Vol. 6, No. 1, pp 1 - 12, 2025
DOI: 10.55969/paradigmplus.v6n1a1

PARADIGM *Plus*

Detection of Cassava Plant Disease using Deep Transfer Learning Approach

Samson Adebisi Akinpelu [1,✉], Odunayo Emmanuel Olasoji [2], Akindayo Akindolani [3], Korede Israel Adeyanju [4], Sunday Adeola Ajagbe [5], and Gbadegesin Adetayo Taiwo [6]

[1]*University of Kwazulu-Natal, Durban, South Africa*
`samson.akinpelu@fuoye.edu.ng`
[2]*Federal University Oye-Ekiti, Oye-Ekiti, Nigeria*
`odunayoemmanuel1996@gmail.com`
[3]*McAnderson Institute of Technology, Derby, United Kingdom*
`dayo@mcandersoninstitute.tech`
[4]*Sheffield Hallam University, Sheffield, United Kingdom*
`deyanjukorede@gmail.com`
[5]*Abiola Ajimobi Technical University, Ibadan, Nigeria*
`saajagbe@pgschool.lautech.edu.ng`
[6]*University of Salford, Manchester, United Kingdom*
`g.a.taiwo@edu.salford.ac.uk`

Abstract

Small-scale farmers use cassava as an essential crop for food and nutrition security, owing to its capacity to flourish under adverse situations. In numerous African countries, it serves as a significant source of carbohydrates. Leaf diseases can sometimes damage cassava crops, constraining overall output and farmers' revenue. The ongoing research on cassava disease is fraught with challenges, including a low detection rate, extended processing time, and inadequate precision. This research employs deep transfer learning with Visual Geometry Group (VGG16) models for the diagnosis of Cassava leaf diseases. An experimental study is conducted on a dataset of 5,656 images of cassava, categorized into four distinct disease classifications. Two of the most sophisticated predictions were generated: one identified the healthy leaf, while the other detected the diseases present on the unhealthy leaf. Our suggested deep transfer learning model attains a promising accuracy of 88% and an F1-score of 82% on the public plant disease dataset from the Kaggle repository, achieved through effective hyperparameter fine-tuning. The results of this study strongly advocate for additional research and practical application of deep learning models in plant disease diagnostics.

Keywords: Deep learning · Cassava Disease · Convolutional Neural Network · Farming · VggNet Model

Received: 11 February 2025 · Accepted: 7 April 2025 · Published: 28 April 2025.

1 Introduction

Deep learning is a computer method used to tackle problems defined by complex patterns that would generally be unfeasible for a human programmer to directly identify and convert into a program. It also relates to the automatic recognition of noteworthy patterns in data, functioning as a beneficial tool in disease diagnosis that helps alleviate the adverse effects of plant diseases on total food production. The importance of this result is heightened when considering worldwide demographic data. The global population currently stands at 7.6 billion, projected to increase to 10 billion by 2050. Despite the projected population growth, merely 11.58% of the landmass—17.25 million sq. km, or 6.66 million sq. km—is allocated for agriculture, providing insufficient space for the expanding human populace. Central Intelligence Agency, 2016; United Nations, Department of Economic and Social Affairs, Population Division, 2017 The typical individual consumes approximately 2940 kcal of food daily.

Cassava plant is an annual root crop cultivated in several countries. It is the most extensively planted root crop, yielding an edible tuber that serves as the third primary source of carbohydrates for around 800 million people globally, following rice and maize. It is often classified as sweet or bitter based on the concentration of cyanide compounds, with global production estimated at approximately 203 million megatonnes. As a predominant root crop globally, It supplies about 40% of the caloric intake for the African people [1]. In 2014, around 145 million tons of cassava were cultivated across 17 million hectares in Africa. This plant is regarded as essential for food security particularly in regions where there is shortage of food and revenue, due to its robust yield under conditions of low soil fertility and erratic rainfall [2]. The challenges faced by peasant farmers, which has be threatening their agricultural productivity, include change in climate, volatility of market, and outbreaks as result of pest.

The 16th century marked the introduction of cassava from South America to Africa, where it initially faced few pest and disease challenges. The most economically detrimental pests were two arthropods inadvertently introduced from the neotropics in the 1970s: the cassava mealybug and the cassava green mite [3]. Cassava viral diseases encompass brown streak and mosaic disease. Mosaic illness was the inaugural ailment documented in Tanzania at the close of the 19th century. In East Africa, the emergence of a virulent strain of the virus in the 1990s, identified as East African cassava mosaic virus (EACMV-UG or UgV), combined with the susceptibility of local cultivars, constituted a substantial threat to food security in the region, forcing farmers to abandon cultivation [4]. Notwithstanding incremental advancements in the management of CMD and CBSD, these two diseases have become the foremost obstacles to cassava cultivation and food security in sub-Saharan Africa, resulting in annual losses over US $1 billion [5]. Timely identification in the field is an essential preliminary measure for regulating the detection and spread of cassava diseases.

The traditional method of disease detection relies on agricultural extension organizations; however, these methods are costly to implement and constrained in nations with inadequate manpower and logistical resources. Advancements in unmanned aerial vehicles (UAVs), smartphone technology, and internet accessibility in these regions provide novel instruments for automatic image recognition in the diagnosis of plant diseases in the field, facilitating extensive early detection. Previous research has demonstrated the automated detection of leaf images for agricultural diseases in wheat and apples [6], as well as on datasets comprising both healthy and unhealthy plants [7]; unmanned aerial vehicles (UAVs) have also utilized similar technologies. Automated image identification by feature extraction has demonstrated encouraging outcomes in identifying cassava infections [8]; nevertheless, feature extraction is resource-intensive and necessitates specialized expertise for optimal results. Models must be efficient and optimized for constrained processing power to leverage smartphone technology. Deep transfer learning, wherein a model trained on an extensive image dataset provides an efficient solution for deep learning challenges by directly applying weights and reducing processing requirements [9, 10]. To this end, this work examined the feasibility of fine-tuning a pre-trained deep learning model to identify cassava disease occurrences using an in-field dataset of

5,756 cases. In other words, we utilized deep transfer learning with Visual Geometry Group (VGG16) models for diagnosing Cassava leaf diseases. An experimental investigation is performed on a dataset of 5,656 photographs of cassava, classified into four unique illness categories. Two highly advanced predictions were produced: one recognized the healthy leaf, while the other identified the diseases affecting the unhealthy leaf.

The rest of this paper is structured as follows: Section 2 provides an overview of the related works and discusses deep transfer learning with respect to plants diseases detection; Section 3 offers the methodology for the deep transfer learning with respect to plants diseases detection system. Section 4 provides the findings and its thorough explanation; Section 5 then wraps up the paper and offers future direction.

2 Related Work

Cassava is a starchy root plant commonly referred to as manioc. Individuals in impoverished nations depend heavily on it for nourishment due to its substantial carbohydrate content. It flourishes in tropical places globally owing to its robustness against extreme weather and unfavorable climatic conditions. Cassava roots have been cultivated predominantly by many continents, such as Latin America, Africa, etc [11]. Approximately 500 million individuals in tropical locations, predominantly in Africa, depend on manioc as their primary source of sustenance. In Asia and Latin America, cassava output is mostly utilized for agricultural purposes and as livestock feed. Human consumption is a significant portion of manioc production in Africa [12]. The root is the mostly consumed part of cassava plant. It can be ground, grated, or utilized whole to produce flour or starch, incorporated into bread, crushed or grated into meal, or transformed into an alcoholic beverage. The agricultural organization forecasted that cassava output in sub-Saharan Africa would attain 161 million tons in 2018, representing a 2% rise over 2017. Cassava is vulnerable to numerous viral diseases, including green mottle, cassava symptomless, vein mosaic, frog skin-associated, Colombian symptomless, Ivorian bacilliform. Early symptom of these diseases encompasses mottling, twisted and malformed leaves, and a decrease in plant size. They devastate cassava plants and cause economic loss by preventing fruit production [13].

The disease markedly diminishes tuber yield, depending on its severity and the plant's age during infection [14]. Artificial Intelligence (AI) methodologies are employed in precision agriculture to swiftly detect the onset of these illnesses [15].

Recent research indicates that deep learning methodologies, particularly convolutional neural networks (CNN) which has exceptional ability to extract significant features from images, thereby surpassing traditional algorithms. Moreover, its results can be enhanced when its parameters are optimized [16]. Previous findings reveal that deep learning algorithms are extensively utilized by academics and researchers for the diagnosis of diverse plant diseases, including those impacting banana, tomato, rice, and citrus. This may be ascribed to the efficacy of these algorithms in addressing issues related to image classification. Ramcharan et al. [17] developed a convolutional neural network (CNN) to categorize five diseases based on photos of cassava infections. The optimal model has an accuracy of 98% CBSD, BLS disease, 96% for mosaic, and 95% for green mite damage. The overall accuracy of the optimal model was 93%. Their research shown that transfer learning approaches provide a swift, economical, and accessible means for detecting plant illnesses. Ramcharan et al. [17] presented a smartphone-based DCNN detection model with an accuracy of 94%, whereas [18] used the exact dataset and attained an accuracy of 96% and corresponding F-measures. Sambasivam and Opiyo [19] achieve an accuracy of 93% for cassava plant disease through predictive models of a machine learning and dataset augmentation to mitigate substantial class imbalance.

Abdullakasim et al. [8] examined and identified brown leaf spot in cassava utilizing artificial neural networks (ANN). Their methodology accurately detected 89.92% of healthy plants and 79.23% of diseased leaves. They examined merely two classrooms and overlooked further ailments. Coulibaly et al. [20] proposed a method that integrates feature selection with transfer learning to classify mildew disease in pearl millet. The authors employed deep learning to efficiently and engagingly examine precision agricultural data. The advantage of their technology is in its capacity to enhance agricultural yield for farmers.

Ramcharan et al. [17] utilized deep convolutional neural networks to identify several illnesses in cassava. The confusion matrix and classification accuracy of the proposed technique are both outstanding. The constraint of their methodology is that the system's efficacy was exclusively evaluated against k-Nearest Neighbor (kNN) and Support Vector Machine (SVM). Moreover, the only performance evaluation metrics included in that study were accuracy and the confusion matrix. The available data is insufficient to adequately assess the efficacy and robustness of any categorization approach. Lu et al. [21] suggested an active automated method for detecting wheat diseases via a supervised learning framework. The proposed model has exceptional accuracy, exceeding that of conventional CNN models. The proposed model's shortcomings encompass a limited number of wheat disease images in the database employed for their research. Accuracy is the sole metric employed to assess model performance, and it is insufficient to validate the system's efficacy. Ferentinos [22] presented a Deep Convolutional Neural Network model for the identification of plant diseases. The dataset contains around 87,848 images, encompassing 25 distinct plant species classified into 58 broad groups of damaged and healthy specimens. The algorithm provides substantial categorization accuracy and serves as a rapid advice tool for farmers.

Abayomi-Alli et al. [23] generated more plant images through augmentation techniques and the MobileNetV2 neural network to classify cassava diseases. Nonetheless, there was no comparison between the results obtained prior to and subsequent to the augmentation of leaf images. Capizzi et al. [24] proposed a radial basis function neural network (RBPNN) for the diagnosis and classification of plant leaf diseases. Zhang et al. [25] introduced a multi-attention network utilizing anti-aliasing to augment the precision of cassava leaf disease classification by enhancing feature quality in coarseness label classification, achieving a classification accuracy of 95.63%. Nevertheless, the approach incurs significant computing costs. We introduce a transfer learning-based approach that effectively resolves the significant shortcomings noted in the previously described methodologies. We demonstrate the application of hyperparameter optimization alongside deep transfer learning for the detection and classification of cassava mosaic disease.

3 Methodology

The identification of a suitable feature to distinguish between different diseases is essential due to the specific characteristics of the image. The human perceptual approach for diagnosing cassava diseases from leaf images depends on pixel intensity distribution, textural features, and several supplementary indications. In the past, the appearance of leaves allowed farmers to identify the type of disease and the suitable pesticide to utilize, owing to their profound knowledge and skill. The future of agriculture is advancing towards digitalized smart farming. A deep learning network is proposed to automate visual feature extraction and disease classification, as illustrated in Figure 1.

3.1 Functional Components of the Proposed VggNet Model

The proposed model comprises of input layer, 4 convolution layers, Max-pooling, Fully connected layer, Dropout layer, Dense layer and Softmax activation function.

1° **Input Layer**: The input layer received the leave cassava image (Img_cassava of size, z), with (z) the dimension of the image. The leave image first goes through the preprocessing stage where the size of image is made fit for the model. We utilize 224 x 224 x 3 as the standard input dimension for the proposed VGG16 model.

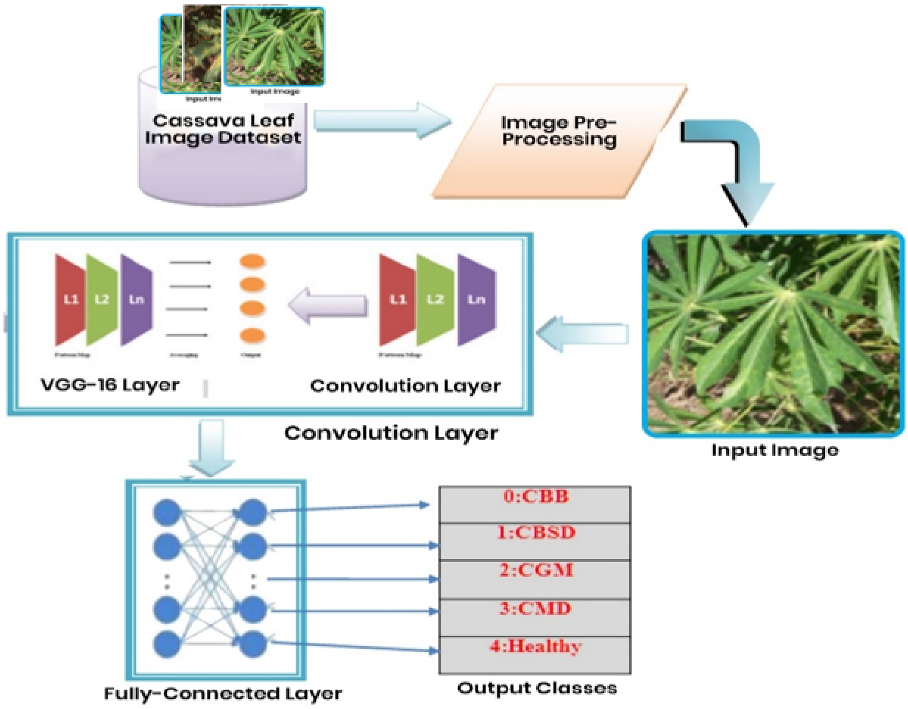


Figure 1: The Proposed model architectural framework

2° **Convolutional Layers**: The convolutional layers employed filters on the input to extract local features. For each convolutional layer (r), the feature map Fr (x, y) was calculated utilizing a 2D convolution operation as computed in equation 1.

$$F_r(x,y) = \sum_{i=1}^{k_x}\sum_{j=1}^{k_y}(x+i, y+j)\cdot W_r(i,j) + b_l \tag{1}$$

where $W_r(i,j)$ represents the convolutional filter of size (kx×ky), and br denotes the bias term. This process generated feature maps that emphasized significant patterns in the leave image.

3° **Rectified Linear Unit**: Thereafter, the output from the convolutional layers was subjected to an activation function for a Rectified Linear Unit (ReLU) to account for non-linearity as depicted in equation 2.

$$F'_r(x,y) = \max(0, F_r(x,y)) \tag{2}$$

This guaranteed that solely positive activations were sent to the subsequent layer.

4° **Dropout Layers**: The dropout layer of the network enable the model to generalized well on unseen data through the training the model on different subsets of neurons. It prevents overfitting. The use of dropout leads to better generalization on unseen data. By training the model with different subsets of neurons, it becomes more adaptable and performs better when faced with new inputs.

5° **Max-Pooling Layers**: Max-pooling was utilized to diminish the feature maps' spatial dimensions while maintaining key characteristics. The pooling process is defined in Equation 3

$$P_r(x, y) = \max_{(i,j)\in\mathbb{R}} F'_r(x + i, y + j) \tag{3}$$

where R represents the pooling window, commonly sized (2×2).

6° **Fully Connected Layers**: Following the processing of features by the layers of convolutions, they were flattened and sent via fully connected (dense) layers to generate the final detection of cassava disease.

7° **SoftMax Output Layer**: A SoftMax activation function was ultimately applied to the output of the fully connected layers to forecast the probability distribution across the cassava disease classes and class with the greatest likelihood was chosen as the predicted cassava disease.

8° Hardware Specification: Table 1 contains the details of the hardware specifications environment in this study.

Table 1: Hardware Specification

S/N	Operating Systems	Ubuntu 18.04
1	RAM	4.00GB
2	Processor	Intel® Core TM i3 6100U, CPU @2.30 GHz, 2.30GHz
3	Type of the system	16-bits OS, x-64 based processor

3.2 Dataset Acquisition

This research utilized dataset of images for cassava diseases from Kaggle public repository. The dataset comprises 5,656 photos, featuring an uneven distribution of 316 healthy cassava leaves and four categories of diseased cassava leaves: CBB (466), CBSD (1,443), CGM (773), and CMD (2,658). The images were captured by professionals in farming domain and labeled by experts, as shown in Figure 2. The dataset was standardized using a pre-processing technique to ensure conformity with model requirements. The training to test set ratio is 80:20 to ensure effective model generalization and prevent overfitting.

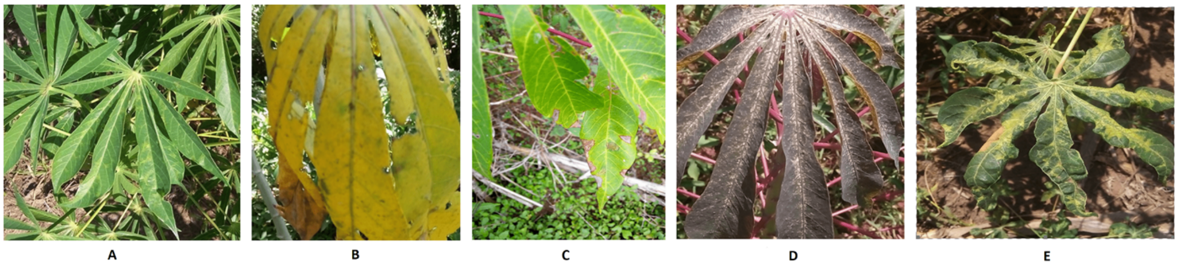


Figure 2: Images of healthy and unhealthy Cassava Leaf. (A) CBB, (B) CBSD, (C) CGM, (D) CMD, and (E) Healthy

3.3 Evaluation Metrics

To examine the performance of our proposed model in this study, we utilized the standard evaluation metrics. These metrics include accuracy, F1-Score and Precision and they are computed using Equations 4, 5, and 6 respectively. The accuracy indicates the percentage of accurate prediction of cassava disease from the total number leave image in the dataset, and Precision is the ratio of true and false positive predictions to the ratio of positive predictions, whereas the F1-score is the simple harmonic mean of recall and accuracy.

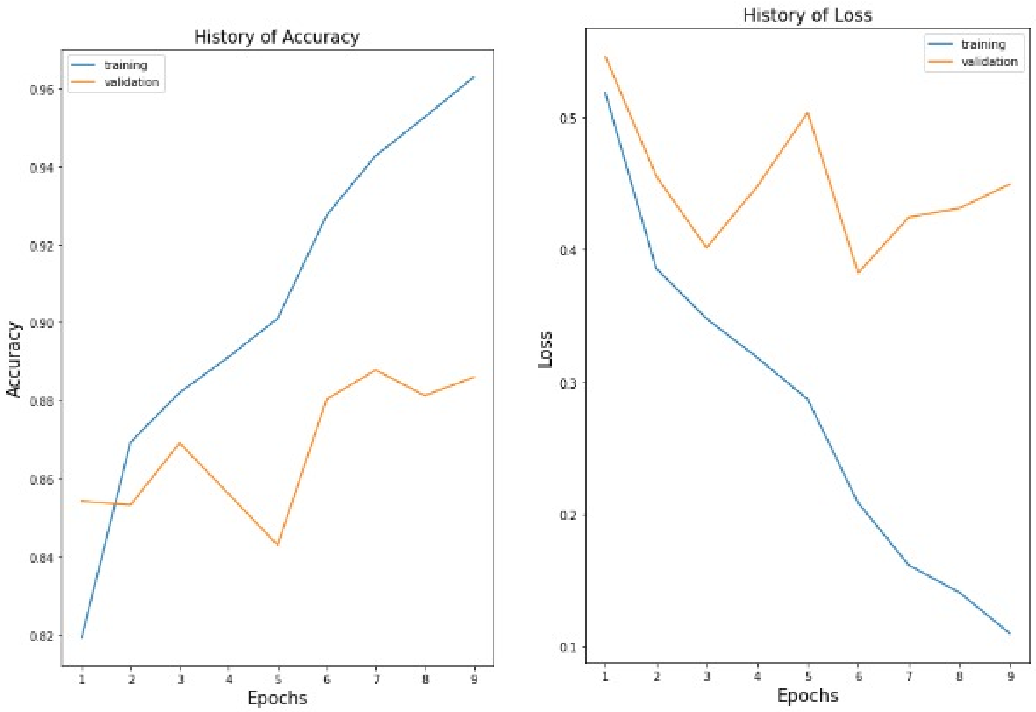
$$Accuracy = \frac{Numberofcorrectpredictions}{Numberoftotalpredictions} \tag{4}$$

$$F1Score = \frac{Precision * Recall}{Precision + Recall} \tag{5}$$

$$Recall = \frac{Numberoftruepositive}{Numberoftrupositive + Numberoffalsenegative} \tag{6}$$

4 Results and Discussion

This section assessed the VGGNet model's performance on the dataset and the training, validation and loss plot is indicated in Figure 3. Using the Adam optimizer and categorical cross entropy as the loss function, the model was trained across 40 epochs at a learning rate of 0.001. The model learn salient features for detection of cassava diseases and recognition of healthy leaf with minimal epoch



(a) Training and Validation Accuracy

(b) Loss Plot

Figure 3: Performance

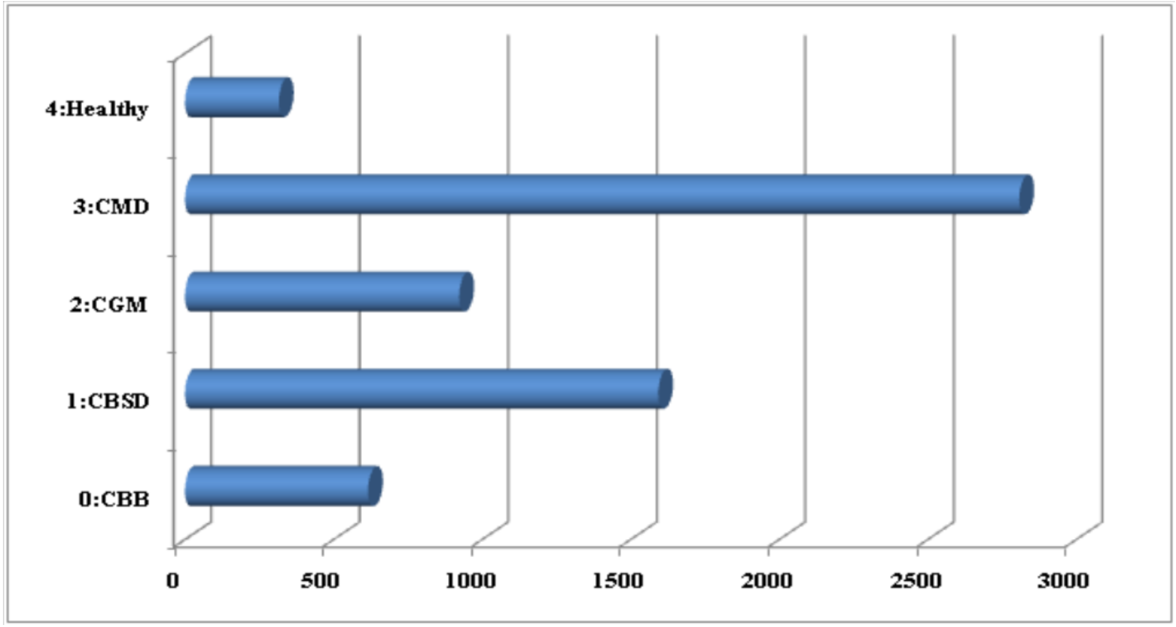


Figure 4: Chart showing class-wise prediction of cassava Leaf Image

after hyperparameter tuning. The validation and training plot confirm the performance of the training, though it suffers little fluctuation at higher number of the epoch. This noticeable fluctuation had an impact on the convergence. The loss plot achieves minimal loss value of 0.211. The model nevertheless obtains a competitive accuracy of 88% on validation data, which is the despite the variations in validation accuracy. This indicates that the VGG16-based method works well, although its generalization performance might be enhanced by additional optimization.

The chart in Figure 4 demonstrates the ability of the model to detect healthy cassava and different classes of diseases for the non-healthy ones. The recognition of CMD disease recorded the highest, followed by CBSD among other classes, while the lowest was recorded on the healthy class. The test on selected cassava leaf images carried out further attest to the performance of the model as shown in Figure 5. Out of 12 cassava leaf images that the model was suggested to, 8 were correctly predicted while 4 were misclassified. The number of wrong predictions is significantly lower compared to the number of correct predictions.

The performance comparison with other existing study is shown in Table 2. The model in the study achieved higher accuracy over others, though they are deep learning based as well. It indicate that the model is resilient to identify discriminative feature for cassava disease detection more than others.

Table 2: Hardware Specification

Techniques	Accuracy Reported	References
Custom CNN	77%	[26]
DRNN	52.87%	[27]
PCNN	46.24%	[27]
DenseNet	80.52%	[28]
MobileNet	65%	[29]
Deep transfer Learning	88%	Ours

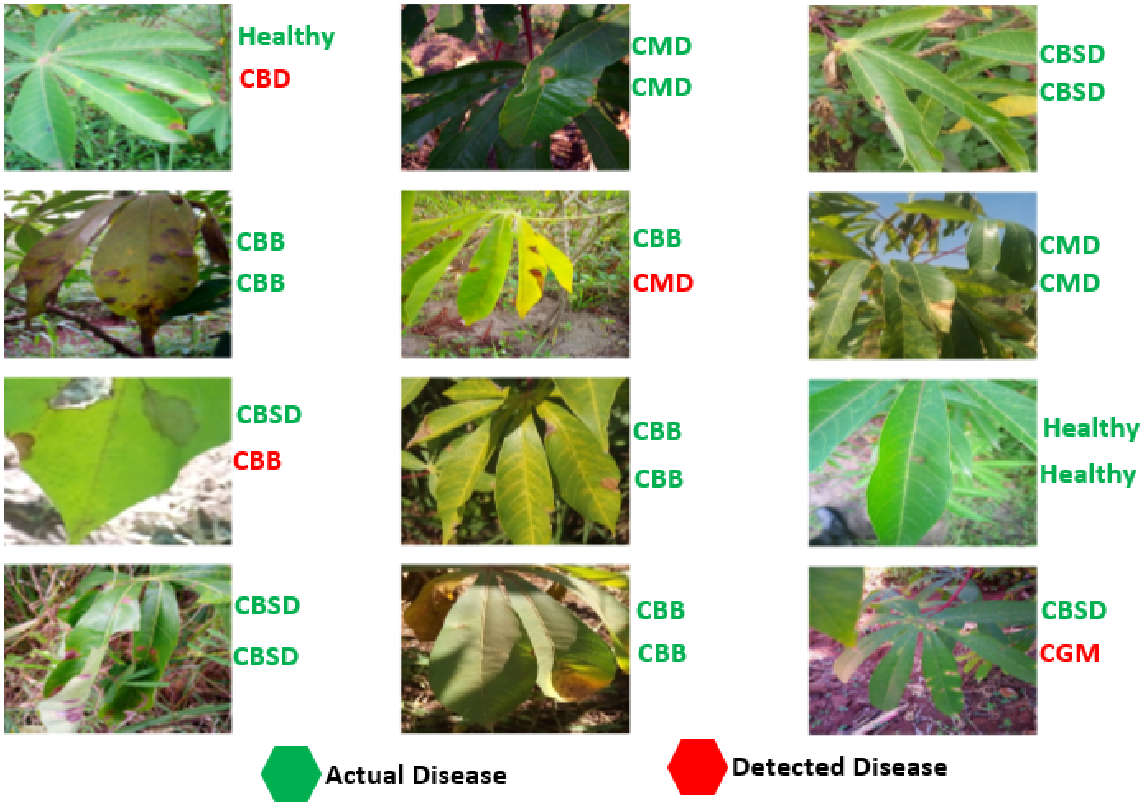


Figure 5: Model test prediction on selected cassava leaf Images

The findings imply that VGGNet is a strong and efficient option for this field, surpassing both sophisticated designs like DenseNet and lightweight systems like MobileNet. Its exceptional performance supports its promise as a trustworthy approach for detecting cassava diseases, advancing both disease management and agricultural technology. This study employs a deep learning methodology using VGG16 to detect cassava diseases from more than 5,000 images of cassava leaf specimens. After fine-tuning, our system attained an accuracy of 88% and an F1-score of 82%, exceeding the performance of other leading approaches, like MobileNet (65%) and DenseNet (80.52%). The results indicate the effectiveness of deep convolutional neural networks in extracting robust features for precise classification in agricultural applications.

5 Conclusion

Early diagnosis of diseases affecting cassava can avert production shortages of this vital crop and influence agricultural technology. Despite the traditional approach employed by farmers and agricultural experts to identify diseases affecting cassava survival resulting in considerable progress, it is plagued by a significant degree of misclassification. This research presents a deep learning approach utilizing VGG16 to identify cassava illnesses from over 5,000 photos of cassava leaf samples. Upon fine-tuning, our system achieved an impressive accuracy of 88% and an F1-score of 82%, surpassing other state-of-the-art methods such as MobileNet (65%) and DenseNet (80.52%). In agricultural applications, the results demonstrate the efficacy of deep convolutional neural networks in extracting robust characteristics for accurate classification. The comparative research underscores the VGG16 model's efficacy in addressing the issues associated with cassava disease recognition, presenting a viable solution for practical applications in smart agriculture and food security. The study identifies areas for enhancement, particularly with the improvement of generalization performance, despite its accomplishments. Techniques such as enhanced regularization, model interpretability, and data augmentation could further augment the model's robustness. Future work through optimization of the model has tendency of zeroing the wrong prediction and increase the accuracy of the model.

Acknowledgments

Acknowledge the Federal University, Oye-Ekiti, Nigeria and the University of Zululand South Africa where the experiment were conducted

Competing Interests

The authors declare that they have no competing interests.

Funding

No funding was received for this project.

Availability of Data and Material

The dataset used for this study is available in the Kaggle repository at https://www.Kaggle.com/datasets/leoalves2/healthcare-dataset-stroke-data

References

[1] W. G. Adebayo, "Cassava production in africa: A panel analysis of the drivers and trends," *Heliyon*, vol. 9, no. 9, 2023.

[2] M. N. Kiboi, F. Ngetich, M. Mucheru-Muna, J. Diels, and D. Mugendi, "Soil nutrients and crop yield response to conservation-effective management practices in the sub-humid highlands agro-ecologies of kenya," *Heliyon*, vol. 7, no. 6, 2021.

[3] S. Tatineni and G. L. Hein, "Plant viruses of agricultural importance: Current and future perspectives of virus disease management strategies," *Phytopathology®*, vol. 113, no. 2, pp. 117–141, 2023.

[4] G. A. Taiwo, A. Alameer, and T. Mansouri, "Review of farmer-centered ai systems technologies in livestock operations," *CABI Reviews*, vol. 19, no. 1, 2024.

[5] J. P. Legg, P. L. Kumar, T. Makeshkumar, L. Tripathi, M. Ferguson, E. Kanju, P. Ntawuruhunga, and W. Cuellar, "Cassava virus diseases: biology, epidemiology, and management," in *Advances in virus research*, vol. 91, pp. 85–142, Elsevier, 2015.

[6] S. R. Dubey and A. S. Jalal, "Adapted approach for fruit disease identification using images," *International journal of computer vision and image processing (IJCVIP)*, vol. 2, no. 3, pp. 44–58, 2012.

[7] S. P. Mohanty, D. P. Hughes, and M. Salathé, "Using deep learning for image-based plant disease detection," *Frontiers in plant science*, vol. 7, p. 215232, 2016.

[8] W. Abdullakasım, K. Powbunthorn, J. Unartngam, and T. Takıgawa, "An images analysis technique for recognition of brown leaf spot disease in cassava," *Tarım Makinaları Bilimi Dergisi*, vol. 7, no. 2, pp. 165–169, 2011.

[9] S. Akinpelu and S. Viriri, “A robust deep transfer learning model for accurate speech emotion classification,” in *International Symposium on Visual Computing*, pp. 419–430, Springer, 2022.

[10] C. Y. Daramola, S. A. Akinpelu, E. O. Akinyemi, S. A. Ajagbe, G. A. Akinpelu, and M. O. Adigun, “Malicious query recognition using chosen machine learning techniques,” *SN Computer Science*, vol. 6, no. 3, p. 281, 2025.

[11] E. Moses, J. Asafu-Agyei, K. Adubofour, and A. Adusei, “Guide to identification and control of cassava diseases,” *CSIR-Crop Research Institute, Kumasi, Ghana*, 2008.

[12] P. C. Chikoti, R. M. Mulenga, M. Tembo, and P. Sseruwagi, “Cassava mosaic disease: a review of a threat to cassava production in zambia,” *Journal of Plant Pathology*, vol. 101, no. 3, pp. 467–477, 2019.

[13] A. K. Gautam and S. Kumar, “Techniques for the detection, identification, and diagnosis of agricultural pathogens and diseases,” in *Natural remedies for pest, disease and weed control*, pp. 135–142, Elsevier, 2020.

[14] A. Maredza, F. Allie, G. Plata, and M. Rey, “Sequences enhancing cassava mosaic disease symptoms occur in the cassava genome and are associated with south african cassava mosaic virus infection,” *Molecular Genetics and Genomics*, vol. 291, pp. 1467–1485, 2016.

[15] M. S. Farooq, S. Riaz, A. Abid, K. Abid, and M. A. Naeem, “A survey on the role of iot in agriculture for the implementation of smart farming,” *Ieee Access*, vol. 7, pp. 156237–156271, 2019.

[16] A. Darwish, A. E. Hassanien, and S. Das, “A survey of swarm and evolutionary computing approaches for deep learning,” *Artificial intelligence review*, vol. 53, no. 3, pp. 1767–1812, 2020.

[17] A. Ramcharan, K. Baranowski, P. McCloskey, B. Ahmed, J. Legg, and D. P. Hughes, “Deep learning for image-based cassava disease detection,” *Frontiers in plant science*, vol. 8, p. 1852, 2017.

[18] I. Sangbamrung, P. Praneetpholkrang, and S. Kanjanawattana, “A novel automatic method for cassava disease classification using deep learning,” *Journal of Advances in Information Technology Vol*, vol. 11, no. 4, pp. 241–248, 2020.

[19] G. Sambasivam and G. D. Opiyo, “A predictive machine learning application in agriculture: Cassava disease detection and classification with imbalanced dataset using convolutional neural networks,” *Egyptian informatics journal*, vol. 22, no. 1, pp. 27–34, 2021.

[20] S. Coulibaly, B. Kamsu-Foguem, D. Kamissoko, and D. Traore, “Deep neural networks with transfer learning in millet crop images,” *Computers in industry*, vol. 108, pp. 115–120, 2019.

[21] J. Lu, J. Hu, G. Zhao, F. Mei, and C. Zhang, “An in-field automatic wheat disease diagnosis system,” *Computers and electronics in agriculture*, vol. 142, pp. 369–379, 2017.

[22] K. P. Ferentinos, “Deep learning models for plant disease detection and diagnosis,” *Computers and electronics in agriculture*, vol. 145, pp. 311–318, 2018.

[23] O. O. Abayomi-Alli, R. Damaševičius, S. Misra, and R. Maskeliūnas, “Cassava disease recognition from low-quality images using enhanced data augmentation model and deep learning,” *Expert Systems*, vol. 38, no. 7, p. e12746, 2021.

[24] G. Capizzi, G. Lo Sciuto, C. Napoli, E. Tramontana, M. Woźniak, *et al.*, “A novel neural networks-based texture image processing algorithm for orange defects classification,” *International journal of advanced computer science and applications*, vol. 13, no. 2, pp. 45–60, 2016.

[25] J. Zhang, B. Zhang, C. Qi, I. Nyalala, P. Mecha, K. Chen, and J. Gao, "Maianet: Signal modulation in cassava leaf disease classification," *Computers and Electronics in Agriculture*, vol. 225, p. 109351, 2024.

[26] J. Srivastava *et al.*, "Cassava leaf disease detection using deep learning," in *2022 IEEE International IOT, Electronics and Mechatronics Conference (IEMTRONICS)*, pp. 1–7, IEEE, 2022.

[27] E. Mwebaze, T. Gebru, A. Frome, S. Nsumba, and J. Tusubira, "icassava 2019 fine-grained visual categorization challenge," *arXiv preprint arXiv:1908.02900*, 2019.

[28] H. Ayu, A. Surtono, and D. Apriyanto, "Deep learning for detection cassava leaf disease," in *Journal of Physics: Conference Series*, vol. 1751, p. 012072, IOP Publishing, 2021.

[29] R. Surya and E. Gautama, "Cassava leaf disease detection using convolutional neural networks," in *2020 6th international conference on science in information technology (ICSITech)*, pp. 97–102, IEEE, 2020.