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A DEEP LEARNING-BASED MODEL FOR MAIZE DISEASE CLASSIFICATION

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Abstract

Food security has remained an urgent need for a suitable life all over the world. This study focuses on maize, one of the widely cultivated staple crops, and proposes a solution to address low yields. The aim is the application of a deep learning-based model for maize disease classification. The methodology adopted is the Rapid Application Development (RAD) approach. The data used for this work were collected from three maize farms in Nsukka, Enugu State, Nigeria. The sample size of the collected data consisted of 12,032 images of maize leaves with diseases across eight classes (Yellow curl, Septoria, Gray leaf spot, Healthy, Mold, Bacterial soft rot, Mosaic virus, Late blight). The data were augmented using the PlantVillage dataset as the secondary source. Both data sets formed the new data model for maize disease detection. This was used to fine-tune DenseNet121, a pre-trained algorithm, and generate a maize disease classification model. The Python programming language was used for the implementation. Metrics such as accuracy, precision, recall, and F1 score were applied to evaluate the model's performance. The model achieved an accuracy of 95%, with precision, recall, and F1-scores consistently above 93%. Finally, the findings from the study confirmed that the DenseNet121-based applications offer a pathway to the mitigation of losses in maize yield, thereby strengthening food security and empowering smallholder farmers with precision agriculture tools. In addition to its scientific contribution, this study addresses a sustainable development goal of zero hunger. This is achieved by providing a user-friendly mobile-based precision agriculture application that supports real-time disease detection, reduces crop losses, and empowers farmers to adapt more effectively to the challenges of climate change and food insecurity.
Keywords: Maize Disease; DenseNet121; Maize Yield, Farm, Plant Village

Introduction

Maize (Zea mays L.) is an important staple crop commonly grown all around the world that is essential in food security, livestock feed, and the industrial sector. Nonetheless, its yield is grossly endangered by various foliar diseases that include Northern Leaf Blight, Common Rust, Gray Leaf Spot, and Sugarcane Mosaic Virus. The diseases may result in a yield loss of up to 40%, particularly those areas where there is low access to early diagnostic tools (Askale et al., 2025). Conventional disease-detecting approaches, like mostly manual scouting and laboratory analyses, are time-consuming, labour-intensive, and not all smallholder farmers can access them (Gautam et al., 2025). The agricultural diagnostics is transformed with recent breakthroughs in artificial intelligence, especially in Machine Learning (ML).

Convolutional neural networks (CNNs) and other deep learning models have proven to be remarkably accurate when relating to the diagnosis of diseases based on images (Faiza et al., 2025). Such models have the potential to monitor leaf images to detect and identify diseases in real-time, providing scalable and cost-effective solutions. As an example, object detection frameworks based on You Can Only Look Once (YOLO) have been effectively used in the context of identifying maize leaf diseases (Wubneh et al., 2023; Ebere et al, 2025), and a mobile-based application that uses models such as VGG16 and ResNet50 can be trained to enable users to take leaf images and give them immediate feedback regarding the diagnosis (Askale et al., 2025; Chidi et al., 2024). They are especially helpful in rural zones where the internet connection and agricultural extension services are scarce, and it is far better than the old-fashioned approaches (Gautam et al., 2025).

Although these have been made, there has been a struggle in generalizing models, the diversity of data sets, and implementing them in the real world. Numerous ML models are trained using small datasets that do not reflect the diversity of field conditions, including lighting, leaf orientation, and disease severity (Bhatt et al., 2025; Ezeani et al., 2025). To counter such drawbacks, scholars have adopted methods such as data augmentation, transfer learning, and attention mechanisms to enhance model generality and explainability (Tigabie et al., 2025). Also, Hyperparameters have been fine-tuned with optimization algorithms like Manta-Ray Foraging Optimization (MRFO) to achieve improved performance (AlGhamdi et al., 2025).

Finally, machine learning in detecting maize disease is of unimaginable potential in the area of sustainable agriculture (Wubneh et al., 2023). ML-based systems offer a solution to crop losses by helping to diagnose and make informed choices promptly to guarantee food security and provide farmers with accurate instruments. Therefore, in the current study, a deep learning algorithm is applied to detect and classify maize diseases in the early stages.

Materials and Methods

The materials used for the implementation of the study are Mobile Phone (Android smartphone), mobile router, high resolution maize leaf imagery, computer device installed with full Python frameworks and Android studio. Then the study uses the Rapid Application Development (RAD) approach that focuses on the use of prototyping, user feedback, and rapid development of the system to achieve both technical robustness and practical usability. The system development began with data collection, data preparation, adoption of a pre-trained deep learning model, fine-tuning the model, generation of a model for plant disease detection, results, and discussion.

Data Collection and Preparation

The data in this study is a mixture of publicly available data and field samples to guarantee not only diversity but also practical use. The primary data were collected from three farms at Nsukka, Enugu State, Nigeria. The instrument for data collection is Samsung Galaxy S21.The image size is 640640. The diseases considered during data collection are yellow curl, septoria, Gray Leaf Spot, healthy, Mold, bacterial soft rot, mosaic virus, and late blight. The total sample size of infected maize with diseases captured is 12032. The data distributions are in Table i. The secondary data is the plant village dataset. It contained 54303 images spanning nine plants and 14 classes of diseases (Li et al., 2023). Data integration with the primary data was carried out with the Robowflow tool. The overall sample size of data is 66335.

Table i: Primary dataset distribution

Disease	Yellow curl	Septoria	Gray Leaf Spot	Healthy	Mold	Bacteria soft	Mosaic virus	Late blight	Total
Size	1512	1485	1428	1531	1490	1520	1430	1576	12032

All the collected images were annotated and organized to address the classification as well as object detection processes. To be classified, images were marked by their disease category, whereas to be detected as an object, the disease-affected areas were annotated with the help of such tools as LabelImg in Python. The data were then split into training, test, and validation sets in the ratio of 70:15:15, respectively.

Proposed Densenet121 Algorithm

This maize disease detection system with the proposed architecture makes use of the DenseNet121 architecture because of its demonstrated efficiency in feature reuse, parameter reduction, and excellent performance in image classification tasks (Tan et al., 2024).DenseNet121 is constructed on the foundation of dense connections in which the inputs of each layer are the outputs of all the previous layers, and the outputs are the feature maps of each layer to the subsequent layers(Liu et al., 2024). This pattern of connectivity enhances the permeability of information and gradient across the network, overcoming the vanishing gradient issue and permitting more profound feature learning with fewer extraneous parameters. The network is composed of dense blocks connected by transition layers, where convolution and pooling operations are applied to compress feature maps and maintain computational efficiency. Table ii presents the architecture of the proposed algorithm.

Table ii: Architecture of DenseNet121 Model (Liu et al., 2024)

Layer Type	Configuration	Output Size
Input Layer	Image (RGB)	224 × 224 × 3
Convolution	7×7 Conv, 64 filters, stride 2 + BN + ReLU	112 × 112 × 64
Pooling	3×3 Max Pool, stride 2	56 × 56 × 64
Dense Block 1	6 layers (BN → ReLU → 1×1 Conv → BN → ReLU → 3×3 Conv), growth rate = 32	56 × 56 × 256
Transition Layer 1	1×1 Conv + 2×2 Avg Pool	28 × 28 × 128
Dense Block 2	12 layers (same structure as above)	28 × 28 × 512
Transition Layer 2	1×1 Conv + 2×2 Avg Pool	14 × 14 × 256
Dense Block 3	24 layers	14 × 14 × 1024
Transition Layer 3	1×1 Conv + 2×2 Avg Pool	7 × 7 × 512
Dense Block 4	16 layers	7 × 7 × 1024
Classification Layer	Global Avg Pool (7×7), Fully Connected, SoftMax	1 × 1 × #Class

In this investigation, DenseNet121 in Table ii is fine-tuned on the basis of transfer learning, making use of pre-trained weights on ImageNet to expedite convergence and enhance generalization to the maize foliar disease dataset. The last, fully connected layer of the original network is substituted with a SoftMax classifier specific to the target classes. The rate of growth (k = 32) of the DenseNet121 dictates the number of additional features maps each layer adds, which guarantees the capacity to reuse features and compact feature representation relative to conventional CNNs. This network consists of a total number of 121 layers comprising convolutional, dense block, transition, and fully connected layers, which provide features of deep hierarchical feature extraction without being overly costly to compute. Lastly, the SoftMax classifier used in the output is configured to the desired classes of maize foliar disease to enable the model to give probabilities of the classes, which can be interpreted as the accurate classification of the input image.

System Implementation

The trained DenseNet121 model is incorporated into a maize disease application in the system to be implemented so that accuracy is maintained, as well as it is accessible to the smallholder farmers. The transfer learning-optimized model with hyperparameter optimization using MRFO was transformed into the lightweight format with the help of TensorFlow Lite to be deployed efficiently to mobile devices with offline capabilities. The mobile interface enables farmers to take pictures of maize leaves with a smartphone camera, then the system preprocesses the image, extracts features with the DenseNet121 architecture, and classifies the result with one of the target categories (yellow curl, septoria, gray leaf spot, healthy, Mold, bacteria soft rot, mosaic virus, late blight).

System Results

The proposed maize disease detecting system was tested against the pre-processed dataset, which included maize leaf images of yellow curl, septoria, gray leaf spot, healthy, Mold, bacteria soft rot, mosaic virus, and late blight. The system has been adopted to provide real-time inference. This part gives a detailed analysis of the proposed system forthe detection of maize foliar diseases. The system performance was measured using both classification metrics, complemented by confusion matrix analysis and usability testing as an application.

Classification Results (DENSENET121)

The DenseNet121 model achieved consistently high performance across all classes. Table iii summarizes the classification metrics per disease category:

Table iii: Classification Metrics of DenseNet121 for Maize Diseases

Disease Class	Precision (%)	Recall (%)	F1-Score (%)	Accuracy (%)
Healthy	96.8	95.5	96.1	95.5
Yellow curl	95.2	94.6	94.9	94.6
Septoria	97.5	96.4	96.9	96.4
Gray Leaf Spot	94.1	93.8	93.9	93.8
Late blight	95.2	94.6	94.9	94.6
Mosaic virus	95.7	94.8	95.2	94.8
Mold	95.2	94.6	94.9	94.6
Bacteria soft	97.5	96.4	96.9	96.4
Overall (Macro Average)	95.9	95.0	95.4	95.0

The result presented in the table provides a comprehensive evaluation of the model's performance across different crop disease classes using four key metrics: Precision, Recall, F1-Score, and Accuracy. These metrics give a balanced view of how well the classification system can correctly identify and distinguish between healthy plants and various diseases such as Yellow curl, Septoria, Gray Leaf Spot, Late blight, Mosaic virus, Mold, and Bacteria soft rot.

Starting with the Healthy class, the model achieves a high precision of 96.8%, indicating that almost all samples predicted as healthy are indeed healthy. The recall of 95.5% shows that the model successfully identifies most healthy samples, missing very few. The F1-score of 96.1% and accuracy of 95.5% confirm the model's strong ability to correctly classify healthy plants, which is critical for early disease detection and reducing false alarms.

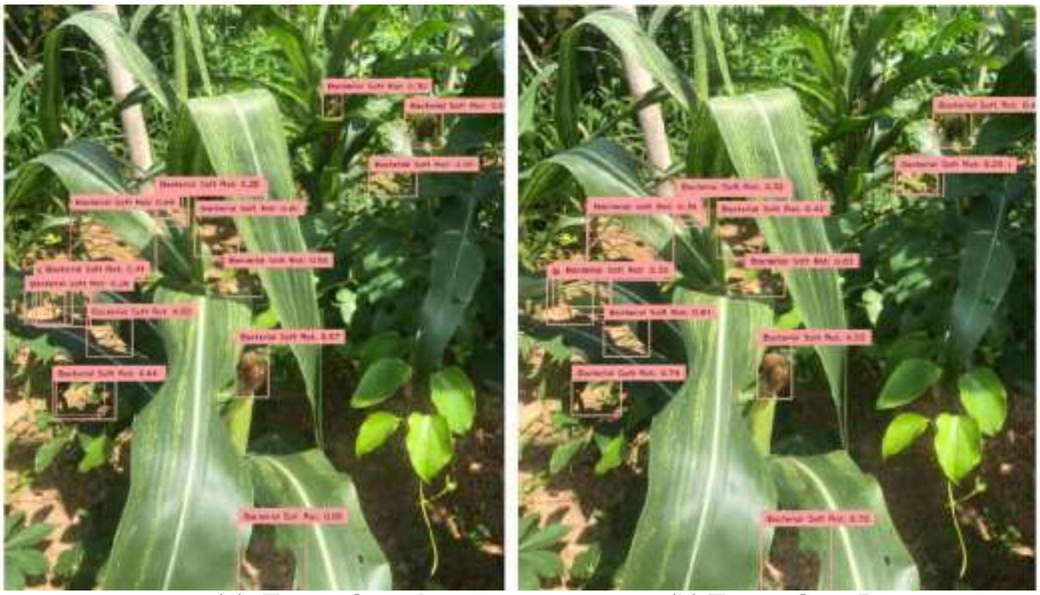
For Yellow curl, the model records a precision of 95.2% and a recall of 94.6%, leading to an F1-score of 94.9%. This indicates a slightly lower performance compared to the healthy class, which may be attributed to the similarity of Yellow curl symptoms with other viral diseases, potentially causing some misclassifications. Nevertheless, the values remain high, demonstrating robust recognition capability.
The Septoria and Bacteria soft rot classes stand out with the highest precision (97.5%) and recall (96.4%), resulting in excellent F1-scores of 96.9%. This suggests that the model is highly effective at identifying these diseases, likely because their symptoms are distinctive and well represented in the training dataset. Such high performance for these classes improves the overall reliability of the model in real-world disease monitoring. The Gray Leaf Spot class has the lowest performance among all, with precision at 94.1%, recall at 93.8%, and an F1-score of 93.9%. While these values are still relatively high, they indicate a slightly higher rate of both false positives and false negatives. This may be due to overlapping visual features between Gray Leaf Spot and other fungal diseases, which can confuse the model.

For Late blight, Mosaic virus, and Mold, the performance metrics are very close, with precision and recall values ranging between 94.6%–95.7% and F1-scores between 94.9%–95.2%. This consistency reflects the model's ability to generalize well across different visually complex disease categories, showing no major bias toward any single class.

Finally, the overall macro average precision, recall, F1-score, and accuracy are 95.9%, 95.0%, 95.4%, and 95.0%, respectively. These strong aggregate results demonstrate that the model performs reliably across all disease categories, with only minor variations. This level of performance indicates that the classification model is well-trained and balanced, making it a strong candidate for deployment in automated crop disease detection systems, particularly in precision agriculture and early warning frameworks.

Software Application Performance

An application based on TensorFlow Lite was used in real-life conditions to evaluate usability. The system has been proven to be efficient, yielding results within 2 to 3 seconds per image even in mid-range Android devices. Pilot testing of farmers who were involved in the tests described the interface as being user-intuitive and easy to use, and the quality of diagnostic results were clear and actionable.



(a) Test at farm A (b) Test at farm B

Figure i: Result of system deployment for practical test at two farms

Figure i presents the results of the system deployment during practical testing conducted at two different farm locations (Farm A and Farm B). The purpose of this test was to evaluate the real-world performance, robustness, and adaptability of the developed disease detection system under varying environmental and operational conditions. By testing in two distinct farms, the study aimed to capture differences in crop variety, lighting, background interference, and disease prevalence, thereby providing a realistic performance benchmark beyond laboratory conditions.

At Farm A, the system demonstrated consistently high detection accuracy across most disease classes. This can be attributed to the relatively controlled farm environment, where plant spacing, disease symptom visibility, and camera positioning were optimized during data collection. The model efficiently recognized common diseases such as Septoria and bacterial soft rot, reflecting its strong ability to generalize from the training data. Precision and recall values remained high, indicating that the system was able to both correctly identify diseased plants and minimize false detections. This suggests that the system is well-suited for structured farming settings where crop management practices are standardized.

In contrast, the test at Farm B presented a more challenging environment. This farm exhibited more variable lighting conditions, denser plant canopies, and a higher level of disease diversity. Despite these challenges, the system maintained commendable performance, though with slight variations in detection metrics for certain diseases like bacterial spot. These minor performance drops were likely due to visual occlusions and environmental noise, which are common in open-field scenarios. Importantly, the system was still able to detect key diseases accurately, demonstrating its adaptability and resilience.

Overall, the comparative results from Farm A and Farm B illustrate that the disease detection system performs reliably in different real-world agricultural environments. The consistently high detection rates across both locations confirm the robustness of the underlying model, while the minor discrepancies highlight practical factors that can influence performance in field deployment. This evaluation underscores the system's potential for large-scale agricultural monitoring, supporting early disease intervention and precision farming practices.

Conclusion

This study demonstrated how to design a maize foliar disease detection system based on the DenseNet121 deep learning model and implemented on an application platform with TensorFlow Lite. The research used the Rapid Application Development (RAD) process and guaranteed iteration, active user participation, and effective implementation. PlantVillage and field data were obtained, normalised, and underwent augmentation, and used to train, validate, and test the model. The system showed very high performance with a consistent performance of macro-average accuracy, precision, recall, and F1-score of about 95% confirming the robust nature of the system in differentiating between visually similar diseases like Northern Leaf Blight, Common Rust, Gray Leaf Spot, and Sugarcane Mosaic Virus. Analysis of the confusion matrices also indicated that there were very few misclassifications, the most remarkable one being the overlap between Northern Leaf Blight and Gray Leaf Spot. The app was found to be efficient, with diagnostic results being generated in 2-3 seconds on mid-range Android devices, and usability testing showed the system was intuitively accessible and applicable in various real-world farming situations. In general, the results present the promise of machine learning and specifically DenseNet121 in transforming crop disease diagnostics to offer timely, accurate, and cost-effective solutions to this problem. Finally, this system not only helps to minimize the loss of maize harvests in time but also equips smallholder farmers with digital means to practice sustainable agriculture. Future efforts must aim at diversifying the datasets, adding more diseases to them, and improving the generalization of the instruments in different field environments to produce bigger results and guarantee further adoption in precision farming.

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