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Image Segmentation Deep Learning Model for Early Detection of Banana Diseases

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ABSTRACT

Bananas are among the most widely produced perennial fruits and staple food crops that are highly affected by numerous diseases. When not managed early, Fusarium Wilt and Black Sigatoka are two of the most detrimental banana diseases in East Africa, resulting in production losses of 30% to 100%. Early detection of these banana diseases is necessary for designing proper management practices to avoid further yields and financial losses. The recent advances and successes of deep learning in detecting plant diseases have inspired this study. This study assessed a U-Net semantic segmentation deep learning model for the early detection and segmentation of Fusarium Wilt and Black Sigatoka banana diseases. This model was trained using 18,240 banana leaf and stalk images affected by these two banana diseases. The dataset was collected from the farms using mobile phone cameras with the guidance of agricultural experts and was annotated to label the images. The results showed that the U-Net model achieved a Dice Coefficient of 96.45% and an Intersection over Union (IoU) of 93.23%. The model accurately segmented areas where the banana leaves and stalks were damaged by Fusarium Wilt and Black Sigatoka diseases.

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Introduction

Agriculture is crucial for developing countries' economies, and identifying plant diseases early is essential. Traditional eye observation is the primary method for identifying and detecting plant diseases. This study aims to improve this by automating disease detection using deep learning. This method distinguishes between healthy and diseased plant parts using features like color difference, boundaries, and shapes (Singh and Misra 2017). This study uses deep learning for the early detection of banana diseases using images of leaves and stalks from the field.

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Bananas are a significant global production, with 124 million metric tons produced in 2021 (FAOSTAT 2023). They serve as staple foods and cash crops, providing a sustainable food supply and household food security (FAO 2001, 2021). However, diseases like Fusarium Wilt and Black Sigatoka cause significant yield losses, ranging from 30% to 100%, in banana production areas (Bubici et al. 2019; Vézina and Van den Bergh 2020; Nations 2017)

Black Sigatoka, also known as Black Leaf Streak Disease (BLSD), is a leaf spot disease caused by a heterothallic and airborne fungus called *Pseudocercospora fijiensis* (Vézina and Van den Bergh 2020). It starts 10–14 days after infection with small, pale-yellow spots on young banana leaves, which enlarge, turn brown, and have light gray centers within days with yellowed surrounding tissue (Soares et al. 2021). The disease can be controlled using weekly fungicide applications on farms (Vézina and Van den Bergh 2020). Figure 1 shows how Black Sigatoka affects the banana plant.

Fusarium Wilt, also known as Panama disease, is a destructive banana disease caused by the soil-borne fungus *Fusarium oxysporum* f.sp. *cubense* race 1 (Foc). The infection starts in the roots and spreads to the corm (Okungbowa and Shittu 2014; Vézina 2022). Symptoms include wilting and yellowing older leaves, followed by new ones (Jackson 2014; Viljoen et al. 2016). As the disease progresses, yellowed leaves collapse, forming a dead leaf covering around the pseudostem. This continues until all leaves fall and dry up, leading to the plant's death. The splitting of the pseudostem's base is another common sign. Figure 2 shows the effects of Fusarium wilt on banana

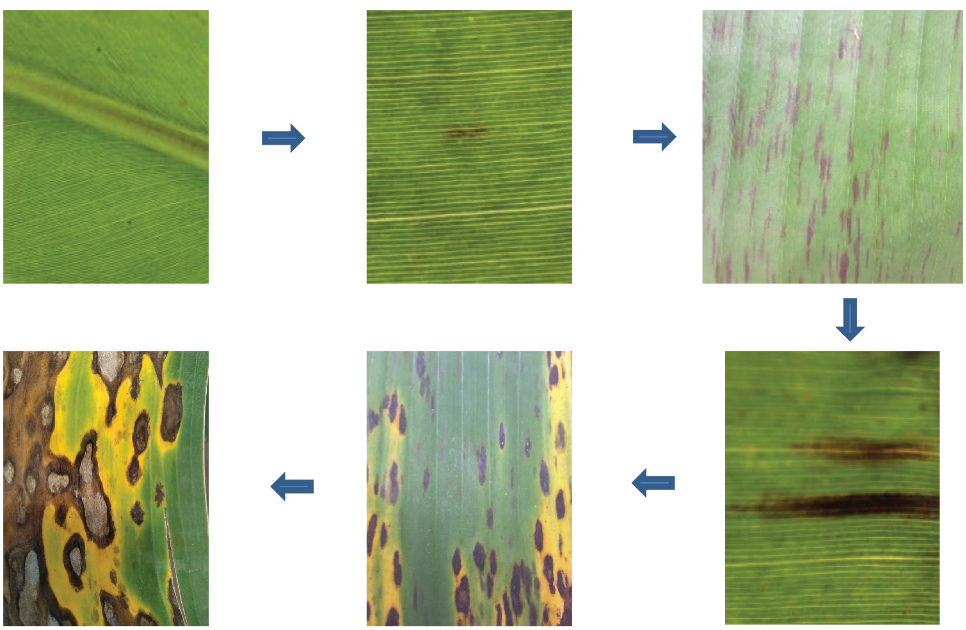


Figure 1. Different stages in which Black Sigatoka develops and affects the banana leaves.

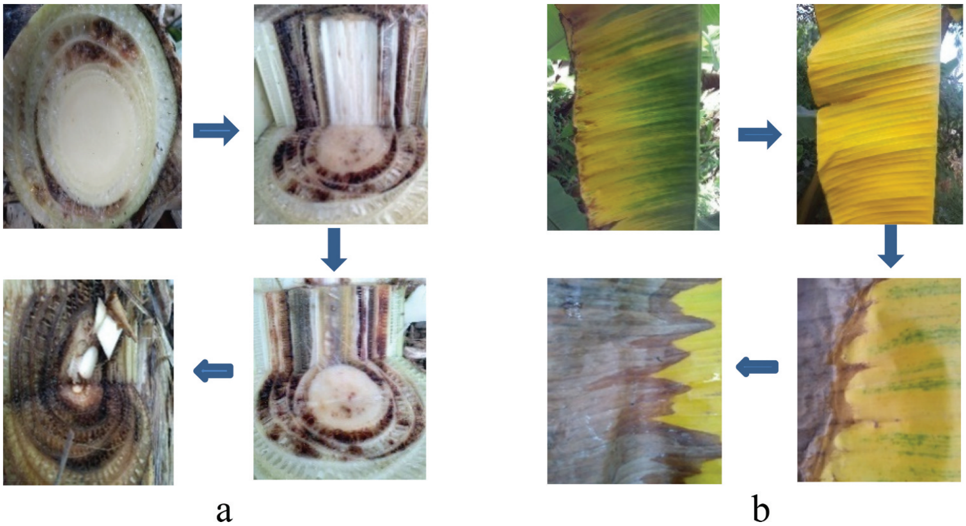


Figure 2. Fusarium wilt damage on banana plants (a) fusarium wilt infected banana stalk (b) fusarium wilt infected banana leaves.

stalks and leaves. Chemical pesticides and fungicides cannot control the fungus. To ensure bananas can be grown, resistant cultivars should be planted on affected soil or start plantations on unaffected land (Vézina 2022).

U-Net is a network that has an encoder-decoder symmetric structure. The left encoder side of the architecture is called the contracting path which is used for feature extraction. It consists of several convolution and pooling operations to sample down the image. The right decoder side is called the expansive path and it's used for upsampling, to restore the original image's shape, and to predict every pixel. To combine the features of various levels in both the encoder and the decoder, skip connections are used to link the encoder and the decoder (Zhang and Zhang 2023). U-Net has shown remarkable performance in medical and natural images, and its lightweight design with 28 M parameters makes it highly suitable for diseased leaf image segmentation (Farahani and Mohseni 2021; Zhang and Zhang 2023). It was also assessed for banana disease segmentation due to its ability to separate diseased areas from cluttered backgrounds, high accuracy, and short experiment runtimes. U-Net was used because it provides farmers with the information they need concerning diseased areas on the banana plant. U-Net seems to work well enough for the problem.

The recent advances and successes of deep learning in detecting plant diseases have inspired this study. The objective of this study was to assess a U-Net image segmentation deep learning model for the early detection and localization of Fusarium Wilt and Black Sigatoka banana diseases using semantic segmentation. The model is assessed for its ability to localize infected areas in banana leaf or stalk images, in addition to detecting them. This study's contribution is the dataset collected from the field and the methods used to train a U-Net image segmentation model that could localize the effects of Fusarium Wilt and Black Sigatoka banana diseases on banana leaf and stalk images.

Computer vision through deep learning techniques has been applied in several studies to detect and classify banana plant diseases. Selvaraj et al. (2019) developed an AI-based system to detect banana plant diseases using a large dataset of 30,952 annotated images from southern India and Africa. The study included Xanthomonas Wilt, Bunchy disease, Black Sigatoka, Fusarium Wilt, Yellow Sigatoka, and Corm Weevil diseases. The model classes included each disease, dried or old leaves, and healthy plants. The detection models were built using Faster R-CNN based on ResNet50 and InceptionV2 and an independent MobileNetV1 convolutional neural network architecture using transfer learning. Six models were built from each architecture to represent diseases according to plant parts, utilizing images from various banana plant parts (including the corm, fruit bunch, leaves, cut fruit, pseudostem, and entire plant). Faster R-CNN models based on ResNet50 on the pseudostem, leaves, fruit bunch, and entire plant had better performance, with mean Average Precision (mAP) of 99%, 70%, 97%, and 73%, respectively. However, the study struggled with unbalanced data and limited images to train the model properly for Bunchy Top disease (902 images), Black Sigatoka disease (980 images), Yellow Sigatoka disease (1066 images), Fusarium Wilt disease (1726 images), and Corm Weevil disease (701 images). Also, there is still a need to detect the exact location and shape of Black Sigatoka and Fusarium Wilt diseases.

Bhuiyan et al. (2023) proposed a lightweight and fast convolutional neural network called the BananaSqueezeNet model for diagnosing Pestalotiopsis, Sigatoka, and Cordana banana diseases using 937 images from Bangladesh. The model achieved 96.25% accuracy, 96.25% recall, 96.53% precision, 96.17% F1-score, 98.75% specificity, and 95.13% MCC. Despite the good performance, the study used a few images that could not have been sufficient to train the model.

Selvaraj et al. (2020) utilized machine learning and aerial images to detect banana diseases like bunchy top disease and Xanthomonas Wilt. They trained models using high-resolution satellite imagery and unmanned aerial vehicle (UAV) data. The random forest model achieved an accuracy of 97%. A mixed object detection (RetinaNet) and classification model achieved accuracies of 99.4%, 92.8%, 93.3%, and 90.8% for banana bunchy top disease, Xanthomonas Wilt, healthy banana cluster, and individual banana plants classes respectively.

Despite numerous studies addressing plant leaf disease detection, few have focused on developing systems capable of segmenting infected areas. Deng et al. (2023) utilized the Multi-scale Convolution Module UNet (MC-

UNet) to segment bacterial spot, late blight, early blight, and leaf mold tomato diseases, using 6,372 images. The MC-Unet model had 6.67 M parameters, it achieved an accuracy of 91.32% and a mean average precision (mAP) of 88.42%.

Dong et al. (2024) proposed a platform for large-scale image phenomics analysis of disease in plant science called Plant Phenomics Analysis of Disease (PlantPAD). It includes 421,314 images, 63 crops, and 310 diseases. PlantPAD includes well-annotated image data, and in-depth disease information, and provides PDDD-PreTrain which is a plant disease pre-training model based on deep learning technology for diagnosing plant diseases. PlantPAD offers applications like intelligent disease diagnosis, disease education, and efficient disease detection and control.

Dong et al. (2023) suggested a series of commonly used pre-trained models support image-based plant disease diagnosis called PDDD-PreTrain. This study used a dataset of over 400,000 images from 40 plant species collected in the field and online and categorized into 120 disease categories. The experiments included plant disease diagnosis such as plant disease identification, plant disease detection, and plant disease segmentation. Several pre-trained models were used in this study.

Huang et al. (2023) proposed a knowledge distillation approach for plant disease detection to provide an efficient and lightweight diagnosis of several diseases in various crops. The study created two approaches to construct four distinct lightweight models as student models: the Mobile-YOLOR-v1, Mobile-YOLOR-v2, YOLOR-Light-v1, and YOLOR-Light-v2 models; and they used the YOLOR model as the teacher model. The study used a multistage knowledge distillation method to enhance lightweight model performance which achieved a mAP@ .5 of 60.4% in the PlantDoc dataset with small model parameters.

Luck et al. (2020) suggested a Macrophenomics facility comprised of a set of methods and equipment for automating the segmentation and quantification of powdery mildew disease. The facility was optimized for quantifying powdery mildew disease on barley and wheat. The facility could score the visible powdery mildew disease symptoms 5–7 days after inoculation automatically. The system was capable of measuring the percentage of diseased leaf area with high accuracy and repeatability, and it could theoretically process up to 10,000 individual samples every day.

Most of these studies presented models that performed very well. However, the lack of a sufficient number of images to train the model properly was the shortcoming of several studies. Also, to the best of the researchers' knowledge, none of the studies addressed the segmentation of Black Sigatoka and Fusarium Wilt banana diseases. Therefore, this research proposes an image segmentation model for segmenting these banana plant diseases at early stages using a dataset collected from the field.

Materials and Methods

The Dataset

The dataset for this study was collected from the fields in the Arusha, Mbeya, Kagera, Kilimanjaro, and Dar es Salaam regions of Tanzania because of banana availability and disease prevalence. The study used Samsung SM-A715F/DS phone cameras under normal settings to capture images of banana leaves and stalks affected by Fusarium Wilt and Black Sigatoka diseases, as shown in Figure 3, guided by plant pathologists and agricultural experts and were labeled. The resolution of the images differed from image to image. Some of the images had a high resolution of 4624×3468, while others had a low resolution of 640×288. The shooting height of the images ranged from 10 to 50 centimeters from the banana plant. The dataset was collected early in the morning to avoid shadows from sunlight. The images comprised three classes: Fusarium Wilt-infected banana leaves and stalks; Black Sigatoka-infected banana leaves; and healthy banana leaves. Only two classes were used to train the U-Net image segmentation deep learning model, as the healthy class was represented by the diseased images' background (unlabeled part). To support further research in detecting and segmenting Fusarium Wilt and Black Sigatoka banana diseases, the dataset used in this work is freely available in an open-access repository, https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/LQUWXW, and more information about the dataset is reported by (Mduma and Leo 2023). Table 1 summarizes the number of images collected. Figure 4 shows examples of Fusarium Wilt-infected banana leaves and stalks and Black Sigatoka-infected banana leaves.

Figure 3. Data collection in the field.

Table 1. Total number of images collected.

Banana Images	Number of images collected
Black Sigatoka infected Leaves	10,137
Fusarium Wilt infected Leaves and stalks	10,724
Total	**20,861**

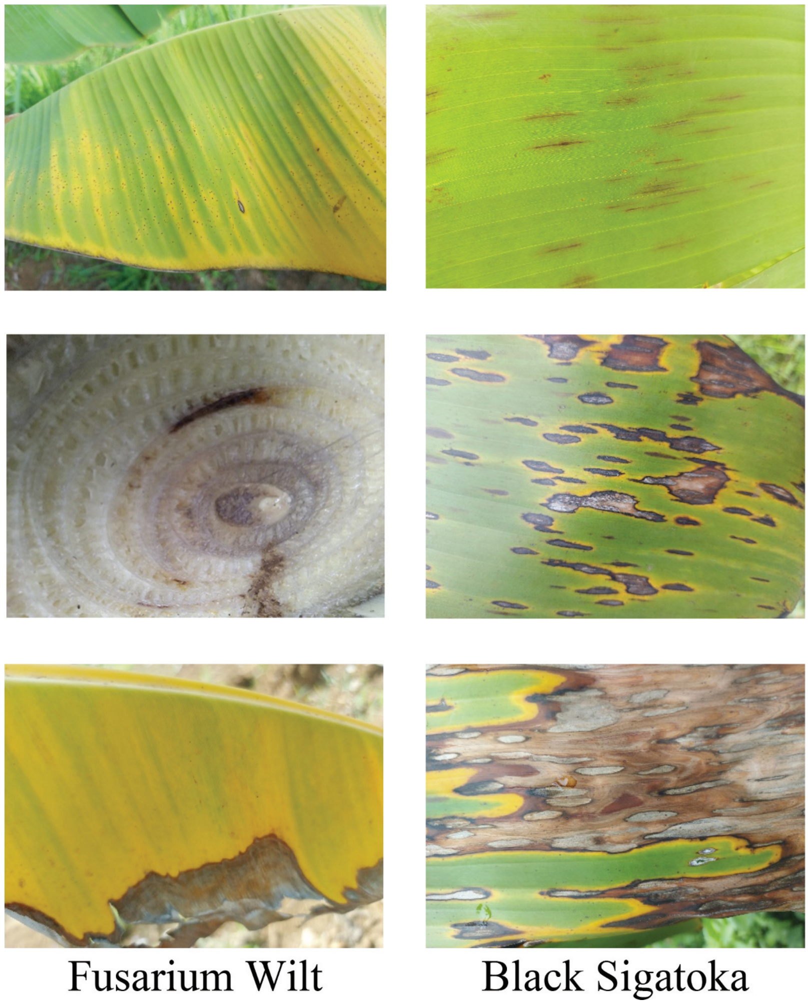


Figure 4. Examples of the dataset's images.

Research Framework

The research framework in Figure 5 explains how this study utilized an image dataset of banana leaves and stalks from the field for model development and validation. The optimized model was obtained after several experiments with hyperparameter tuning based on the model's performance provided by the evaluation metrics.

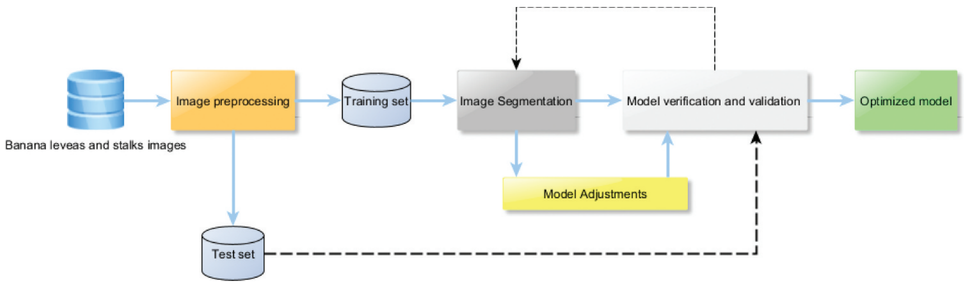


Figure 5. The research framework.

Image Pre-Processing

Image pre-processing helped prepare the image dataset so that it could be used effectively in model training and validation.

Cropping, Data Cleaning, and Image Renaming

The image dataset was manually cropped to remove the background and unwanted items and focus on the banana leaf or stalk. Open-source and easy to use tools VisiPics and Duplicate Photo Finder were used to remove 2621 duplicates from the dataset, with VisiPics removing strictly similar images and Duplicate Photo Finder removing images searched against the "same picture" filter. Table 2 summarizes the removed duplicates.

Only clean images were used in model training. The number of clean images used in model training was obtained using the following formula:

$$C = T - D \tag{1}$$

Where

C denotes the clean images.

T denotes the total number of collected images.

D denotes the duplicate images.

Images were renamed with image numbers to avoid confusion and simplify handling. For instance, Black Sigatoka images were renamed from BS_1.jpg to BS_9120.jpg, using the open-source and user-friendly Bulk Rename Utility software.

Table 2. A summary of removing duplicates.

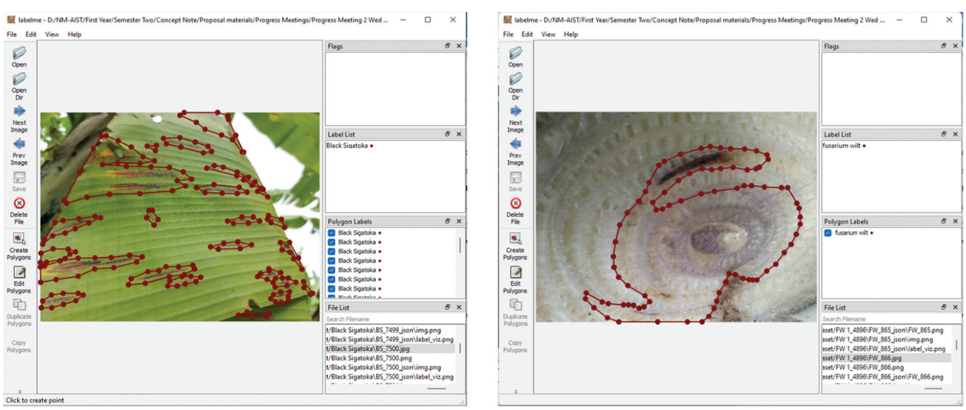
Banana Images	Before Removing Duplicates	After Removing Duplicates	Duplicates found and deleted
Black Sigatoka infected leaves	10,137	9,120	1,017
Fusarium Wilt infected leaves and stalks	10,724	9,120	1,604
Total	**20,861**	**18,240**	**2,621**

Image Annotation

Image annotation is the manual process of assigning labels to images or collections of images. It involves a human operator finding interesting objects and adding details like shapes and labels. Image segmentation algorithms require images to have masks around regions of interest with labels for accurate predictions. For semantic segmentation 18,240 clean images were annotated using LabelMe (Russell et al. 2008) open-source software. An irregular polygon was manually drawn around areas in banana leaf and stalk images displaying disease symptoms. These polygons were given label names for each class, such as "Black Sigatoka" for Black Sigatoka disease symptoms and "fusarium wilt" for Fusarium Wilt symptoms. Each image contained at least one polygon. The images were saved together with their corresponding annotation files with similar names but different extensions. LabelMe saves its annotations in JSON format, which were converted to PNG format annotations and were used in the U-Net model for semantic segmentation. Figure 6 illustrates the annotation process in LabelMe software.

Assessed Model

This study focused on developing a semantic segmentation deep learning model for the segmentation of banana diseases using U-Net. U-Net was trained and yielded the best performance in several International Symposium on Biomedical Imaging (ISBI) challenges (Ronneberger, Fischer, and Brox 2015) in semantic segmentation.



(a) (b)

Figure 6. The manual annotation process of the image dataset using LabelMe (a) annotating a Black Sigatoka infected banana leaf image; (b) annotating a fusarium wilt infected banana stalk image.

U-Net Model for Semantic Segmentation

Semantic segmentation classifies every pixel in an image without separating instances of the same class. The U-Net model assessed for semantic segmentation, extends the fully convolutional network architecture to use a few annotated training images (relying excessively on data augmentation) and still yields precise segmentations (Ronneberger, Fischer, and Brox 2015). Figure 7 illustrates the architecture of the U-Net model.

Model Training

The U-Net model was trained on two classes of images, Black Sigatoka and Fusarium Wilt, with their PNG format image masks. Due to the large dataset and high computing time, especially when resizing and converting each image and its mask into NumPy array values, the model was divided into 25 groups to handle smaller images at a time. The first 12 groups had 500 images, groups 13 to 24 had 250, and group 25 had 120 images with their corresponding masks for each Black Sigatoka and Fusarium Wilt. An 80% training set and a 20% validation set were randomly selected from all groups. The output weight from the previous group was used as the input weight for training the next group.

U-Net Model Hyper-Parameter Tuning

The study used a custom U-Net model with 32 convolutional filters in the initial layer, which was doubled after every one of the four layers in the contraction path. The images were rescaled or normalized to an interval of zero to one and resized to 512×512 pixels. The training dataset size was increased by using data augmentation. Data

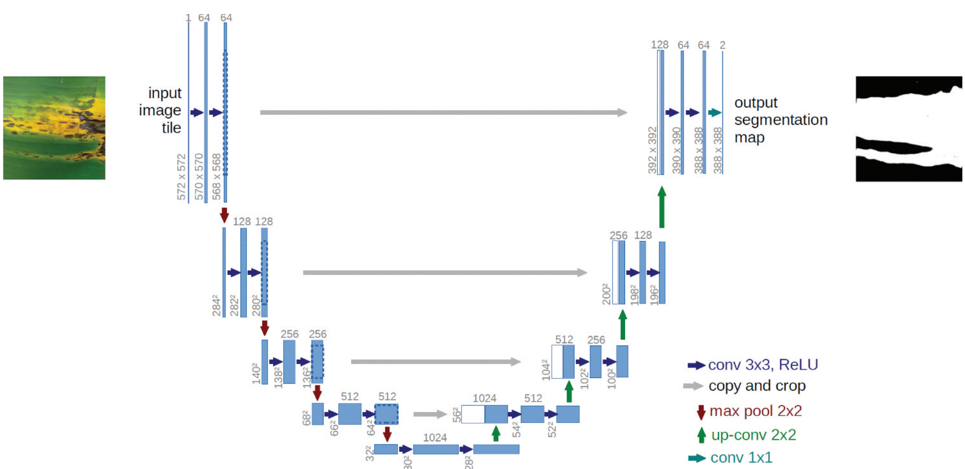


Figure 7. U-Net architecture.

argumentation techniques included rotation of 5.0 degrees, height and width shift range of 0.05, shear range of 40, zoom range of 0.2, vertical and horizontal flipping, and fill mode of constant. Data augmentation was applied equally to both images and annotations. The U-Net model experiment used 100 epochs, an SGD activation function, an IoU threshold for a minimum detection probability of 0.5, and a learning rate of 0.01.

The process of rescaling or normalizing the images to a range of zero to one was done using the following transformation:

$$x = \frac{x - x_{min}}{x_{max} - x_{min}} \tag{2}$$

Where

X ranges between 0 and 255.

X_{min} is 0.

X_{max} is 255.

Therefore, the formula becomes.

$$x = \frac{x}{255} \tag{3}$$

The SGD optimizer in Keras features a present learning rate scheduler that lowers the learning rate throughout the stochastic gradient descent optimization algorithm. Equation 4 shows how the learning rate was decreased.

$$lr = \frac{lr * 1}{1 + decay * epoch} \tag{4}$$

Where

Lr is the learning rate

Decay is the learning rate decay over each update

Epoch is when all the images are passed in training the model once

U-Net Loss Function

Ronneberger, Fischer, and Brox (2015) state that "the energy function is computed by a pixel-wise soft-max over the final feature map combined with the cross-entropy loss function." U-Net transforms the segmentation problem into a multiclass classification problem, and each pixel is assigned to a certain class. U-Net gives the background labels that separate touching items a lot of weight. The loss weighting scheme helps U-Net distinguish touching objects of the same class. Hence, U-Net can separate individual spots of Black Sigatoka within a binary segmentation map.

The loss is defined as

$$L = \sum_{i=1}^{m} -(y_i \log(p_i) + (1 - y_i)\log(1 - p_i)) \tag{5}$$

Where

L is the U-Net loss.

m is the number of pixels in an image.

i is the index of a pixel.

y_i is the binary indicator i.e. the ground truth or real value of the i-th pixel whose value is 0 or 1.

log is the natural log.

p_i is the predicted probability/value of the i-th pixel. Its value ranges from 0 to 1.

U-Net Evaluation Metrics

Intersection over Union (IoU): IoU is the proportion of the overlapping area (the point where the predicted mask and the ground truth mask meet) to the union area (where the predicted mask and the ground truth mask are joined). When the IoU exceeds a predetermined threshold, the prediction is True Positive (TP), and when it falls short of that threshold, it is False Positive (FP). This metric is chosen because it is the main metric that evaluates how accurate an image segmentation model is. The following formula gives the Intersection over Union (IoU):

$$IoU = \frac{Overlapping\ Area}{Union\ Area} \tag{6}$$

Dice Coefficient: The dice coefficient measures the overlap between the expected and actual mask, ranging from zero (no spatial overlap between the predicted mask and ground truth) to one (complete overlap), and is defined as follows:

$$Dice\ Coefficient = \frac{2 * Overlapping\ Area}{Total\ number\ of\ pixels\ in\ both\ images} \tag{7}$$

Experiment Setting

The experiments were done on a PC with Windows 11 Pro and one Intel(R) Core (TM) i5-8250 U CPU @ 1.60 GHz 1.80 GHz, with 8GB of RAM. The notebook was run on Google Colab Pro Plus with a Tesla T4 GPU and 54.8GB of RAM. Python 3 and the TensorFlow backend were used to implement the network.

Results and Discussion

The model's efficiency is crucial for its performance. The first 12 model group experiments had training times ranging from 162.47 to 175.63 minutes. The training times between groups 13 and 24 ranged from 89.16 to 93.57 minutes due to less data, while the training time for group 25 was 87.77 minutes due to having the least data.

Loss Results

U-Net group 8 had the least validation loss and training loss. Figure 8 shows the loss over epoch graph for the U-Net group 8 model. The graph shows that the training loss has a decreasing trend during training with small fluctuations, while the validation loss also decreases but with milder fluctuations hitting a minimum of 0.0583. This suggests that both early in the training process and later on, the U-Net model fits well on the features of our dataset. U-Net group 8 model had the best performance because it obtained the lowest loss value when compared to other groups.

Evaluation Metrics Results

The U-Net semantic segmentation model was evaluated using the Dice coefficient and Intersection over Union. Table 3 displays the evaluation metrics findings for all carried-out model experiments. The best-performing group was U-Net group 8, which achieved a Dice coefficient of 96.45% and an Intersection over Union of 93.23%. The average performance for all U-Net groups was a Dice coefficient of 90.996% and an Intersection over Union of

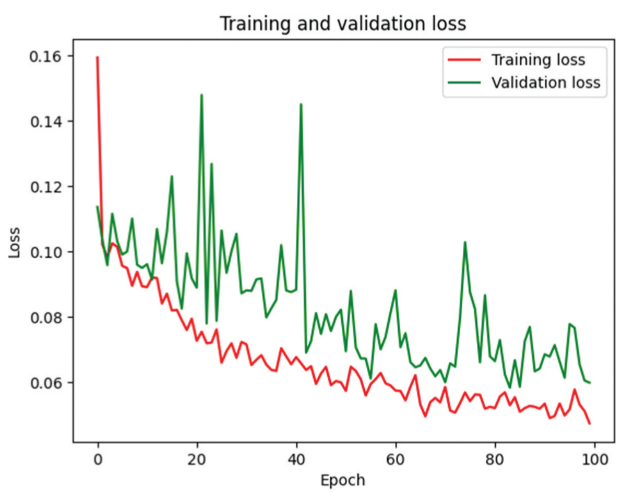


Figure 8. Loss over epoch graph for U-Net group 8 model.

Table 3. Evaluation metrics results.

Model Group	IoU (%)	Dice Coefficient (%)	Validation IoU (%)	Validation Dice Coefficient (%)
U-Net group 1	86.71	92.21	87.31	93.08
U-Net group 2	86.98	92.47	87.99	93.57
U-Net group 3	83.97	90.67	87.82	93.42
U-Net group 4	87.51	92.73	91.41	95.49
U-Net group 5	88.01	92.98	91.38	95.47
U-Net group 6	92.86	95.97	91.62	95.58
U-Net group 7	92.77	96.01	91.71	95.65
U-Net group 8	93.28	96.25	93.23	96.45
U-Net group 9	82.90	90.05	83.49	90.90
U-Net group 10	85.09	91.38	84.06	91.29
U-Net group 11	84.42	90.51	80.34	89.05
U-Net group 12	89.72	93.72	87.48	93.20
U-Net group 13	70.26	80.77	78.96	87.83
U-Net group 14	75.41	84.83	75.01	85.55
U-Net group 15	91.77	95.33	92.46	95.94
U-Net group 16	81.51	88.35	77.13	86.97
U-Net group 17	74.07	84.18	72.68	84.10
U-Net group 18	73.29	83.43	73.71	84.76
U-Net group 19	77.96	86.77	78.07	87.66
U-Net group 20	81.45	88.61	79.22	88.11
U-Net group 21	76.03	85.53	76.64	86.70
U-Net group 22	79.41	87.42	84.30	91.26
U-Net group 23	84.92	90.80	86.52	92.73
U-Net group 24	83.08	89.97	80.72	89.22
U-Net group 25	89.51	93.99	83.39	90.93

83.866%. Similar results were obtained by (Loyani, Bradshaw, and Machuve 2021) when they segmented a tomato plant paste called tuta absoluta using a U-Net model. Their model achieved a Dice Coefficient of 82.86% and an Intersection over Union of 78.60%. Also, similar results were obtained by (Wang et al. 2023) who achieved a Dice metric of 92% and a Mean Intersection over Union of 86.15% when they segmented pear leaf diseases using an MFBP-UNet model. The dice coefficient usually has a higher value than Intersection over Union in the same segmentation performance. Figure 9 shows the Intersection over Union over epoch graph for the U-Net group 8 model. The training Intersection over Union and validation Intersection over Union increase steadily with some fluctuations, with milder fluctuations for the validation Intersection over Union. At the 100th epoch, the training Intersection over Union is near 0.94, while the validation Intersection over Union is near 0.92. This trend shows that the model learned the dataset features well and could segment the diseased areas well. Figure 10 shows the Dice Coefficient over epoch graph for the U-Net group 8 model. The training and validation Dice Coefficients increase steadily with some fluctuations, with milder fluctuations for the validation Dice Coefficient. At the last epoch, the training Dice Coefficient was slightly over 0.96, while the validation Dice Coefficient was near 0.96. This trend shows that the model fits well on the data and could segment the diseased areas well. A preliminary experiment was conducted using the Mask R-CNN model for the instance segmentation of

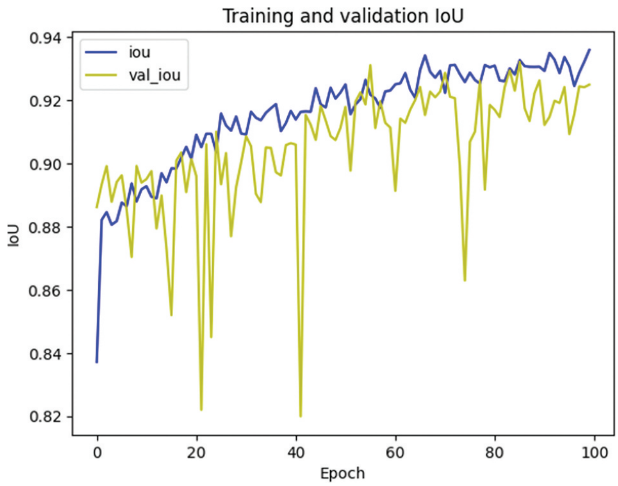


Figure 9. Intersection over union over epoch graph for U-Net group 8 model.

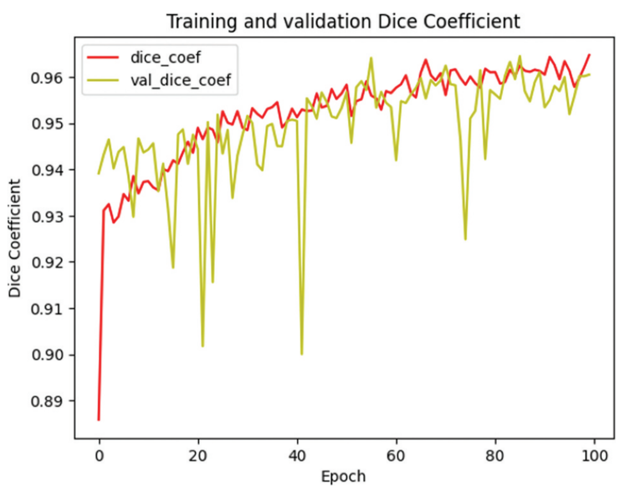


Figure 10. Dice coefficient over epoch graph for U-Net group 8 model.

Fusarium Wilt and Black Sigatoka banana diseases achieving a mean Average Precision (mAP) of 0.04529.

The U-Net model could segment the two banana diseases well. Figure 11 shows the segmentation predictions for banana leaves and stalks affected by Fusarium Wilt and Black Sigatoka diseases. In Figure 11, bottom row shows the original images, and the second row from the bottom displays the ground truths from the annotations. In the second row from the bottom, the white part represents the area labeled as having the disease during annotation, while the black part represents the healthy background area. The third row from the bottom is the predictions from the U-Net model, while the top row is the predictions overlayed on top of the original image. In the third row from the bottom, the white area represents the

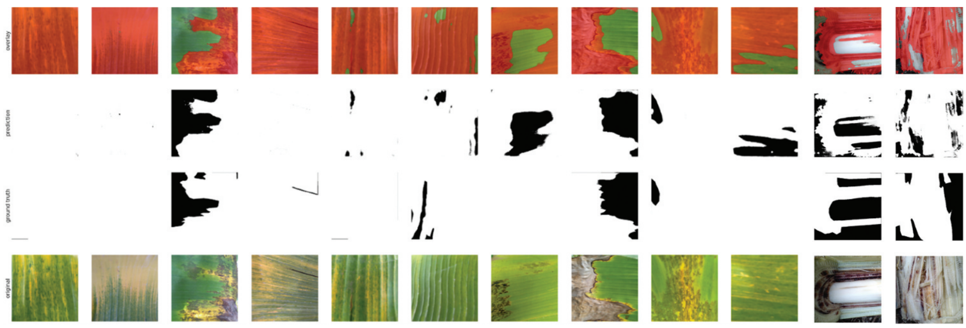


Figure 11. Segmentation predictions from the U-Net model.

areas the model predicted to have the disease and segmented them, while the black areas represent the areas left out by the model as healthy. In the top row, the red overlays are the areas predicted by the model to have the disease. From Figure 11, the model could segment the areas where the leaves were not green, signifying the presence of disease, and leave out healthy green areas. From the study all images had either Black Sigatoka disease or Fusarium Wilt disease, so every image had only one class. Figure 12 shows the segmentation prediction results provided by the preliminary experiment conducted using the Mask R-CNN model to segment Fusarium Wilt and Black Sigatoka diseases.

Complexity and Overhead Analysis of the Proposed Approach

The U-Net model performs well in the semantic segmentation of banana diseases. The proposed approach of training the model in groups of images helps to accommodate many images at the cost of performing many experiments. For example, to accommodate 18,240 images in training the model, 25 experiments were conducted to train the model, with the output of the previous experiment used as input for the next. A single experiment could accommodate up to 1000 images and their corresponding annotations, with 500 images for each class. More

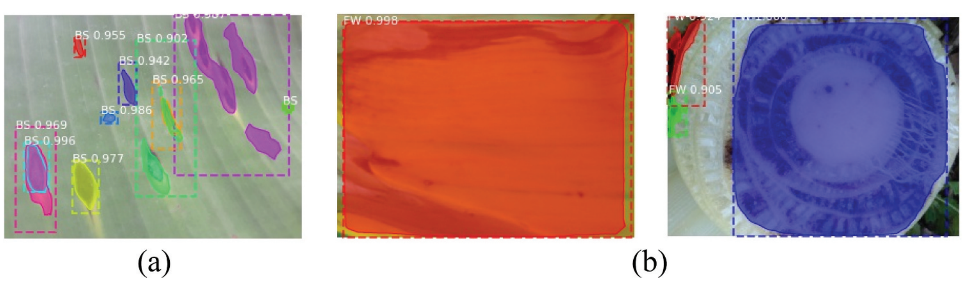


Figure 12. Segmentation predictions from the mask R-CNN model (a) segmentation of Black Sigatoka infected banana leaf; (b) segmentation of fusarium Wilt infected banana leaf and stalk.

resources were required in terms of cost and time for these experiments, and many computing units were purchased to support all 25 experiments, which took 3,204.86 minutes to complete.

Conclusion

The study aimed to develop a deep-learning image segmentation model for early detection of Fusarium Wilt and Black Sigatoka banana diseases. The U-Net image segmentation deep learning architecture was assessed for semantic segmentation. The average performance achieved by all the U-Net groups was a Dice coefficient of 90.996% and an Intersection over Union of 83.866% in segmenting the two banana diseases. The standard deviation for all the U-Net groups was 3.737 for the Dice coefficient and 6.221 for the Intersection over Union. The result for the best performing U-Net model group which was U-Net group 8 achieved a Dice Coefficient of 96.45% and an Intersection over Union (IoU) of 93.23% in segmenting the two banana diseases. This result of U-Net group 8 was the best since it was not contained within the error of all the experiments. The model accurately segmented areas where banana leaves and stalks were damaged by these diseases. The industrial significance of the proposed approach is that it can localize affected areas of banana plants, and this information could be used to quantify the extent of the disease. This study demonstrates that deep learning can be effectively used for the early detection of banana diseases, allowing farmers to take necessary measures to minimize their negative effects and increase yields. The assessed model when deployed can be practically used and benefit farmers without prior knowledge of the symptoms or extension officer services, enabling them to detect and localize the presence of these diseases early. This study adds to the body of knowledge to aid extension officers and farmers in making informed decisions for increasing banana productivity.

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Data Availability Statement

The data that support the findings of this study are openly available in ["Harvard Dataverse"] at https://doi.org/10.7910/DVN/LQUWXW.

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