugarcane leaf images of size 224x224 pixels and with 3 color channels (RGB) are used as input for the model. (2) Feature extraction by DenseNet: These images are processed by a pre-trained DenseNet201 network, which extracts features and generates a tensor with dimensions 7x7x1920. (3) Global Average Pooling: The tensor with dimensions 7x7x1920 is then passed through a global average pooling layer, which reduces its spatial dimensions to a 1D feature vector of length 1920. (4) Feature Vector: The resulting 1D feature vector of length 1920 represents the extracted features from the original image. This feature vector can be utilized for classification tasks or further analysis.

Non-trained parameters are parameters from a DenseNet model that was previously trained on the ImageNet dataset. This means that this model will not be retrained on our sugarcane leaf dataset, but will only be used to extract features. Figure 4 shows the result of the extracted feature with DenseNet.

D. SVM Classifier

The Support Vector Machine (SVM) is a highly effective machine learning method commonly employed for classification purposes [29], [30]. In this particular case, we will utilize SVM with a Radial Basis Function (RBF) kernel to classify sugarcane leaf diseases. The classification will be based on features obtained from leaf images using DenseNet201. SVM works by finding the best possible hyperplane to separate the classes of data in the feature space. SVM has several advantages [31], such as: (1) SVM works very well on high-dimensional data, (2) only support vectors are used to define the hyperplane, which makes SVM efficient in memory usage, (3) flexibility with kernel tricks, which allows SVM to handle data that cannot be separated linearly using various kernel functions. Equation (3) provides the SVM classifier used to identify sugarcane leaf disease.

$$f_{svm} = W_t \varphi(X) + b \tag{3}$$

Where:

 W_t is the Weight vector, φ is the mapping function. This mapping function is utilized to transform any input function into a different dimensional space, allowing for easier separation. The hyperplane is determined in a manner that the distance from this hyperplane to the nearest data points on each side is referred to as support vectors. SVM employs the values of training images to effectively classify the test images.

In the context of our research on sugarcane leaf disease classification, SVM provides a valuable alternative to deep learning models. By training an SVM on features extracted from sugarcane leaf images, we can establish a baseline performance and gain insights into the discriminative power of different feature representations. Furthermore, the interpretability of SVM, particularly in terms of identifying key support vectors, can offer valuable insights into the characteristics that distinguish between different types of sugarcane leaf diseases.

	ø	1	2	3	4		. 191	7 191	3 1919	labe	l class_name
0	0.847739	-2.314642	0.092679	-0.091092	-0.955365		0.35584	4 -0.83548	-0.436520) :	1 Brown Spot
1	-0.250167	-1.694962	-0.757211	-0.859588	-0.251926		. 0.45925	9 -0.92760-	0.269685	; ;	5 Healthy Leaves
2	-0.722426	0.058019	-0.421527	1.543183	1.431694		0.10274	6 -0.43681	6 -0.456827	, ,	4 Grassy shoot
3	-0.964689	0.961297	-0.500415	-1.182934	-0.311018		0.02358	9 -1.03873	0.385875	5 :	1 Brown Spot
4	0.888123	-1.423313	0.682042	-0.881504	-0.024084		0.09783	7 -0.56695		3 :	Brown Spot
5056	1.423925	0.333624	0.680174	0.252873	0.182745		0.26059	3 -1.04925	5.360555	5 1	B smut
5057	-0.429540	0.515739	0.247367	-0.618209	-0.799404		0.06821	0 -0.56726	3 -0.242481		7 Sett Rot
5058	0.465609	-0.134720	1.704435	1.158391	0.476919		0.41648	9 -0.62361	2 -0.392101		9 Viral Disease
5059	0.860506	-0.222202	0.793266	-0.826927	-0.547490		0.45497	9 2.11289	-0.750824		9 Viral Disease
5060	-0.981769	-1.364537	-0.864806	0.193189	-0.352845		. 2.06403	0 -0.23958	-0.629246	5 (6 Pokkah Boeng
Test	Features:										
	0	1	2	3	4		1917	1918	1919	label	class_name
0	-0.138217	-0.275116	-0.488731	-0.615674	-0.285898		0.141569	2.347857	-0.739270	7	Sett Rot
1	-1.210788	0.196905	-1.577767	0.079174	-0.663701		1.584132	-0.380390	-0.570599	1	Brown Spot
2	-0.621318	-0.246845	1.306906	0.169843	-0.505938		-0.550605	-0.518433	-0.987112	10	Yellow Leaf
3	-0.999639	0.790370	-0.407534	-1.278010	-1.171175		2.933522	-0.458572	3.822210	7	Sett Rot
4	1.975550	-0.826348	0.341429	-0.409560	0.301260		-0.563775	-0.803422	-0.667758	9	Viral Disease
			•••						•••		
1682	-0.875493	0.387759	0.834994	1.080153	0.615527		-0.118104	-0.722831	0.273377	1	Brown Spot
1683	-0.437115	0.359102	0.411693	0.337784	-0.229967		-0.125983	0.170598	-0.486848	7	Sett Rot
1684	2.507182	0.161079	0.156198	-1.159944	1.378058	•••	-0.488205	1.589317	0.123696	9	Viral Disease
1685	0.578854	-0.224218	0.867036	0.208694	0.161440		-0.047778	-0.334052	0.360971	0	Banded Chlorosis
1686	0.383961	-0.529268	0.360777	0.085967	0.252259		-0.493214	0.485812	0.172873	10	Yellow Leaf

[1687 rows x 1922 columns]

Fig. 4. Result of the extracted feature

Train Features:

E. Evaluation

The Confusion Matrix (CM) is the most commonly used method to figure out the achievement of classification models in machine learning [32]. CM represents the comparison between predicted and actual values from the classification model The CM can be used to calculate several important metrics such as accuracy, f1-score, precision, and recall, which help to evaluate the performance of the DCNN-SVM model.

From these components, we can calculate several important classification evaluation metrics:

 The accuracy of the predictions of the model, which is calculated according to equation (4), is represented as a percentage of correctly predicted samples.

$$Acc = \frac{t_p + t_n}{t_p + t_n + f_p + f_n} \tag{4}$$

2) Precision is calculated as Equation (5) and displays the percentage of positive data samples accurately predicted by the model.

$$pre = \frac{t_p}{t_p + f_p} \tag{5}$$

 Recall, also known as sensitivity or true positive rate, imply the percentage of positive samples that the model accurately predicts. Equation (6) can be used to calculate it.

$$recall = \frac{t_p}{t_p + f_n} \tag{6}$$

 The F-1 Score describes the weighted average precision compared to the weighted average recall, and it can be represented by Equation (7).

$$f1 - score = 2\frac{pre * recall}{pre + recall}$$
(7)

Where:

 t_p represents the number of true positive samples, t_n represents the number of true negative samples, f_p represents the number of false positive samples, and f_n represents the number of false negative samples.

F. Experiment Set Up

In this experiment, the data was split into training and testing sets with a ratio of 75% for training and 25% for testing. The distribution of this split data is shown in Table III and Figure 5. The experiments in this research used the Python programming language, and the libraries used such as OpenCV, Sci-kit Learn, TensorFlow, and Keras. This experiment was performed using a PC with the following specifications: CPU processor core i7 gen 9th, DDR4 16 GB, and GPU NVIDIA GeForce GTX 1660 Ti.

TABLE III DISTRIBUTION OF SPLIT DATASET Classes in dataset **Training set** Testing set Banded Chlorosis 354 117 1275 Brown Spot 447 Brown Rust 234 80 Dried leaves 262 81 Grassy Shoot 267 79 Healthy Leaves 314 116 Pokkah Boeng 234 63 Sett Rot 447 175 Smut 249 67 Viral Disease 505 158 Yellow leaf 890 304 Total 5061 1687



(b)

Fig. 5. Dataset distribution. (a) Distribution of images per categories, (b) Proportion of images per categories

III. RESULT AND DISCUSSION

A. Result

In this chapter, we will be presenting the outcomes of our study on sugarcane leaf disease detection. Specifically, we implemented a hybrid DCNN+SVM model and will be discussing the results obtained. We will cover various aspects, such as the classification reports, confusion matrix, and RoC plots. Analyzing these results will allow us to assess the effectiveness of the model in detecting sugarcane leaf diseases. Table IV summarizes precision, recall, and F1-scores per class.

The classification results indicate that the model

demonstrates a remarkable overall accuracy of 96.74%. This clearly highlights the model's effectiveness in accurately classifying sugarcane leaf diseases. Moreover, the model exhibits exceptional performance consistency across classes, as evidenced by its high weighted average precision, recall, and F1 score of 96.75%, 96.74%, and 96.72% respectively.

The model's performance in each class appearance is remarkable across multiple categories. For instance, in the 'Brown Spot' category, it achieved a precision of 98.67%, a recall of 99.55%, and an F1 score of 99.11%, indicating its exceptional ability to identify this particular disease. Additionally, the model demonstrated flawless precision, recall, and F1 score in the 'Grassy Shoot' category, showcasing its flawless classification of this disease.

CLASSIFICATION REPORT FOR DCNN-SVM MODEL								
	precision	recall	F1-score	support				
Banded Chlorosis	0.9492	0.9573	0.9532	117				
Brown Spot	0.9867	0.9955	0.9911	447				
Brown Rust	1.000	0.9875	0.9937	80				
Dried leaves	0.9872	0.9506	0.9686	81				
Grassy Shoot	1.000	1.000	1.000	79				
Healthy Leaves	1.000	0.9655	0.9825	116				
Pokkah Boeng	0.8545	0.7460	0.7966	63				
Sett Rot	1.000	1.000	1.000	175				
Smut	0.7639	0.8209	0.7914	67				
Viral Disease	0.9490	0.9430	0.9460	158				
Yellow leaf	0.9711	0.9934	0.9821	304				
Accuracy			0.9674	1687				
Macro (avg)	0.9511	0.9418	0.9459	1687				
Weighted (avg)	0.9675	0.9674	0.9672	1687				

TABLE IV

However, there are a few categories that exhibit lower performance. The 'Pokkah Boeng' category, in particular, achieved a precision of 85.45% and a recall of 74.60%. These figures indicate the difficulties in accurately identifying this disease. Likewise, the 'Smut' category demonstrated a precision of 76.39% and a recall of 82.09%, suggesting that the model is more prone to misclassifying this disease compared to other categories.

1) Summary of Model Performance and Findings

Overall, despite some limitations in classifying certain diseases, the model exhibited strong overall performance. Its remarkable accuracy across most classes highlights its practical utility in identifying sugarcane leaf diseases in realworld scenarios. These findings establish a robust foundation for future improvements and adjustments aimed at enhancing accuracy, particularly for diseases that showed lower classification performance.

2) Confusion Matrix Analysis

Figure 6 illustrates the confusion matrix (CM) for the DCNN-SVM model. The matrix predominantly features diagonal elements, indicating that the model accurately classified most instances within each class. Each diagonal element reflects the number of instances correctly predicted for that specific class. The diagonal plot indicates very favorable results from the CM. However, the most significant misclassification occurred between the classes 'Pokkah Boeng' and 'Smut.'

In the case of the true class 'Pokkah Boeng,' it was incorrectly classified as 'Smut' 16 times. This consistent misclassification suggests that the model struggles to differentiate between these two classes. Several factors contribute to this issue: (1) Similarity of Visual Features: 'Pokkah Boeng' and 'Smut' share similar visual characteristics, complicating their distinction by the model; (2) Insufficient Training Data: There are fewer training samples for 'Pokkah Boeng,' leading to an imbalance between the samples of 'Pokkah Boeng' and 'Smut,' which may bias the model toward classifying instances as 'Smut'; (3) Limitations in Feature Extraction: The features extracted by DenseNet may not effectively capture the subtle differences between these diseases, resulting in misclassifications.

For the true class 'Smut,' it was misclassified 7 times as 'Pokkah Boeng,' 3 times as 'Viral Disease,' and once as 'Yellow Leaf.' The misclassification of 'Smut' as 'Pokkah Boeng' and other categories indicates that it is challenging for the model to classify correctly. Contributing factors include: (1) Confusion with 'Pokkah Boeng': This aligns with previous observations that these two diseases are often confused, likely due to their similar appearance or a lack of distinguishing features in the dataset; (2) Confusion with Other Diseases: Misclassifications as 'Viral Disease' and 'Yellow Leaf' suggest that 'Smut' may exhibit symptoms or visual features that overlap with these other diseases.

3) RoC Curve Evaluation

Figure 7 presents the ROC curve for the DCNN-SVM model. The performance of the classification algorithm is evident from the position of the ROC curve on the graph, which shows a significant upward trend, indicating that the classification algorithm performs well. All classes achieved an AUC score of 1.00, demonstrating that the model has a perfect ability to differentiate between different classes. This means that for each class, the model accurately classifies all positive instances as positive and all negative instances as negative without any errors.

						Confu	ision I	Matrix	¢				
	Banded Chlorosis -	112	0	0	0	0	0	0	0	0	1	4	
	Brown Spot -	1	445	0	0	0	0	0	0	0	0	1	- 40
	BrownRust -	0	0	79	0	0	0	0	0	0	0	1	- 35
	Dried Leaves -	0	2	0	77	0	0	0	0	0	0	2	- 30
el	Grassy shoot -	0	0	0	0	79	0	0	0	0	0	0	- 25
le Lab	Healthy Leaves -	0	0	0	0	0	112	0	0	0	4	0	
Tru	Pokkah Boeng -	0	0	0	0	0	0	47	0	16	0	0	- 20
	Sett Rot –	0	0	0	0	0	0	0	175	0	0	0	- 15
	smut -	0	0	0	0	0	0	8	0	55	з	1	- 10
	Viral Disease -	5	3	0	0	0	0	0	0	1	149	о	- 50
	Yellow Leaf -	0	1	0	1	0	0	0	0	0	0	302	
		Banded Chlorosis -	Brown Spot -	BrownRust -	Dried Leaves -	Grassy shoot -	Healthy Leaves -	Pokkah Boeng -	Sett Rot -	smut -	Viral Disease -	Yellow Leaf -	- 0

Fig. 6. Confusion matrix for DCNN-SVM model

 TABLE V

 DETAILS OF VARIOUS STUDIES IN SUGARCANE LEAF DISEASE DETECTION

Predicted Label

Article reference	Dataset availability	Number of images	Number of Classes	Method	Accuracy (%)
[33]	Private	14724	2	CNN	95.40
[34]	Private	240	2	VGG+SVM	90,29
[35]	Private	910	4	DCGAN+transfer learning	99.00
[36]	Private	2569	5	Emsemble deep learning	86.53
[37]	Private	5048	6	InceptionV3	86
[38]	Private	3508	3	SVM RBF	88
[39]	Plant village dataset + private dataset	2095	6	CNN+transformer	87.64
Proposed architecture	Sugarcane leaf dataset	6748	11	DCNN+SVM	96.74

TABLE VI

	Accuracy	precision	recall	F1-score
DenseNet201-Logistic Regression	0.9609	0.9624	0.9609	0.9612
DenseNet201-Random Forest	0.9443	0.9447	0.9443	0.9438
DenseNet201-Decision Tree	0.8121	0.8132	0.8121	0.8115
DenseNet201-Naïve Bayes	0.5483	0.6793	0.5483	0.5187
DenseNet201-SVM+Linear Kernel	0.9591	0.9593	0.9591	0.9591
DenseNet201-SVM+Poly Kernel	0.9621	0.9617	0.9621	0.9615
DenseNet201-SVM+Sigmoid Kernel	0.8785	0.8840	0.8785	0.8781
DenseNet201-SVM+RBF Kernel (proposed)	0.9674	0.9675	0.9674	0.9672



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4) Comparative Study of Sugarcane Leaf Disease

Table 5 details various studies on sugarcane leaf disease detection. With an accuracy rate of 96.74%, it demonstrates that the combination of DCNN and SVM (the proposed architecture) is effective for classifying sugarcane leaf diseases. This accuracy surpasses most other studies, except one that achieved 99% using a DCGAN-transfer learning method. Notably, this study addresses a larger number of classify more complex disease categories. With a dataset comprising 6,748 images, this research utilizes a sufficiently large dataset to provide adequate training data, even though larger datasets exist (e.g., 14,724 images). Nonetheless, this dataset size is adequate for achieving high accuracy.

By integrating the feature extraction capabilities of DCNN with the classification strengths of SVM, this approach yields highly competitive results in detecting sugarcane leaf diseases. It achieves excellent accuracy while effectively classifying a wide range of classes, positioning it as a superior solution in this field.

B. Ablation Studies

In this research, we will conduct an ablation study comparing various classification methods applied alongside DenseNet for feature extraction. The models under consideration include DenseNet combined with Logistic Regression, Random Forest, Decision Tree, Naive Bayes, and several configurations of Support Vector Machines (SVM) using different kernels: linear, polynomial, and sigmoid. By analyzing the performance of these combinations, we aim to identify which classification methods yield the best results in detecting diseases in sugarcane leaves.

The significance of this study lies in its potential to refine model architectures by pinpointing the most effective combinations of feature extraction and classification techniques. Understanding the strengths and weaknesses of each approach will not only enhance disease detection accuracy but also contribute to the broader field of agricultural machine learning applications. Through this systematic evaluation, we hope to provide valuable insights that can guide future developments in plant disease identification.

Table VI displays the outcomes of ablation studies carried out to assess the performance of different classification methods integrated with DenseNet201 for identifying diseases in sugarcane leaves. The evaluation metrics, including accuracy, precision, recall, and F1-score, offer a detailed insight into the effectiveness of each model.

1) Performance Overview

DenseNet201-Logistic Regression: This combination achieved an accuracy of 96.09%, with precision at 96.24%, recall at 96.09%, and an F1-score of 96.12%. These results indicate that Logistic Regression performs well when paired with DenseNet201, effectively balancing sensitivity and specificity.

DenseNet201-Random Forest: The Random Forest model yielded an accuracy of 94.43%, with precision and recall both at approximately 94.43% and an F1-score of 94.38%.

While still effective, this approach shows a notable drop in performance compared to Logistic Regression.

DenseNet201-Decision Tree: This model recorded a significantly lower accuracy of 81.21%, with precision and recall values around 81.32% and 81.21%, respectively, leading to an F1-score of 81.15%. The Decision Tree's performance suggests that it may not be as effective in handling the complexities of disease classification as other methods.

DenseNet201-Naïve Bayes: The Naïve Bayes classifier exhibited the lowest performance among the tested models, achieving an accuracy of only 54.83%. Its precision was relatively high at 67.93%, but recall was low at 54.83%, resulting in an F1-score of 51.87%. This indicates that Naïve Bayes struggles significantly with this classification task.

DenseNet201-SVM (Linear Kernel): This model achieved an accuracy of 95.91%, with precision at 95.93%, recall at 95.91%, and an F1-score of 95.91%. The linear SVM shows strong performance, comparable to Logistic Regression.

DenseNet201-SVM (Polynomial Kernel): The polynomial kernel SVM performed slightly better than the linear variant, achieving an accuracy of 96.21%, precision at 96.17%, recall at 96.21%, and an F1-score of 96.15%. This suggests that the polynomial kernel can capture more complex relationships in the data.

DenseNet201-SVM (Sigmoid Kernel): The sigmoid kernel SVM recorded an accuracy of 87.85%, with precision at 88.40%, recall at 87.85%, and an F1-score of 87.81%. While better than Naïve Bayes and Decision Trees, its performance is still inferior to the other SVM configurations.

DenseNet201-SVM (RBF Kernel - Proposed): This proposed model achieved the highest performance metrics, with an accuracy of 96.74%, precision at 96.75%, recall at 96.74%, and an F1-score of 96.72%. The RBF kernel SVM demonstrates superior capability in classifying diseases compared to all other methods evaluated.

2) Analysis

The findings from these ablation studies reveal several important observations. The integration of DenseNet201 with SVM using the RBF kernel stands out as the most effective approach for detecting diseases in sugarcane leaves, achieving the highest accuracy and balanced metrics across all evaluation criteria. Logistic Regression and Polynomial SVM also performed well, demonstrating their robustness when paired with deep learning-based feature extraction. These results highlight the potential of combining advanced classification methods with deep learning architectures to enhance disease detection capabilities.

On the other hand, simpler models like Decision Trees and Naïve Bayes showed significantly lower performance, suggesting they may not be suitable for applications requiring the recognition of complex patterns. This contrast emphasizes the importance of selecting appropriate classification algorithms that complement deep learning frameworks like DenseNet201. Overall, this ablation study provides valuable insights into how different classification methods interact with DenseNet201's feature extraction capabilities, offering guidance for future research aimed at optimizing plant disease identification systems in agriculture.

C. Discussion

The implementation of DenseNet201 for feature extraction in this study has yielded promising outcomes in detecting diseases in sugarcane leaves; however, several limitations must be acknowledged.

Dataset Imbalance: A primary limitation is the potential imbalance within the dataset. When certain classes are underrepresented, it can lead to biased models that perform poorly on minority classes. This imbalance may cause the model to prioritize majority classes, thereby diminishing its ability to accurately detect less frequent diseases.

Limited Applicability: While DenseNet201 has proven effective for sugarcane leaves, its performance on other crops remains uncertain. The specific features learned from sugarcane may not transfer effectively to other plant types, which restricts the model's applicability in a broader agricultural context.

Computational Demands: DenseNet201 is a complex model that requires substantial computational resources for both training and inference. This high demand for computational power may not be feasible in all agricultural settings, particularly in developing regions where access to advanced hardware is limited.

Interpretability Issues: Although DenseNet201 excels at feature extraction, the interpretability of these features is constrained. Understanding which specific features influence the model's predictions can be challenging, complicating efforts to provide explanations or insights into the reasoning behind certain predictions.

To address these limitations and build upon the findings of this research, several areas for future work are proposed.

- Dataset expansion and augmentation: To mitigate the issue of dataset imbalance, future work should focus on expanding the dataset with more images, especially for underrepresented classes. Data augmentation techniques could also be employed to synthetically increase the size of the minority classes, helping to create a more balanced dataset.
- 2) Transferability to other crops: Future research could explore the transferability of the DenseNet201-based model to other crops. This could involve fine-tuning the model on datasets from different crops or developing a generalized model capable of detecting diseases across multiple types of plants. Testing the model's performance on a variety of crops will provide insights into its robustness and potential for broader agricultural applications.
- Development of lightweight models: Given the 3) computational demands of DenseNet201, future work could involve developing or exploring more lightweight models that require fewer resources while still maintaining high accuracy. Models such as MobileNet or EfficientNet could be considered as alternatives, especially for deployment in resourceconstrained environments. Improving Feature Interpretability: It is important to enhance the interpretability of the features extracted bv DenseNet201. A technique like Grad-CAM (Gradientweighted Class Activation Mapping) can be utilized to visualize the regions of the input images that have the most influence on the model's decision-making process.

This would make the model's predictions more transparent and improve understanding.

- 4) Real-time disease detection: In order to make disease detection more practical for agricultural applications, future research should focus on developing real-time detection systems. This would involve optimizing the model for faster inference times and integrating it into mobile applications or low-power devices that can be directly used by farmers in the field.
- 5) Multi-modal approaches: To improve the robustness of disease detection, future work should explore multimodal approaches that combine image data with other types of data. This could include environmental factors (such as temperature and humidity) or plant metadata (such as growth stage and nutrient levels). Integrating these additional data sources has the potential to enhance the accuracy and reliability of the disease detection system.

IV. CONCLUSION

The approach used in this research combines DenseNet for extracting features and SVM with an RBF kernel for classification, proving to be effective in identifying diseases in sugarcane leaves with a high accuracy rate of 96.74%. However, issues with misclassification between different disease categories remain. To improve the model's performance and ensure more precise and dependable detection, it is expected that using high-quality datasets and advanced methods will be advantageous. The results of this study provide a strong foundation for further progress in plant disease detection using deep learning and machine learning techniques. Future studies could focus on enlarging the dataset by including more images that depict diverse environmental conditions and diseases, which would enhance the model's capability to identify more intricate patterns. Moreover, investigating other deep learning models or creating new hybrid structures could lead to better outcomes in disease identification.

DATA AVAILABILITY STATEMENT

The data used in this research is the public sugarcane leaf dataset which can be accessed on the URL page: https://data.mendeley.com/datasets/355y629ynj/1.

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