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MALARIA PARASITE DETECTION USING VGG-16

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ABSTRACT

Malaria, caused by the Plasmodium parasite and transmitted through mosquito bites, is a significant global health challenge, with African nations accounting for 94% of cases and deaths. In 2019, the disease caused 409,000 deaths, 67% of which were among children under five. While a precise diagnosis is crucial, conventional techniques—like examining stained blood smears under a microscope—require a lot of resources, including trained staff and lab equipment that is sometimes unavailable in low-resource environments. In order to overcome these obstacles, this work uses deep learning methods for automated malaria identification. Prior machine learning techniques, such as random forests and decision trees, have demonstrated respectable accuracy but are not stable or scalable. The suggested approach makes use of convolutional neural networks (CNNs) and the VGG-16 architecture to enhance diagnostic efficiency and accuracy via transfer learning. In settings with limited resources, this automated methodology provides a scalable and effective method for diagnosing malaria from blood smear pictures by reducing dependency on human expertise. This strategy could revolutionize malaria diagnostics by improving speed and accuracy, resolving significant shortcomings of conventional techniques, and aiding international efforts to eradicate this fatal illness.

Keywords: Deep learning, Malaria Parasite, Detection, Machine Learning

INTRODUCTION

Malaria, according to the World Health Organization (WHO), is endemic in many nations. Malaria is a deadly disease that spreads easily (WHO, 2021). When a human is bitten by a mosquito, a virus known as the Plasmodium parasite, which lives in the insect's body, enters the victim's circulation and causes the disease (Rahman *et al.*, 2019). Malaria has plagued civilization for thousands of years, and humans have often been at danger for the disease. In 2019 alone, there were 409,000 malaria-related deaths and 229 million new cases, according to WHO statistics. The fact that 67% (or 274,000) of malaria deaths were in children under the age of five, making malaria one of the leading causes of child mortality worldwide, is another startling statistic that first springs to mind when looking at these numbers. 94% of all malaria infections and deaths worldwide occur in African countries, making them the disproportionate and indisputable hub of the disease. To prevent malaria from spreading and inflicting further misery throughout the world, a technique for correctly diagnosing the disease has to be developed. Malaria parasites may be identified by looking at a drop of patient blood spread out as a blood smear on a microscope slide under a microscope. The samples are colored to give the parasites a distinctive look prior to testing. This approach "remains the gold standard for malaria laboratory confirmation." However "it depends on the quality of the reagents, the microscope, and the laboratorian's experience."

In order to determine which parasites cause malaria, tests were conducted in Saiprasath et al. (2019) using machine learning techniques. An oil immersion objective lens with a 1000x magnification was used to collect images from 133 subjects. Poor quality, out-of-focus, and hard-to-identify parasite images were eliminated. Bounding boxes for 50,255 photos of malaria parasites from 2703 blood smear pictures are also included in the collection. Each picture was then separated into overlapping patches using the bounding box, and each patch was given a label of either 0 or 1. Twenty-seven blood smear pictures, or 75% of the labeled data, make up the training dataset. Of them, 37550 instances had patches that have been determined to be parasites. About 25% of the entire data, or 676 blood smear photos, are used in the testing dataset. Of them, 16312 cases had patches that have been identified as parasites. Preprocessing and feature engineering are finished before the patient test picture is sent into the machine learning system. The binary classification algorithm is then used to determine the malaria status of the picture patch.

Chavan and Sutkar (2014) employed two machine learning techniques to identify the parasites that cause malaria and evaluate the disease using image processing. The Neural Network (NN) and Support Vector Machine (SVM) classifiers were used in their analysis. For the proposed process, each of them gathered thirty images from labs. The purpose of this study is to use slide pictures of blood smears to differentiate between malaria patients who are infected and those who are not. The accuracy of the NN classifier is 78.53% for this dataset, compared to 98.25% for the SVM classifier.

Bashir, Mustafa, Abdelhameid, and Ibrahem (2017) carried out their experiment to detect malaria parasites. For this study, they employed artificial neural networks (ANN) in conjunction with image processing techniques. The database for this inquiry was created using 77 pictures. The classification strategy's effectiveness was evaluated based on its accuracy, specificity, and sensitivity. For this data set, they obtained 99.65% specificity, 100% sensitivity, and 99.6% accuracy. Mashor, Nasir, and Mohamed (2018) examined the detection of malaria using Giemsa stain" . In this study, certain image processing methods are applied. For example, this technique is used to convert an RGB image to gray scale, which is subsequently screened to improve its quality. The next step is to segment the photos. The next step is feature extraction. For this, they use the K-means method. They developed an automated approach for diagnosing malaria using this. The malaria parasite Plasmodium attacks red blood cells (RBCs) and is spread by mosquitoes. Malaria may be fatal to humans and ranges in severity from mild to extremely hazardous.

Tek, Dempster, and Kale (2006) learned information for stained pixels and the Bayesian pixel classifier were used to train the weighted KNN (K-Nearest Neighbors) technique. A classification of multi-class parasites by lifecycle stage and type was proposed by Tek, Dempster, and Kale (2010). Anggraini et al. (2011) proposed a thresholding technique for detecting Plasmodium in blood smears. Waitumbi et al. (2011) proposed four for Malaria Parasite detection as follows: clump splitting, edge identification, edge joining, and parasite location. Adaptive histogram equalization is the pre-processing method used in this approach. The pixels are divided into erythrocyte, parasite, and background groups using a color segmentation technique based on common supervised classification algorithms. Supervised classification techniques including Support Vector Machines, K-Nearest Neighbour, and Naive Bayes were evaluated using a variety of color models, including the RGB (Red, Green, and Blue), normalized RGB, HSV (Hue Saturation Value), and YCbCr models. In recent years, new techniques for diagnosing malaria have surfaced, including fluorescence microscopy detection, rapid antigen, and PCR (Polymerase Chain Reaction) technology that may identify certain nucleic acid sequences (Haditsch, 2004). Despite this, light microscopy remains the most widely used and popular diagnostic method (Thung & Suwardi, 2011) . Sowmya, Mohan, and Soman (2015) locates edges using sparse banded filter matrices, whereas Pooja, Mamtha, Sowmya, and Soman (2016) employs X-ray image classification to detect the tumor.

Due to the fact that a lab specialist is needed to make the diagnosis, this process is "inefficient in some circumstances due to the absence of lab equipment." Researchers have employed machine learning techniques, such as random forests, support vector machines, and decision tree classifiers, among others, to categorize the malaria parasite with a reasonable degree of accuracy. However, prior approaches for categorizing malaria parasites from thin blood smears did not exploit the VGG-16 mechanism for transfer learning. This study's main objective is to create a deep learning model for medical image processing that addresses problems with the current malaria detection technique by utilizing VGG-16 and convolutional neural networks.

MATERIALS AND METHODS

The study is divided into three stages. Collecting datasets and appropriately allocating them to training, testing, and validation sets is the main goal of phase 1. In phase two, image processing includes picture scaling and data augmentation. In phase three, CNN and VGG-16 are developed for image classification, and each reference model is assessed using a de facto assessment criterion.

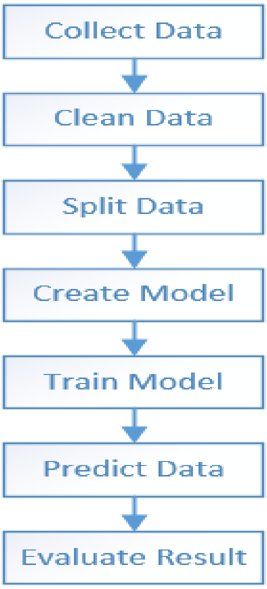


Figure 1: Research Framework

Convolutional Neural Network (CNN)

In order to automatically and adaptively learn spatial hierarchies of input via backpropagation, convolutional neural networks (CNNs), a subtype of artificial neural networks, employ a number of building elements, such as convolution layers, pooling layers, and fully connected layers. CNN has been the preferred technique for computer vision applications ever since the 2012 Image Net Large Scale Visual detection Competition (ILSVRC) object detection challenge's exceptional results were made public. CNN has demonstrated expertise in a number of areas, including medical research. Naturally, radiology professionals are intrigued by CNN's potential, and several research have already been published in areas such as image reconstruction, segmentation, classification, and other tasks.

In order to handle data with a grid pattern, like photos, CNN is a type of deep learning model that automatically and adaptively learns spatial hierarchies of attributes, from low-level to high-level patterns. A typical CNN consists of three different types of layers (or "building blocks"): convolution, pooling, and fully connected layers. While a fully connected layer in order three incorporates the collected features into the output, like classification, convolution and pooling layers in order one and two do feature extraction. A convolution layer is necessary for CNN, which consists of a stack of mathematical processes, including convolution, a specific type of linear operation. Figure 2 shows an example of a CNN design.

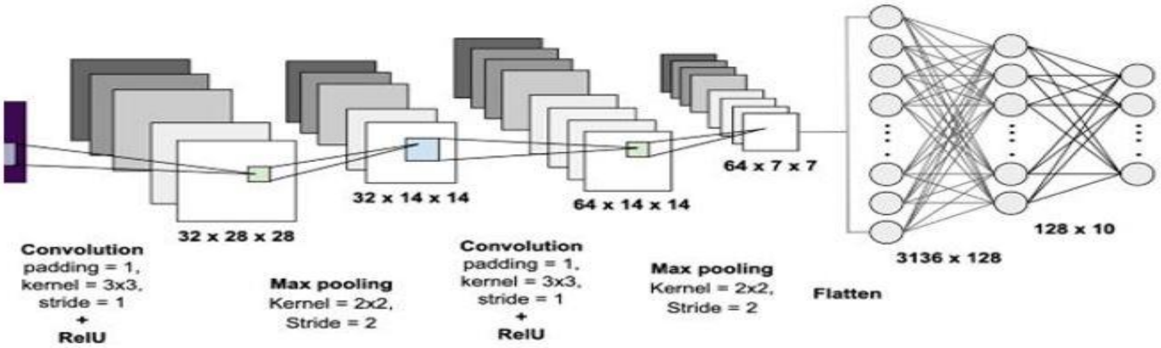


Figure 2: CNN Architecture

Convolutional neural networks are artificial neural networks created especially for image processing. A CNN typically consists of an input layer, an output layer, and hidden layers. They are adept at identifying trends. An ensemble of algorithms that analyze input and provide outputs with the fewest mistakes possible is called a neural network. The nodes are referred to as neural networks because of their structure, which is somewhat like to that of a neuron in the human brain. CNN is widely used in medical imaging because of its exceptional pattern recognition capabilities. This project will make advantage of transfer learning. The model will use transfer learning to examine four different types of convolutional neural networks: EffiecieNet, GoogleNet, Inception, and VGG. To get the best ratings for sensitivity and specificity, the models will be modified. A CNN model architecture typically consists of four layers: the convolutional layer, pooling layer, normalizing layer, and fully-connected layer. The filters make up the convolutional layer of CNN. The pooling layer lowers the parameters, the normalization layer standardizes the inputs, and the fully connected layer completes the layering process. Each convolutional layer of a convolutional neural network (CNN) is followed by an operation known as max pooling. The dimension of pictures is reduced when a layer is added to a model because the output from the previous convolutional layer has less pixels. The output and hidden layers of a CNN both have activation functions. The activation function of a neuron describes its output given a collection of inputs. One popular activation function in deep learning is the rectified linear unit, or ReLU. If an input is less than or equal to 0 in a particular scenario, ReLU will set it to 0. If the input is larger than zero, ReLU will output it. If it is more positive, the neuron is more active. It converts the input to a number that is extremely near to zero if it is truly negative. Nevertheless, it shifts it to a value that is extremely close to one if the input is positive enough. The sigmoid will change an input that is nearly zero into a number between zero and one.

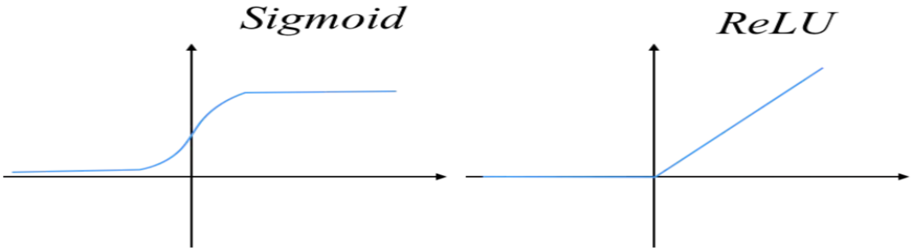


Figure 3: Activation functions Sigmoid and ReLU graphical representation

VGG-16

The VGG16 Convolutional Neural Network (CNN) architecture is simple and widely utilized in ImageNet, a large visual database project used in research on visual object identification software. The VGG16 Architecture was developed and presented by Karen Simonyan and Andrew Zisserman of the University of Oxford in their paper Very Deep Convolutional Networks for Large-Scale Image Recognition. The Visual Geometry Group (VGG), a team of scientists from the University of Oxford, created this structure, which has 16 layers, as indicated by the number 16. The network's simplicity—just three 3x3 convolutional layers placed on top of one another—makes it noteworthy. The max-pooling layers regulate the rising depth and volume size. Two fully connected Two fully connected layers with 4096 nodes each are followed by a softmax layer . The VGG16 architecture is seen in figure 4.

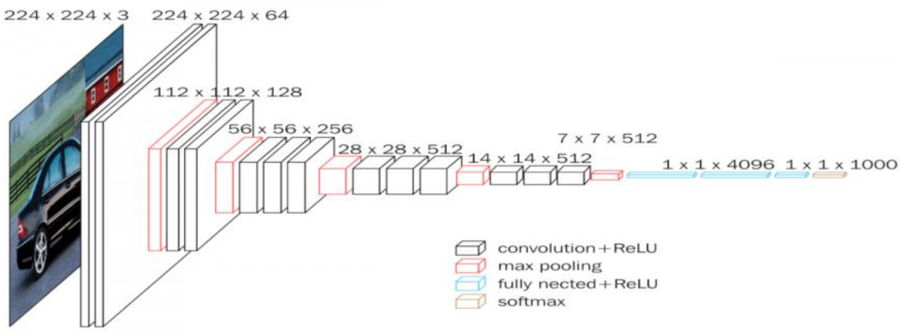


Figure 4: VGG-16 Architecture

Experimental Setup

Operating System: Windows 10 Home
Laptop Model: HP Pavilion
Processor: Intel® corei5 (8th Gen) CPU @1.60GHz
Installed Random Access Memory (RAM): 12.0 GB
System Type: 64-bit Operating system, x64 based processor
Python 3
Anaconda
Jupyter notebook
Google Colabs

Dataset

This project required a large dataset, which was going to be difficult to find. The search was extended online following interviews with the directors of the pathology departments at several hospitals and medical facilities in Nigeria. This effort will be delayed since the samples were collected from Nigerian hospitals and testing institutions. Most of these testing companies delete their data as well. Because of this, we used the following dataset from the official NIH website for our research: The dataset utilized was the detection of malaria parasites in thin blood smear pictures uploaded to Kaggle. There are 2756 parasitized (abnormal) and 2757 normal (uninfected) pictures in the patient blood smear dataset. Additionally, as shown in Table 1 below, the dataset was split into a ratio:The Searchable Image Dataset indicates that the cells have some kind of abnormality, thus the images are classified as either normal (number 0) or abnormal (number 1). It will be necessary for the deep learning model to distinguish between normal and aberrant photos. The images in the folder with the number 0 depict blood smears that are normal and free of malaria parasites, whereas the images in the folder with the number 1 depict aberrant blood smears that contain malaria parasites.

Table 1: Divided Images

Category	Total Images (T)	Training Images (0.8*0.8*T)	Validation Images (0.2*0.8*T)	Testing Image (0.2*T)
0(Uninfected)	2757	1764	441	551
1(Parasitized)	2756	1763	440	551

Data Splitting

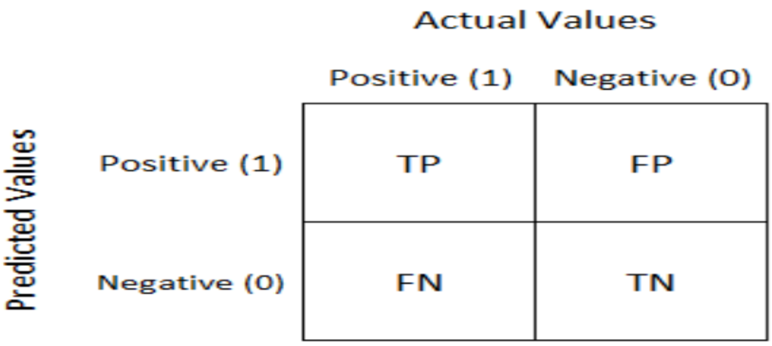
It's critical to comprehend how well a deep learning model performs throughout training. As a consequence, three data groups are produced. These sets are used for training, testing, and validation. The training set is the collection of data used to train the model. A training set can be used to change the weights of a neural network. The validation set is used to determine the best model to use or the ideal parameters. The output of each model is compared to the validation set.

Data Augmentation

Data augmentation is the process of creating new data based on modifications to your current data. By creating unique and unique situations for training datasets, data augmentation can increase the effectiveness and output of deep learning models. A deep learning model's accuracy and performance are enhanced with a sizable and adequate dataset. Costly and time-consuming data collection and classification may be necessary for machine learning techniques. Businesses can lower these operational costs by improving datasets through the use of data augmentation techniques. In this study, images are used as the data, and flipping and rotating the image yielded more information for training. Three changes were applied to the original image: a 90° rotation, a vertical flip, and a horizontal flip.

Evaluation Metric and Validation Technique

The confusion matrix may be used to summarize the performance of a classification method. Classification accuracy by itself may be misleading if the dataset has more than two classes or if the number of observations in each class is not equal. By computing a confusion matrix, the advantages and disadvantages of the categorization paradigm may be better appreciated. A confusion matrix is a collection of prediction results for a classification problem. Count values are used to report the proportion of accurate and inaccurate predictions for each class. The confusion matrix shows the prediction result of the classification model. It provides you with information on the errors your classifier is making, and more importantly, what kinds of errors it is producing. Figure 2 displays the confusion matrix.



		Actual Values	
		Positive (1)	Negative (0)
Predicted Values	Positive (1)	TP	FP
	Negative (0)	FN	TN

Figure 5: Confusion Matrix

i. True Positive: The machine predicted positive and it's true.
ii. True Negative: The machine predicted negative and it's true.
iii. False Positive (Type 1 Error)- The machine predicted positive and it's false.
iv. False Negative (Type 2 Error)- The machine predicted negative and it's false.

Deep Learning Model Creation

The dataset was used to train a seven-layer convolutional neural network that was constructed using the Keras API. A list of layers provided to the sequential constructor was used to form the model. There is only one input and one output in this sequential model. Convolution blocks with a max pooling layer (tf.keras.layers) comprise the sequential model.Every one of them (tf.keras.layers) has MaxPooling2D.Conv2D. With just one unit above it, a fully connected layer (tf.keras. layers) is activated by a sigmoid activation function ("sigmoid"). Optimizer='The optimizer, sometimes called RMSProp, is a method for changing a neural network's weights in order to reduce losses and improve accuracy. The output of the machine learning model is compared to the anticipated outcome using a loss function. It is known as "binary crossentropy." We give the model the metrics parameter.Compile for each training session in order to track training and validation accuracy. The entire number of rounds in a dataset is called an epoch. It was trained during 50 epochs.

Transfer Learning VGG-16

The VGG16 Convolutional Neural Network (CNN) architecture is simple and widely utilized in ImageNet, a large visual database project used in research on visual object identification software. The VGG16 Architecture was developed and presented by Karen Simonyan and Andrew Zisserman of the University of Oxford in their paper "Very Deep Convolutional Networks for Large-Scale Image Recognition" . The VGG16 model in ImageNet, a dataset with over 14 million pictures split into 1000 classes, achieved an accuracy of 92.7% in the top five tests. During the 2014 ImageNet Large Scale Visual Recognition Challenge (ILSVRC), it was one of the most popular models . A VGG pre-trained model using an RMSprop optimizer and a learning rate of 0.001 was used to classify the training dataset. After 50 epochs, its accuracy was 86%.

RESULTS AND DISCUSSION

The CNN was tested on test data using the keras evaluate function. The function was passed one argument which served as the path to the folder containing the testing images. The function returned a test loss of 52% and a test accuracy of 83%.

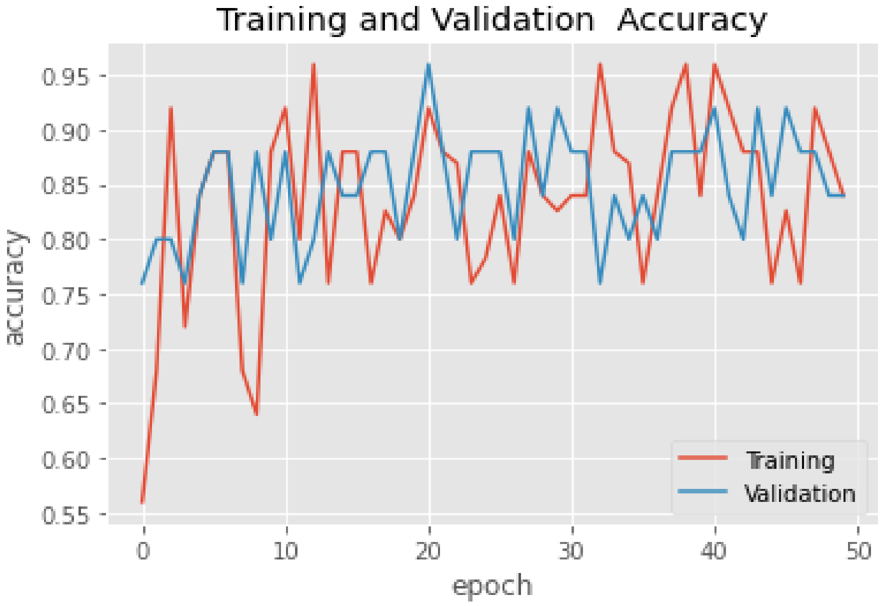


Figure 6: Training and Validation graph (50 EPOCHS)

Accuracy of VGG-16

The CNN VGG-16 was tested on test data using the keras evaluate function. The function was passed one argument which served as the path to the folder containing the testing images. The function returned a test loss of 60% and a test accuracy of 86% as seen in figure 7.

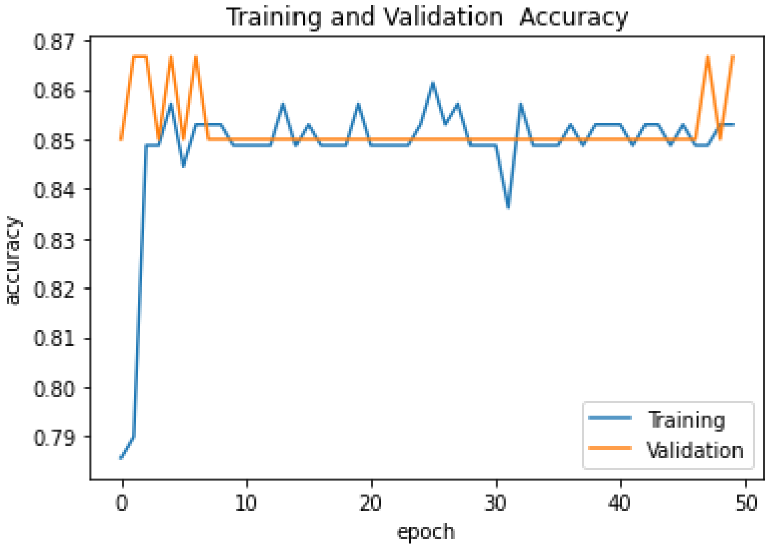


Figure 7: Training and Validation graph (50 EPOCHS)

Result Comparison

Table 2: Accuracy Comparison

Algorithm	**Accuracy**
Proposed CNN	83%
VGG-16	86%
Neural Network classifier	78.53%
Naïve Baiyes	85%

Table 2 shows a comparison of the proposed CNN and transfer learning approach with other malaria detection parasite. From the result in Table 2 VGG-16 outperforms other technique with an accuracy of 86%.

CONCLUSION

In conclusion, this work demonstrates the transformative potential of leveraging deep learning techniques, specifically convolutional neural networks (CNNs) and the VGG-16 architecture, for the automated diagnosis of malaria. By addressing the limitations of conventional diagnostic methods and prior machine learning approaches, this strategy offers a scalable, accurate, and resource-efficient solution tailored for low-resource settings. The implementation of transfer learning enhances diagnostic precision while reducing reliance on human expertise and laboratory infrastructure. This automated methodology holds promise for significantly improving malaria detection, expediting treatment, and contributing to global efforts aimed at eradicating the disease, particularly in regions most affected by this deadly illness.

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