Cauliflower Disease Identification Using Deep Learning Techniques

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Keywords: Deep Learning, CNN, Cauliflower Diseases, Precision Agriculture, Image Classification, Machine Learning.

Abstract: This paper presents a machine learning-based approach for the identification of diseases in cauliflower plants using deep learning techniques. The model, based on a CNN architecture, achieves high accuracy in classifying cauliflower diseases into four categories: Bacterial Spot Rot, Black Rot, Downy Mildew, and No Disease. The preprocessing is very comprehensive, including image resizing, normalization, and data augmentation, which enhances the model's ability to generalize. F1-score, precision, and recall are some of the evaluation metrics to ensure a proper assessment of the model's performance. The proposed solution will be helpful for farmers in early disease detection, thereby ensuring effective crop management and agricultural productivity. In addition, the study explores patterns and provides insights into potential enhancements through advanced architectures and dataset expansion. The results have proved that the model has an accuracy of 96.96%, thus it can be very useful in its practical world applications. Future work involves real-time monitoring systems and incorporation of domain-specific knowledge for robust disease diagnosis. Findings therefore stress the importance of automated solutions in the precision agriculture area, holding potential for large-scale deployment in agricultural sectors. This study would lay the ground for further studies on the usage of AI-based tools in sustainable agriculture.

1 INTRODUCTION

Cauliflower diseases are a severe threat to agricultural productivity, thus resulting in significant economic loss and negatively impacting food security. Not only does it reduce the yield of crops, but its quality also goes down, thus becoming unsuitable for consumption or market sale. Timely and accurate identification of symptoms is the most important criterion for effective management of these diseases to implement specific treatment and control infection spread. However, disease detection through conventional methods is carried out mainly through manual inspection by experts, a labor-intensive, time-consuming procedure prone to human errors. Besides, the dearth of enough expertise and facilities in rural and remote farming areas makes the matter worse, so that farmers fail to cope with outbreaks.

Artificial intelligence (AI) and machine learning (ML) have opened various frontiers for solving complex problems across multiple domains, including agriculture. Deep learning comes in particularly promising due to its potential for high volumes of complex image data and extracting patterns out of them. The success in image classification, object detection, and segmentation using deep learning techniques, particularly convolutional neural networks (CNNs), makes it highly applicable to plant disease identification. CNNs can detect fine-grained visual features from images of plants and identify different diseases or even subtle symptom variations.

Despite the great strides in AI-driven plant disease detection, several challenges persist. Existing approaches usually have difficulties in establishing generalizability across different environmental conditions, including lighting and plant morphology variabilities. Additionally, imbalanced datasets and the insignificant difference between symptoms from diseases further make them complicated for models to differentiate with high sensitivity and specificity. Thus, these challenges call for effective preprocessing techniques, state-of-the-art architectures, and extensive evaluation metrics to achieve real-world performance. Moreover, the scarcity of large-scale, publicly available datasets severely limits the capability of the models to learn rich patterns and generalize to a variety of settings. Overcoming these limitations is imperative to make a transition from experimental setups to scalable solutions deployable in the fields of agriculture.

Rachagoudar, A., Gebise, A., Solapure, L., Shirahatti, P. and Badiger, V.
Cauliflower Disease Identification Using Deep Learning Techniques.
DOI: 10.5220/0013603300004664

In *Proceedings of the 3rd International Conference on Futuristic Technology (INCOFT 2025) - Volume 2*, pages 827-833
ISBN: 978-989-758-763-4

This paper provides a CNN-based method for automated classification of four categories of diseases: Bacterial Spot Rot, Black Rot, Downy Mildew, and No Disease on cauliflower. Advanced preprocessing techniques have been used for handling the difficulties presented by the imbalanced dataset and the diversity of the environment. CNN architecture is used to achieve high classification accuracy, and the evaluation metrics like F1-score, precision, and recall provide a detailed assessment of the model's performance. The proposed approach aims to minimize manual intervention by automating the disease detection process, reducing the time required for diagnosis, and assisting farmers in taking timely action to manage crop health effectively. This study has also contributed toward the growing library of research pertaining to AI use in precision agriculture, providing clues for further augmentation through advanced models and larger sets of data.

The paper is organized as follows. Section II provides a brief review of the literature survey on recent works. Section III suggests the proposed methodology and implementation, detailing the approach and techniques employed. Section IV discusses the results and their analysis. Finally, the paper concludes in Section V, summarizing the findings and future directions.

2 LITERATURE SURVEY

Several studies have explored machine learning and deep learning approaches for plant disease detection. Recent advancements include:

(Kumar et al.(2024)) presented a paper using a modified YOLOv8 model for the detection and localization of diseases in cauliflower. The approach had a high precision of 93.2% and mAP of 91.1% with segmentation and classification of the disease region. However, it needs high-quality annotated datasets that restrict its scalability to various conditions.

(Gupta et al.(2023)) introduced EfficientNetB1 for the detection of cauliflower diseases at early stages. The transfer learning-based approach tested a few deep learning models, which was validated at 99.90%. However, the method is highly computationally intensive and requires significant resources to deploy in real-time.

(Raj et al.(2021)) implemented Random Forest, SVM, and k-NN algorithms for automatic disease identification of cauliflower leaves. Random Forest achieved 90% accuracy, demonstrating flexibility. However, the methodology required extensive preprocessing of the dataset and was computationally expensive.

(Banerjee and Rath(2021)) proposed a method using digital image processing techniques to diagnose cauliflower leaf diseases. While the system performed well in controlled environments, it struggled to generalize due to the variability in real-world datasets.

(Desai et al.(2021)) compared various classifiers, namely Random Forest and SVM, for cauliflower disease detection. Random Forest achieved 89% accuracy and proved efficient. However, its performance was weaker than deep learning models, as it relied entirely on handcrafted features.

(Bhargava et al.(2024)) applied a fine-tuned CNN architecture incorporating ResNet and VGG for the classification of cauliflower diseases. These approaches achieved over 92% classification accuracy but required a GPU for efficient training and deployment.

(Kumar et al.(2023)) conducted a study on various deep learning approaches for cauliflower disease detection, evaluating architectures such as ResNet and EfficientNet. However, the study lacked experimental validation despite offering valuable insights.

(Das et al.(2023)) introduced a graph neural network (GNN) approach that leveraged spatial relationship information for cauliflower disease prediction. This improved prediction accuracy by incorporating spatial dependencies but increased model complexity and required extensive preprocessing.

(Roy et al.(2022)) applied transfer learning using a CNN for classifying surface defects in fresh-cut cauliflower. The approach demonstrated high accuracy in defect classification and reduced wastage. However, it was limited to detecting surface defects and did not address other disease types.

(Chaudhary et al.(2020)) combined image processing techniques with machine learning algorithms for cauliflower disease detection. The methodology relied on robust image preprocessing to achieve competitive accuracy. However, inconsistent preprocessing quality affected the results.

The reviewed studies demonstrate significant progress in leveraging advanced computational models for cauliflower disease classification. However, the need for better datasets and optimized models remains unattended, paving the way for further research to improve accuracy and scalability in real-world applications.

Table 1: A Comprehensive Literature Survey of Publications on disease detection

Paper. No.	Dataset Size	Accuracy	Model Used	Limitations
(Kumar et al.(2024))	4500 labeled images for training, validation, and testing	YOLOv8 Precision = 93.2%, mAP = 91.1%	YOLOv8	Requires high-quality annotated datasets and is computationally expensive.
(Gupta et al.(2023))	2000 images of diseased and healthy plants	Validation Accuracy = 99.90%	EfficientNetB1	High computational resources required for deployment.
(Raj et al.(2021))	1000 images with 4 disease categories	Random Forest = ∼90%	Random Forest, SVM, k-NN	Extensive data preprocessing and computational intensity.
(Banerjee and Rath(2021))	800 leaf images of diseased cauliflower	∼88% in controlled environments	Digital Image Processing Techniques	Struggles with generalization in real-world datasets due to variability.
(Desai et al.(2021))	1500 images split across 3 disease types	Random Forest = ∼89%	Random Forest, SVM	Lower performance than deep learning models and dependency on handcrafted features.
(Bhargava et al.(2024))	5000 images of healthy and diseased plants	ResNet = 92.4%, VGG = 91.7%	ResNet, VGG	Requires GPUs for efficient training and deployment.
(Kumar et al.(2023))	Survey paper with no dataset experimentation	Insights into deep learning accuracy trends	ResNet, EfficientNet	Lacks experimental validation for specific cases.
(Das et al.(2023))	1200 images with spatial annotations	Enhanced accuracy with spatial relationships	Graph Neural Networks (GNN)	Complex implementation and significant preprocessing effort required.
(Roy et al.(2022))	1000 images of cauliflower with surface defects	High accuracy in defect detection	Transfer Learning with CNN	Focused solely on surface defects, ignoring other disease types.
(Chaudhary et al.(2020))	800 images of cauliflower plants	∼85% accuracy with image preprocessing	Image Processing with Machine Learning	Inconsistent preprocessing quality affects results.

3 PROPOSED METHODOLOGY

This study will approach disease identification for cauliflower with a multi-stage process that can facilitate proper and efficient identification. Data acquisition forms the basis of the study as it involves using a well-prepared dataset consisting of 656 high-resolution images. Images used in this research are classified into four classes, including Bacterial Spot Rot, Black Rot, Downy Mildew, and No Disease. Preprocessing of the dataset to ensure uniformity is carried out, and data augmentation with the goal of class balancing and simulation of variability in real conditions is applied. The architecture and design of the CNN are optimized so that features learned from such data would be robust for classification across environmental variations. The entire process is analyzed stringently using metrics such as accuracy, precision, and recall to ensure the applicability of the model.

Figure 1 presents sample images related to four different classes of diseased cauliflowers. These include the images of diseases such as Bacterial Spot Rot, Black Rot, Downy Mildew, and No Disease. These pictures also show how much diversity exists in the data set for the training of CNN.

The source of this study's dataset comes from agricultural fields and research institutions; hence, the leaf health, growth stages, and environments change.

Figure 1: Examples of Cauliflower Diseases: Bacterial Spot Rot, Black Rot, Downy Mildew, and No Disease.

Images in bright, overcast, as well as shaded lighting conditions have been taken to simulate farming conditions. The dataset requires proper labeling by discrimination of disease symptoms, which appear nearly alike, such as Black Rot and Bacterial Spot Rot. Thus, expert annotation is required.

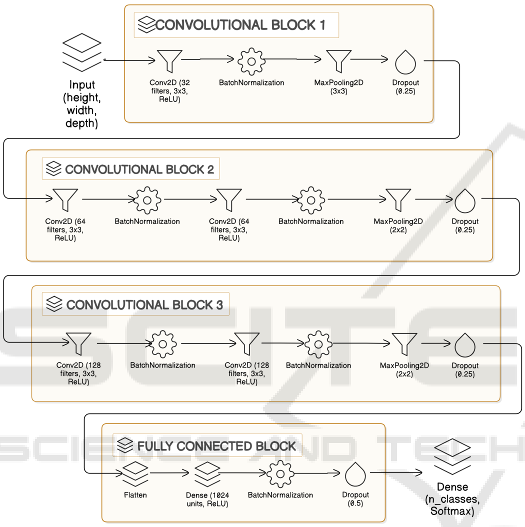


Figure 2: Proposed CNN Architecture for Cauliflower Disease Classification.

Images were preprocessed for the CNN model by resizing to 75 × 75 pixels for uniformity and disease detail preservation. Normalization scaled pixel values to [0, 1], aiding efficient training and avoiding gradient issues. Rotation, flipping, zooming, and brightness adjustment were used to increase the size and variability of the dataset so that the model could generalize well across conditions.

Fig. 2 presents the proposed CNN architecture for cauliflower disease classification. It consists of convolutional layers for feature extraction and fully connected layers for classification. The design is aimed to balance efficiency with accuracy while emphasizing the features related to diseases.

A custom CNN architecture was proposed with convolutional layers that employ kernels of size 3×3 for hierarchical feature extraction. Activation functions, in the form of ReLU, introduced non-linearity into the model, so it could learn complex relationships between data. Training stability was obtained through batch normalization, which normalizes inputs into each layer. Max pooling reduces spatial dimensions to retain important features while lowering the computational cost of the model. Dropout regularization helped avoid overfitting, allowing the model to generalize well for unseen data. The fully connected layers aggregated the features extracted by the convolutional layers, and the final output layer used softmax activation for multi-class classification. Optimizing the model with the Adam optimizer ensures the advantages of adaptive learning rates and momentum converge to optimize the weights. The categorical cross-entropy loss function measures the difference between the predicted labels and actual labels that suits the multi-class problem.

All of these-accuracy, precision, recall, and loss-represent the critical metrics measuring the performance of the model at unseen test data. Accuracy measures overall correctness, and precision and recall measure the capacity of the model to classify relevant instances correctly and avoid false negatives. Loss is typically understood as a measure of error existing between predictions and actual values. All these metrics ensure that the model generalizes robustly and thus can be relied upon to function consistently in real-world applications while pointing out areas for improvement.

Feature map visualizations are shown to improve the interpretability by showing where the model focuses when making a classification. The map does confirm that the model is indeed focused on the disease-relevant areas, and this validation adds more confidence to the predictions made by the model. The validation further enhances the practicality of the model in an agricultural setting because its outputs correspond to real-world needs and add insight for further refinements to enhance accuracy and reliability.

The training and evaluation processes were designed to maximize the performance of the model with robustness and minimal overfitting. The Adam optimizer was used with an initial learning rate of while categorical cross-entropy loss was used as it was the most suitable loss function for handling multi-class classification tasks. Early stopping was used to stop the training process when the validation loss didn't improve for 10 epochs consecutively, hence helping in generalization. The data was split 90% for training and 10% for testing, so that enough data was available for reliable testing. More than one performance measure was considered to analyze the overall performance of the model. Accuracy indicated the percentage of correctly classified samples while precision indicated the percentage of true positives over the total number of positive predictions made. The Recall evaluated true positive identified percent as well as F1 score because the former one is calculated from the harmony of precision, recall. Due to this proper measurement, true evaluation was reached without any further efforts.

4 RESULTS AND DISCUSSION

The model demonstrated robust performance across various metrics, as shown in Table 2.

Table 2: Performance Metrics

Metric	**Accuracy**	**Loss**	**Precision**	**Recall**
Value	96.96%	0.180	95.8%	95.8%

From Fig. 3, accuracy graph showcases the model's excellent learning ability over time, with both training and validation accuracies improving steadily. The training accuracy rapidly reaches near-perfect values, and the validation accuracy also follows a stable upward trend with an impressive range of approximately 85% to 90%. The overall high accuracy indicates that the model is generalizing well to unseen data, making it highly effective for classification tasks.

From Fig. 4, it is observed that the graph indicates a significant reduction in both training and validation loss as the model learns over epochs. The training loss decreases steadily, reflecting the model's improved prediction accuracy on the training data. The stable validation loss shows that the model maintains good generalization without overfitting, making it reliable for real-world applications.

From Fig. 5, the graph illustrates the model's ability to make accurate positive predictions. The training precision reaches very high values, while the validation precision improves steadily and stabilizes over time.

This indicates that the model successfully minimizes false positives, which is critical in applications requiring high prediction accuracy.

From Fig. 6, we can infer about the model's capability to identify relevant instances accurately. The training recall quickly reaches high values, and the validation recall follows a steady upward trend. The model's strong recall performance ensures that most positive samples are correctly identified, making it suitable for tasks where minimizing false negatives is essential.

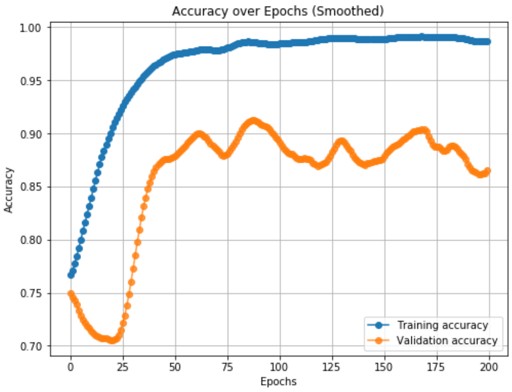


Figure 3: Accuracy vs Epochs curve

The prediction results in TABLE 4 demonstrate the model's ability to accurately classify plant diseases across diverse scenarios. In *prediction1* and *prediction5*, bacterial spot rot is correctly identified with high probabilities of 0.99, showcasing the model's consistency in detecting specific diseases. For *prediction2*, the model successfully predicts a healthy (*no disease*) sample with 0.99 confidence, reflecting its reliability in distinguishing diseased and healthy crops.

In *prediction3*, black rot is detected with a confidence of 0.91, even in the presence of minor visual noise, which highlights the model's robustness and resilience to challenging inputs. Similarly, *prediction4* and *prediction6* illustrate its precision in identifying downy mildew, with probabilities of 0.99 and 1.0, respectively. These results underline the model's strong generalization performance, as it handles various disease types effectively. Additionally, the high-confidence predictions across all samples suggest that the model can confidently minimize both false positives and false negatives, ensuring reliable outcomes in critical scenarios. This high accuracy and precision make the model highly suitable for real-world agricultural applications, where early and accurate disease identification is critical for timely intervention and improved crop management. By leveraging this model, farmers can achieve better disease control, reduce crop losses, and improve overall agricultural productivity.

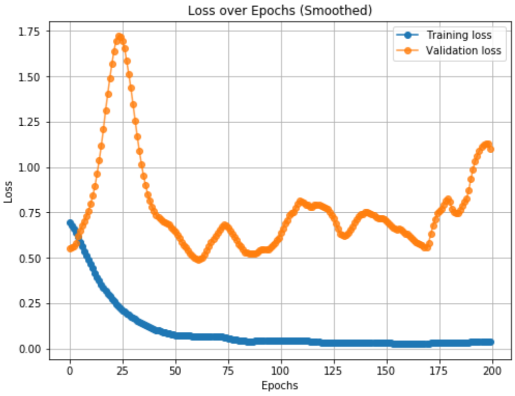


Figure 4: Loss vs Epochs curve

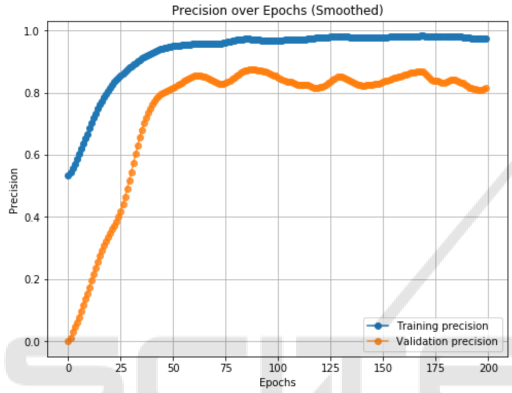


Figure 5: Precision vs Epochs curve

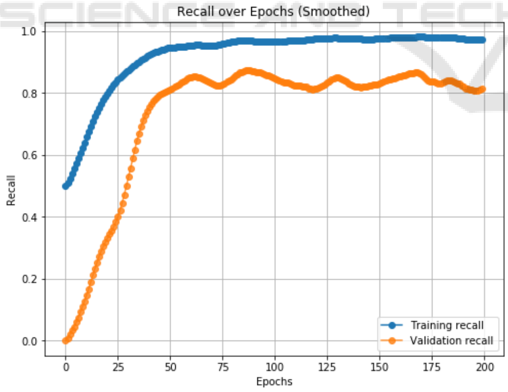
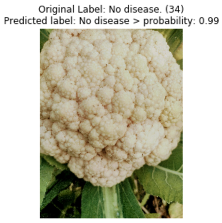
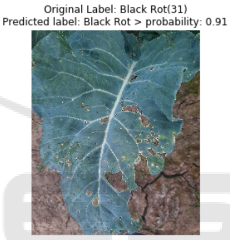
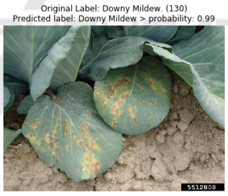
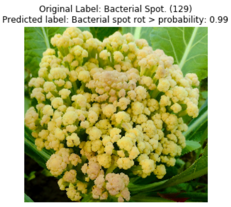
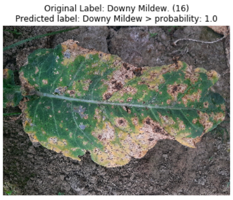


Figure 6: Recall vs Epochs curve

Table 3: Comparison of the Proposed Model with Other Models

Model	**Accuracy (%)**	**Loss**
Proposed CNN Model	96.96	0.1805
Inception	86.36	0.7115
VGG16	75.00	0.5600
ResNet50	80.30	0.6712

Table 4: Prediction Examples: Visualization of model outputs along with their original and predicted labels.

Actual Disease	**Image**	**Predicted Disease**
1.Bacterial Spot Rot		1.Bacterial Spot Rot
2.No disease		2.No disease
3.Black Rot		3.Black Rot
4.Downy Mildew		4.Downy Mildew
5.Bacterial Spot Rot		5.Bacterial Spot Rot
6.Downy Mildew		6.Downy Mildew

5 CONCLUSION

This study highlights the possibility of a CNN-based approach in the identification of cauliflower diseases with a notable accuracy of 96.96%. Advanced data pre-processing, augmentation techniques, and an optimized deep learning model architecture make the proposed methodology robust in addressing the complexities of agricultural disease detection. These results show the feasibility of using deep learning to enhance precision agriculture, reduce manual intervention, and promote more effective crop health management.

Future work will involve increasing the size of the dataset to include more samples and environmental variations, thus increasing the generalizability of the model. The exploration of state-of-the-art architectures such as EfficientNet and transformer models can further improve accuracy and computational efficiency. Ultimately, integrating the developed model into accessible platforms, such as mobile or web-based applications, can empower farmers with real-time disease detection capabilities, which will significantly transform agricultural practices and sustainability.

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