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Enhancing cassava disease detection using CNN models trained from scratch: A comparative study with transfer learning approaches

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Abstract

Agriculture is a vital sector, with farmers playing a crucial role in producing food and supporting the global population. However, plant diseases pose significant challenges, leading to substantial crop yield losses and threatening food security., Artificial intelligence models, particularly convolutional neural networks (CNNs), are widely used for object identification and image classification. Although transfer learning techniques help reduce computation time, CNNs often struggle to differentiate between highly similar images because of the limited flexibility in configuring and fine-tuning parameters. To address issues related to random configuration, feature selection, and model architecture, we present a CNN model with 15 layers, trained from scratch. This approach allows for a setup and design better suited to the task of distinguishing similar images. The proposed model is compared to two other CNN-based transfer learning models, InceptionV3 and VGG16, which are trained solely on the top layers with fixed bottom layers. Experimental results indicate that the proposed model outperformed the other models by 24%, achieving an accuracy of 84% over 50 epochs. The experimental results suggest that the proposed approach can achieve even better performance with additional training epochs, as the model's training graph was still improving.

Key words: *cassava; convolution neural network; transfer-learning model*

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Introduction

The rapid growth of the world's population necessitates an increase in food production (Falcon *et al*., 2022). Efforts to boost crop production are directly tied to this expanding population (Maja & Ayano, 2021). According to population growth estimates, food crop production must increase by 50% by 2050 to meet the projected population growth (Tang *et al*., 2022). Agriculture is crucial, with farmers producing 80% of the world's food and supporting over 90% of the global population (Mukti *et al*., 2019; Serraj *et al*., 2019). However, plant diseases present significant challenges, causing over 30% of crop yield annual losses and threatening food security, and they also cause hundreds of billions of dollars in economic losses (Gai & Wang, 2024). The agricultural sector has increasingly adopted machine learning (ML) and deep learning (DL), leveraging advances in computational systems like Graphical Processing Units (GPUs) (Ahmad *et al*., 2023). This has led to the development of DL models that have revolutionized complex processes such as image processing, enabling the analysis of large datasets (Jiao & Zhao, 2019). Although the use of DL techniques in agriculture is relatively new, it has shown promising results in plant disease diagnosis (Ahmad *et al*., 2023; Boulent *et al*., 2019). These techniques can analyze extensive agricultural data to identify patterns, facilitating early disease diagnosis. Early detection helps manage diseases effectively, reducing yield losses caused by pests and diseases (Sharma *et al*., 2022). Integrating ML and DL in agriculture could potentially bridge the gap between actual and potential yields by managing plant diseases efficiently. Several studies have employed DL and computer vision to differentiate between healthy and diseased plants. For instance, Dey *et al*. (2022) evaluated the performance of four pre-trained deep CNN models that are VGG19, InceptionV3, ResNet50, and VGG16 in identifying symptoms of hispa, brown spot, leaf blast, and NPK deficiency. The study utilized a total of 2,892 images, combining public and field datasets with the backgrounds removed. Among the models, VGG19 achieved the highest accuracy of 91.8%. However, despite this high performance, the uniform image backgrounds limit the model's applicability in real-world scenarios, where backgrounds are typically non-uniform.

Also, Ghosa *et al*. (2020) proposed the use of VGG-16 on classification of three diseases (Rice blast, leaf blight and brown spot). With the dataset of the original 500 field images, this resulted in a total of four classes, including healthy. The model achieved an accuracy of 92.46%. This study used very low number of images despite of its high accuracy; it may not perform well in practical.
Similarly, Latif *et al*. (2022) aimed to diagnose six classes: healthy, narrow brown spot, leaf scald, leaf blast, brown spot, and bacterial leaf blight. They used a dataset of 2,167 images, all with uniform backgrounds, and trained CNN-based models such as GoogleNet, VGG16, VGG19, DenseNet201, and AlexNet. These models were evaluated using different dataset configurations, including non-normalized, normalized, and augmented variations. A modified VGG19 model, trained on the non-normalized augmented dataset, achieved the highest accuracy of 96.08%.

Marzougui *et al*. (2020) proposed a CNN-based architecture for plant disease diagnosis using a dataset of 500 images (healthy and diseased leaves). They used ResNet, GoogleNet, and AlexNet pretrained weights, with ResNet performing best at 98.96% accuracy. Despite the model's good performance, the dataset's diversity and size were insufficient for practical use.
Moreover, Too *et al*. (2019) investigated various DL models for plant disease classification using fine-tuning techniques on the PlantVillage dataset, which comprised 87,000 images across 38 classes. They explored architectures such as VGG 16, Inception V4, ResNet (50, 101, and 152), and DenseNets (121 layers), with DenseNet achieving an accuracy of 99.75%. The homogeneous background of the PlantVillage dataset posed potential limitations for field application.

All the previously discussed studies have utilized Transfer Learning (TL) models based on CNNs, demonstrating significant improvements but facing limitations, especially with related image classes. These limitations include overfitting, exploding gradients, class imbalance, arbitrary configuration, and data scarcity (Du *et al*., 2023; Dyrmann *et al*., 2016; Kim *et al*., 2022; Majeed *et al*., 2016). Because TL models were pre-trained on a large-scale dataset with millions of labelled images, the robustness of transfer TL depends on how similar the pre-trained features are to the target dataset. If the target dataset is small or significantly different in terms of image content, style, or domain, the pre-trained features might not capture the relevant patterns, which will also lead to reduced classification performance (Amin *et al.*, 2023). Additionally, the selection of pre-trained models and layers to fine-tune is often made for convenience rather than specific task needs, potentially leading to suboptimal results. Training a model from scratch can mitigate issues associated with arbitrary configuration, such as feature selection and model architecture, allowing for a setup and design more suited to the task. Also, training from scratch may reduce the risk of misclassification caused by effects of pretrained dataset. While this approach requires a large amount of labeled data and substantial computational resources, it avoids the limitations and biases of pre-trained models.

In this study we propose developing a CNN model with 15 layers, trained from scratch using images of healthy and infected cassava leaves. The model is compared with CNN-based TL models to enhance differentiation between similar infections, specifically bacterial blight and brown spot, with the goal of improving cassava disease detection. The remainder of this work is organized as follows: The materials and methods are described in the next section, followed by the experimental setup in Section 3. Section 4 presents a discussion of these findings. Finally, Section 5 concludes the paper, and Section 6 provides recommendations

Materials and methods

The study area

This study was conducted in Mkuranga District, located in the coastal Pwani region of Tanzania, at 7° 4' 23" latitude, 39° 12' 41" longitude, and an elevation of 65.36 meters. As one of Tanzania's leading cassava-producing districts, Mkuranga was selected for its agricultural significance. Diseased crops were surveyed, and images were collected as data between December 2023 and February 2024.

Data collection and description

The model's accuracy in practical applications can be influenced by key factors, including capture conditions, crop varieties, acquisition dates, and symptom severity. To address this, data collection was carried out on various days and months to capture symptom images under diverse conditions (Boulent *et al.*, 2019). High-quality images were collected to make a total of 9,850 images were initially captured using a Nikon COOLPIX B500 camera with 5400x4000 pixel resolution, between 9 a.m. and 12 p.m. and from 4 p.m. to 5 p.m.

After cleaning and removing blurry or shadowed images, as shown in Figure 1 (a) and (b), the dataset was refined to 4,490 images. The dataset used in this study consist of five plant classes namely; healthy, mosaic, bacterial-blight, green-mite, and brown-spot as shown in Figure 2 (a) – (e). with the following distribution: healthy (773), mosaic (869), bacterial blight (889), green mite (992), and brown spot (967). To balance the dataset to approximately 1,000 images per class, an additional 510 images were incorporated from Mwebaze *et al.* (2019), with the following class distribution: healthy (227), mosaic (131), bacterial blight (111), green mite (8), and brown spot (33).

The final dataset was structured to include both controlled images (with uniform backgrounds) and those captured in real-world, uncontrolled field settings. Training a model solely on low-complexity images would reduce its ability to generalize to more complex field data, so the inclusion of diverse image types was critical for robust model performance (Boulent *et al.*, 2019).

Figure 1

Types of the images deleted during data cleaning.

(a) Blur image

(b) Image with a shadow

Figure 2

Images used in this study.

(a) Healthy

(b) Mosaic

(c) Bacterial-blight

(d) Green-mites

(e) Brown-spot

Pre-processing methods

The dataset was pre-processed by resizing the images to 150×150 pixels to reduce computation time. This was followed by data augmentation to increase the dataset size and help the models learn various features in different dimensions, thereby aiding in the prevention of overfitting (Tang *et al.*, 2020). The data augmentation techniques used in this study included both geometrical transformations such as resizing, cropping, rotation, and horizontal flipping and intensity transformations, including contrast and brightness enhancement, color adjustment, and noise addition. These techniques ensured that the models were exposed to a diverse set of image variations, enhancing their robustness and generalization capabilities.

Convolution neural network

CNNs, which are extensively utilized in computer vision, are a major component of DL. For tasks involving picture-based detection, their capacity to identify visual patterns in image pixels with little to no preprocessing makes them highly valuable. This section provides a description of the CNN models that were employed in the study. VGGNet is a cutting-edge architecture designed to extract features from low-resolution images (Simonyan & Zisserman, 2015). It is composed of sixteen convolutional layers, each of which uses a uniform-sized (3x3) filter, in contrast to larger convolutions. VGGNet reduces the number of parameters and supports two Rectified Linear Unit (ReLU) layers instead of one by employing double-layered 3x3 layers (Coulibaly *et al.*, 2019). VGG16, a variant of VGGNet, with 3x3 convolution layers and 2x2 pooling layers.

GoogleNet offers an alternative to traditional CNNs by introducing an inception module that adds more layers. By using average pooling in place of the fully connected layers at the top of the convolutional network, it significantly reduces the number of parameters (Lu *et al.*, 2021). GoogleNet's architecture aims to minimize memory and energy use. This study also considers InceptionV3, which is an enhanced version of InceptionV1 and InceptionV2 (Minarno *et al.*, 2023). Moreover, XceptionNet fared better on the largest datasets than InceptionV3, even with the same number of parameters. Instead of GoogleNet's conventional inception modules, this model employs depth-wise separable convolutions followed by pointwise convolutions (1x1 convolutions) (Minarno *et al.*, 2023).

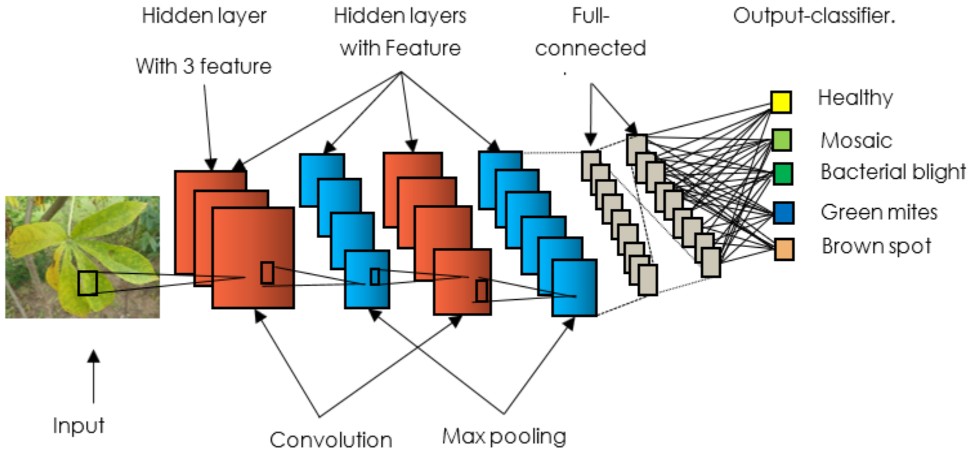
The proposed CNN models

The proposed model architecture consists 15 layers that includes input layer, 6 convolutional layers followed by max pooling layers, dropout layer, flatten layer, two full connected layers and an output layer which produces 7,040,389 trainable parameters.

Figure 3 shows the proposed architecture that has an input of dimension 150x150 pixels, hidden layers, two full connected layers with size 128 and output layer. The output layer consists of five classes that are healthy, mosaic, bacterial-blight, green-mite and brown-spot. The model was trained from scratch to reduce misclassification especially for bacterial-blight and brown-spot that shows near resemblance.

Figure 3

The model architecture of proposed CNN model.



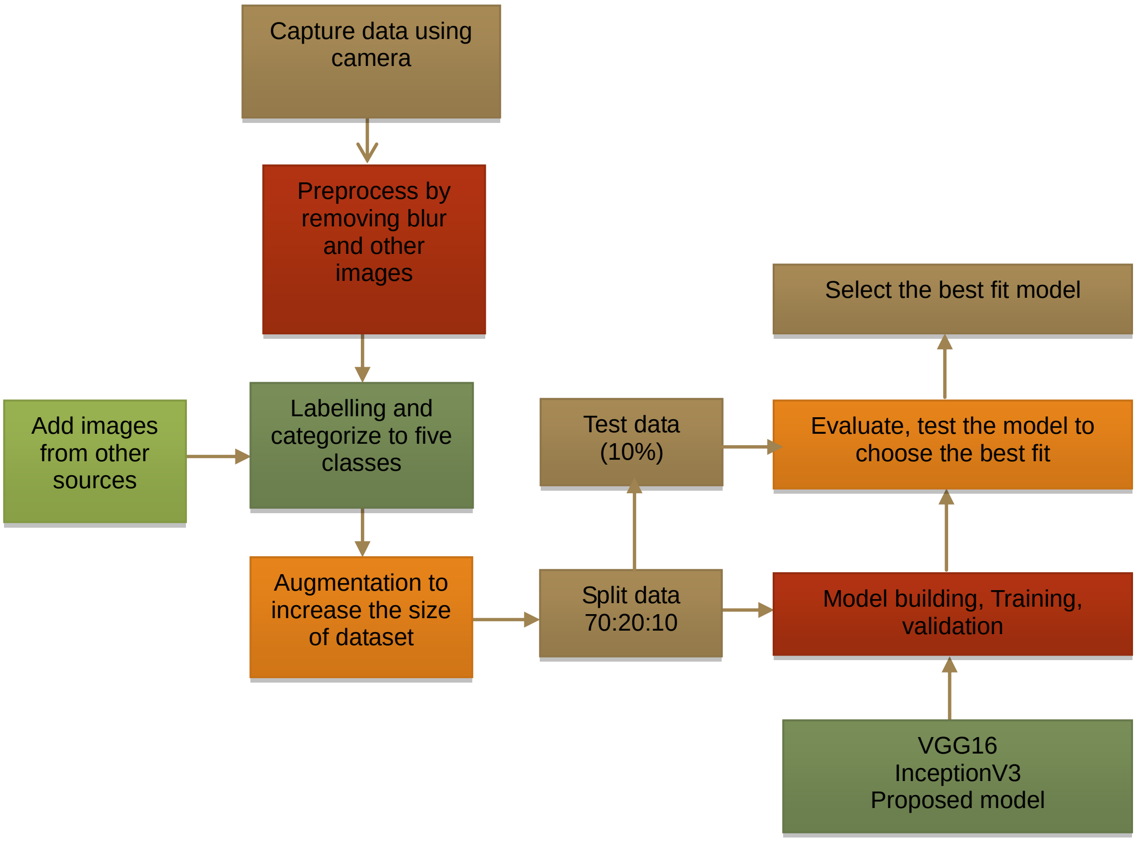
Experimental setup

Figure 4 shows the proposed framework and the procedures followed for model development. First, images were captured using a camera. These images were then pre-processed to remove undesirable ones, such as grainy images. Next, data tagging was conducted, classifying images of various diseases into appropriate folders. To balance the classes with fewer images, additional photos were sourced from other databases.

After data labeling, data augmentation was employed to increase the quantity and diversity of images under different conditions. The dataset was then split into training, validation, and testing sets in a 70:20:10 ratio. All three models that are VGG16, InceptionV3, and the proposed model were trained, and validated using the same dataset for comparison purposes. Finally, the remaining 10% of the dataset was used to assess the models' performance. The models were evaluated and tested to determine the best fit.

Figure 4

The flowchart showing the summarized steps followed on experimental setup.



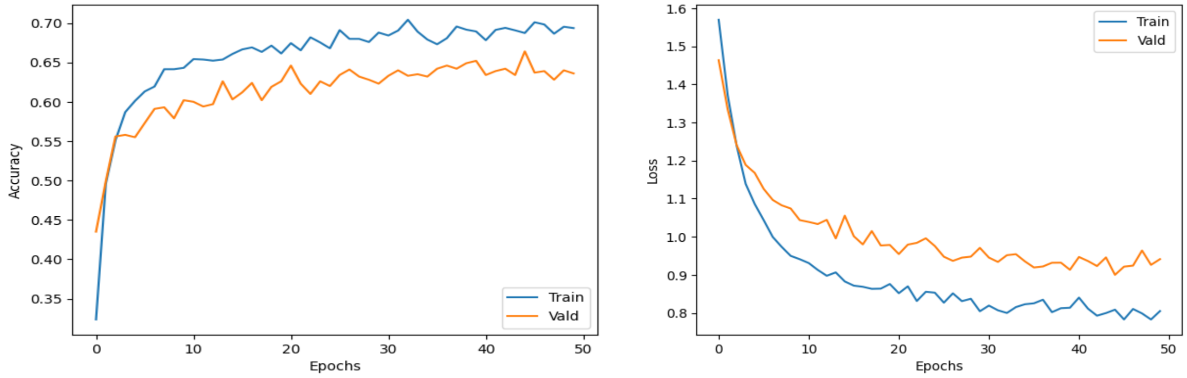
Results

This section compares the performance of CNN-based models trained using TL to that trained from scratch. Figure **5**(a) and (c) show the training curves of the TL models that are VGG16 and InceptionV3 and Figure **5**(b) and 5(d) show the loss curves of the VGG16 and InceptionV3 models. On the other hand, Figure **5**(e) and 5(f) shows the training and loss curves for the proposed model trained from scratch.

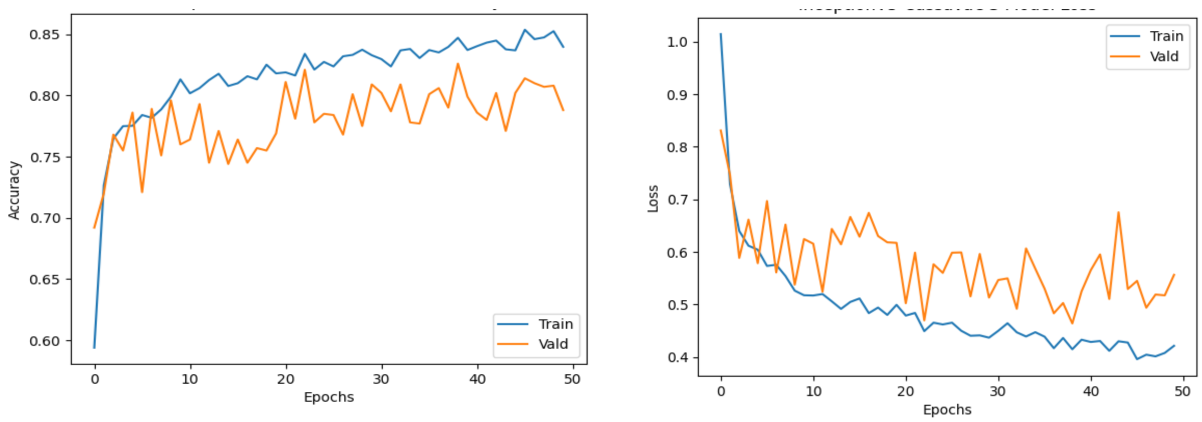
The VGG16 achieved an accuracy of 70% during training and 64% during validation while the InceptionV3 model achieved accuracy of 85% during training and 78% during validation. Moreover, the proposed model achieved an accuracy of 90% during training and 82 during validation. On the other hand, the training and validation loss of the VGG16 and InceptionV3 ranges between 0.4 and 1 while that of proposed model varied between 0.2 and 0.6 for training and validation. All the models were trained for 50th epoch for comparison purpose.

Figure 5

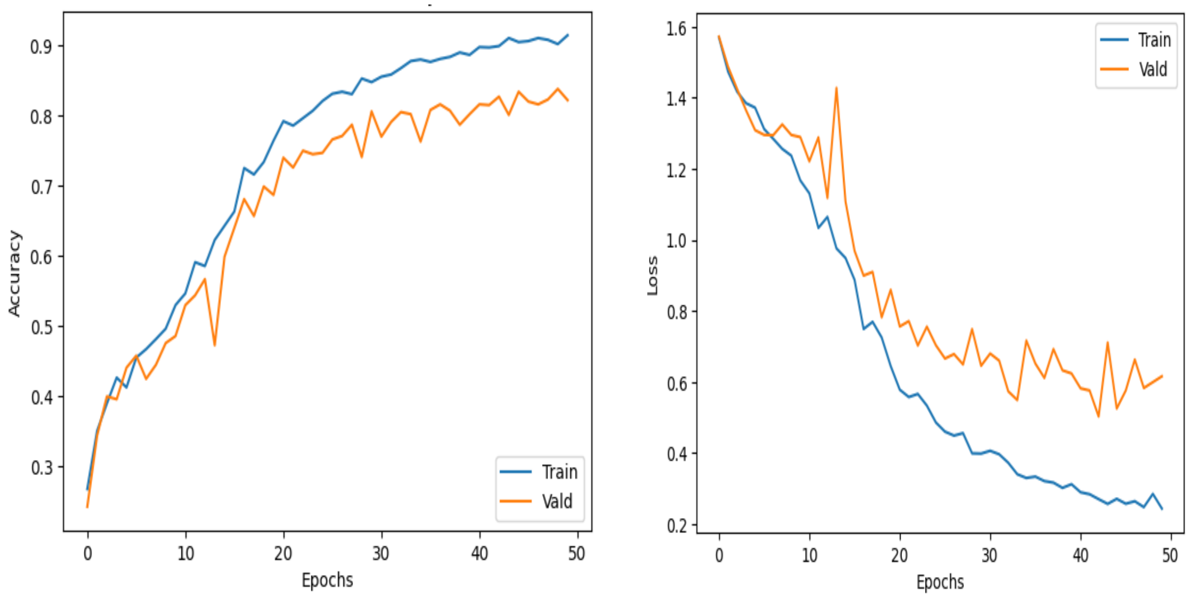
The graphs of training and validation results of the three models, left is accuracy of the model and right depicts the model's Loss.



(a) VGG16 Model Training (b) VGG16 Model Loss



(c) InceptionV3 Model Training (d) InceptionV3 Model Loss



(e) Proposed CNN based Model Training (f) Proposed CNN based Model Loss

Figure 6 shows the confusion matrix for the three models: VGG16, InceptionV3, and the proposed CNN model. Among all three models, the healthy class performed the best, achieving more than 85% detection accuracy. In contrast, the bacterial-blight class performed the worst, with accuracy falling below 52%.

The VGG16 model correctly identified 85 (85%) of images in the healthy class, misclassifying 1(1%) as green-mite and 14 (14%) as brown-spot. For the bacterial-blight class, it correctly identified 15 (15%) of the images, while incorrectly classifying 59 (59%) as brown-spot, 10 (10%) as green-mite, 10 (10%) as healthy, and 1 (1%) as mosaic.

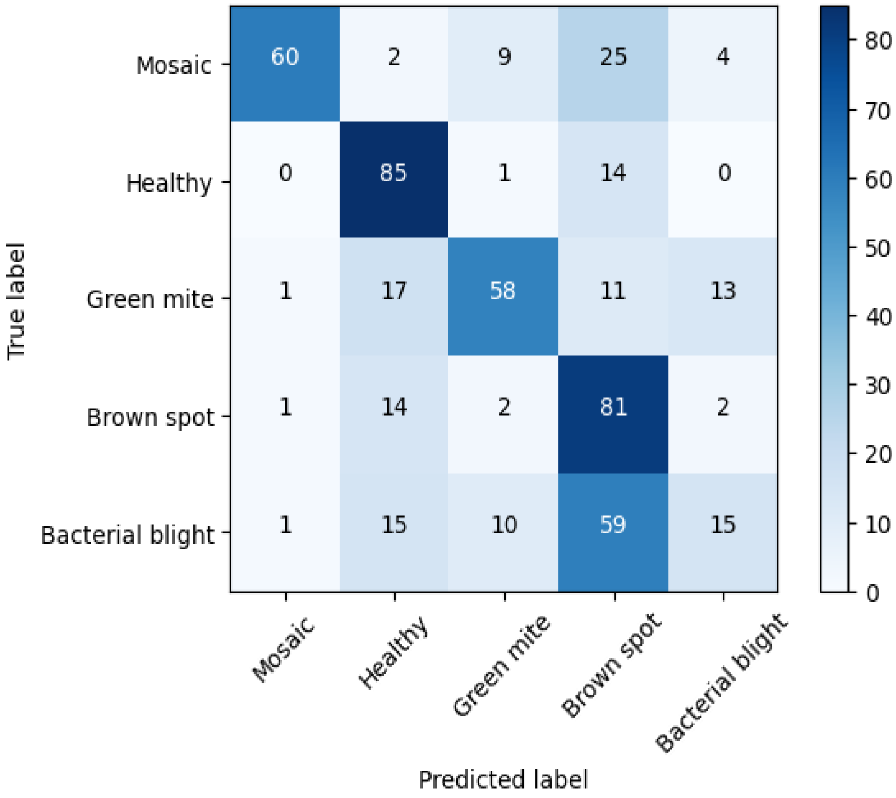
The InceptionV3 model correctly identified 95 (95%) of images in the healthy class, with misclassifications of 1 (1%) as mosaic, 3 (3%) as brown-spot, and 1 (1%) as bacterial-blight. The model also correctly classified 49 (49%) of images in the green-mite and bacterial-blight classes. For the green-mite class, the model incorrectly classified 45 (45%) of images as healthy, 2 (2%) as mosaic, and 4 (4%) as bacterial-blight. Additionally, for the bacterial-blight class, the model misclassified 27 (27%) of images as brown-spot, 5 (5%) as green-mite, 16 (16%) as healthy, and 3 (3%) as mosaic.

The proposed model performed exceptionally well for the healthy and brown-spot classes, correctly identifying 98 (98%). Moreover, the model correctly identified 88 (88%) of images as mosaic and 86 (86%) of images as green-mite. It misclassified 1 (1%) of healthy images as green-mite and 1 (1%) as brown-spot. Additionally, it misclassified 2 (2%) of brown-spot images as bacterial-blight. For the green-mite class, the proposed model correctly identified 86 (86%) of images, while it misclassified 2 (2%) as healthy, 3 (3%) as mosaic, 3 (3%) as brown-spot and 6 (6%) as bacterial-blight. For the mosaic class, the model correctly identified 88 (88%) of images, misclassifying 1 (1%) as healthy, 4 (4%) as green-mite, 6 (6%) as brown-spot, and 1 (1%) as bacterial-blight. On the other hand, the model performed poorly on the bacterial-blight class, correctly identifying 51 (51%) of images, while misclassifying 42 (42%) as brown-spot, 6 (6%) as green-mite, and 1 (1%) as mosaic.

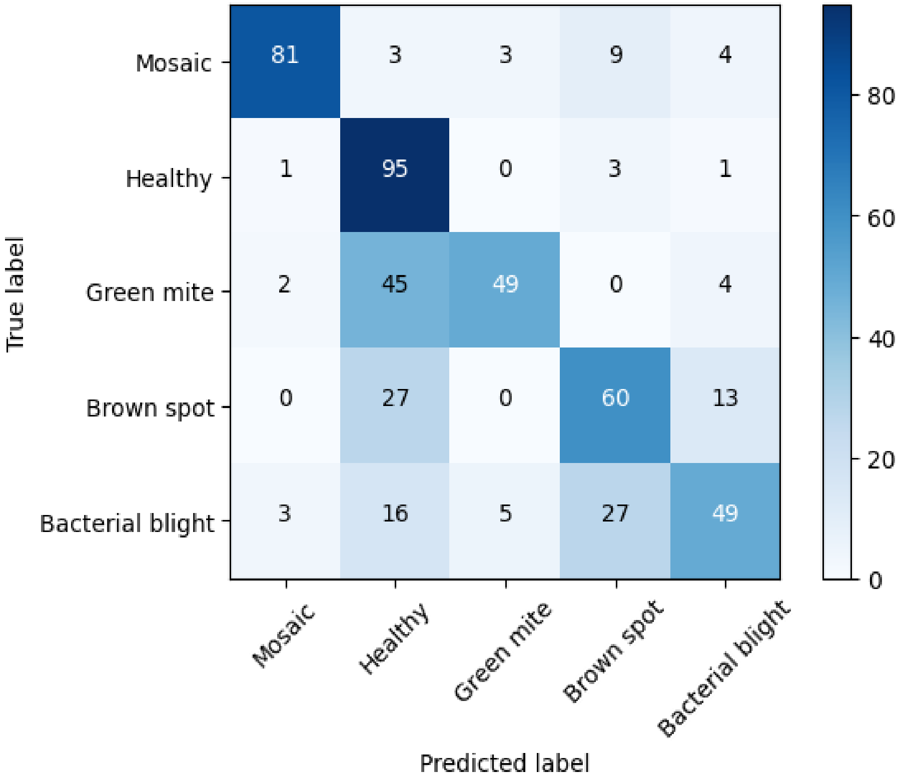
Overall, the confusion matrix highlights the superior performance of the Healthy class across all models and the challenges faced in accurately identifying the bacterial-blight class.

Figure 6

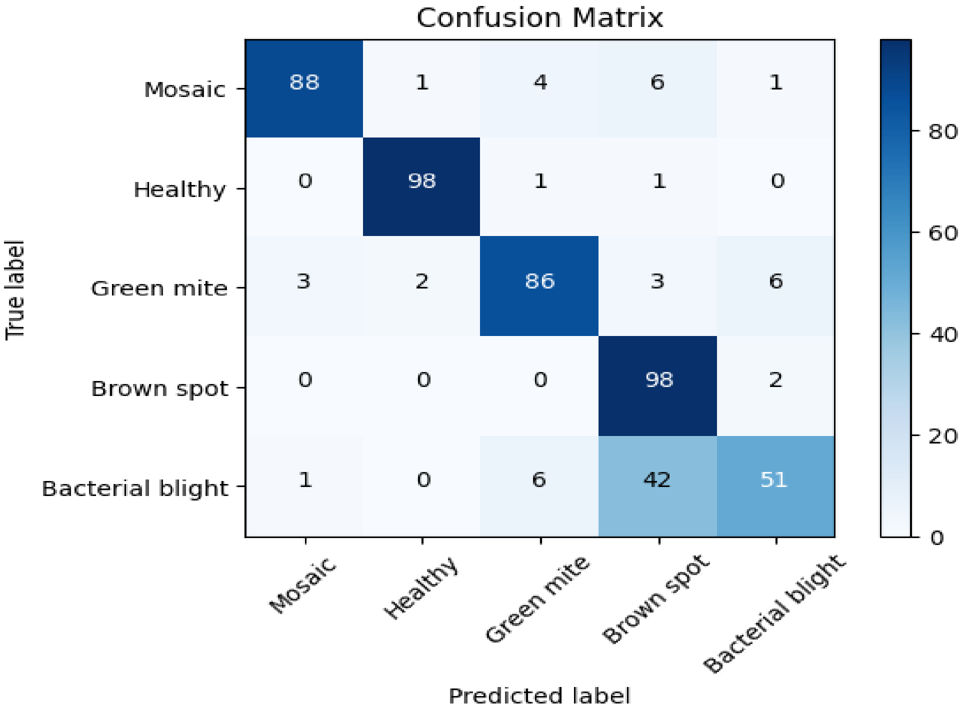
Confusion matrix of the three experimented models.



(a) VGG16



(b) InceptionV3



(c) Proposed model

Overall confusion matrix of the proposed model is shown in Table 1, Precision, recall, F1-score, support, and other performance metrics were used to assess the effectiveness of the proposed CNN model. These metrics offer an in-depth overview of the models' performance in classifying images into various classes, including mosaic, healthy, green-mite, brown-spot, and bacterial-blight. The proposed CNN model excelled in identifying healthy images, achieving a precision of 0.97, a recall of 0.98, and an F1-score of 0.98. These high values indicate that the model is highly accurate in both predicting healthy images and ensuring that most of the healthy images are correctly identified.

Moreover, the model performed well in identifying mosaic images, with a precision of 0.96, a recall of 0.88, and an F1-score of 0.92. This high performance reflects the model's ability to detect mosaic images accurately, although there were still some misclassifications with healthy and brown-spot images. The model showed good performance with precision, recall, and F1-score values of 0.89, 0.86, and 0.87, respectively. However, some images were incorrectly classified as healthy, indicating room for improvement in distinguishing between these classes. In the brown-spot class, the model presented mixed results, with a high recall of 0.98 but a lower precision of 0.65, resulting in an F1-score of 0.78. The high recall indicates that most brown-spot cases were detected, but the lower precision suggests a significant number of false positives, particularly confusing bacterial-blight and other classes. While the model struggled with accurately identifying bacterial-blight images. On bacterial-blight, the proposed CNN model had a precision of 0.85, a recall of 0.51, and an F1-score of 0.64. This indicates a significant challenge in correctly identifying bacterial-blight, as nearly half of the actual bacterial-blight images were misclassified as other classes.

Table 1

Classification report of the proposed CNN model.

Classes	Precision	Recall	F1-score	Support
Mosaic	0.96	0.88	0.92	100
Healthy	0.97	0.98	0.98	100
Green-mite	0.89	0.86	0.87	100
Brown-spot	0.65	0.98	0.78	100
Bacterial-blight	0.85	0.51	0.64	100
Accuracy		0.84		500

Discussion

This study's primary objective is to establish that, when compared to the two TL models used in the experiment, the proposed CNN-based model that was trained from scratch is very successful in diagnosing four cassava diseases. The experimental results reveal that the model trained from scratch outperforms the TL models by achieving an average accuracy of 84%, meaning that the proposed model can give disease classification task by making 84% as correct diagnosis while making 16% as misclassification. On other hand, VGG16 had average accuracy of 60%, therefore it can make misclassifications of diseases by 40% while InceptionV3 has average accuracy of 67%, therefore can make misclassification by 33% of given results.

Furthermore, the results show that the model works well in the healthy and mosaic classes, with good precision and recall scores, confirming its ability to distinguish such cases. However, bacterial blight and brown spot were more difficult, with lower precision and recall values, particularly for bacterial blight. Misclassification patterns also evolved, with healthy leaves occasionally mistaken for green mites and bacterial blight usually misidentified as brown spot. High accuracy in such models is critical because it enables reliable cassava disease diagnosis from images, allowing for prompt and informed agricultural decision-making. Improvements could focus on these difficult classes to increase the model's utility in real-world scenarios.

The proposed model has certain limitations.

Because it was trained from scratch, it requires a larger dataset to learn effectively, increasing the risk of overfitting since it relies solely on the training data to define its weights without leveraging prior training knowledge (Sabha *et al.*, 2024). Nonetheless, this approach enables the creation of customized architectures specifically designed for the task, which can enhance performance. For example, such architectures could be adapted to process more than three colour channels, manage varying scales, or integrate multiple models trained with different hyperparameters or datasets. However, training from scratch also demands substantial computational resources and time, making it costly and resource-intensive (Boulent *et al.*, 2019). Additionally, the model is limited to detecting or classifying only four diseases (mosaic, bacterial blight, green mite, and brown spot), along with healthy plants. This narrows its applicability, excluding other diseases like cassava brown streak and cassava anthracnose. While the model's 84% accuracy is encouraging, it ideally needs to reach closer to 99% for greater reliability.

Conclusion

This study highlights the importance of using a CNN-based model trained from scratch for datasets containing related images. The proposed model, with a 15-layer architecture and 7,040,389 parameters, was trained over 50 epochs and compared against two other CNN-based models, VGG16 and InceptionV3. Unlike the proposed model, which was fully trained from scratch, the top layers of VGG16 and InceptionV3 were trained while keeping their lower layers fixed. For consistency, all models were trained for 50 epochs. In testing, the proposed model outperformed the others, achieving an average accuracy of 84%, compared to 60% for VGG16 and 67% for Inception V3. Moreover, it yielded higher F1 scores across multiple classes: 0.92 for mosaic, 0.98 for healthy, 0.87 for green-mite, 0.78 for brown-spot, and 0.64 for bacterial-blight. In contrast, the F1 scores for VGG16 and Inception V3 ranged from 0.22 to 0.87 across all classes. These experimental results indicate that the proposed model could achieve even better performance with additional training, as its training graph was still improving at the end of 50 epochs. Future work could involve training on larger and more diverse datasets and expanding the model's application to other crops, which could improve its robustness and generalizability. affordability.

Recommendation

This study recommends the utilization of the CNN model architecture as described in section "The proposed CNN models" training it from scratch. This process should be performed with more epochs and diverse datasets with large number of images so as to attain high accuracy. This will contribute to effective cassava diseases management since accurate diagnosis through visual assessment will be improved. Additionally, further researches and investments should be conducted with other intensive diseases diagnosis methods such as molecular characterization and detection of pathogens should be used for more accurate disease detection for even those plants with asymptomatic characters of diseases of cassava in Tanzania, leading to the development of more informed management strategies (Saokham *et al.*, 2021).

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability

The datasets analyzed in the paper are available on request.

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