Deep Learning for Malaria Diagnosis: Leveraging Convolutional Neural Networks for Accurate Parasite Detection

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Abstract— malaria is one of the most severe diseases worldwide. However, the current diagnostic method that involves examining blood smears under a microscope is unreliable and heavily relies on the examiner's expertise. Recent attempts to use deep-learning algorithms for malaria diagnosis have not produced satisfactory results. But, a new CNN-based machine learning model has been proposed in a research paper that can automatically detect and predict infected cells in thin blood smears with 94.63% accuracy. This model accurately accentuates the region of interest for the stained parasite in the images, which increases its reliability, transparency, and comprehensibility, making it suitable for deployment in healthcare settings.

Keywords— Deep Learning , CNN, Malaria, Blood disease, Machine learning.

1 Introduction

Malaria is a disease that affects a large portion of the world's tropical and subtropical regions and can be fatal. The disease has been well-known to humans for a long time and is transmitted by the parasite vector and mosquito species Anopheles. The parasite in the mosquito's saliva is injected into the bloodstream of the victim when it feeds on blood. The two most harmful parasite species responsible for malaria among individuals are P. falciparum and P. vivax [1][2].

According to the World Health Organization (WHO), around 247 million people suffered from malaria globally in the year 2021[3], and the disease caused approximately 619,000 deaths, with most fatalities occurring among children below the age of five. To eliminate malaria and reduce its devastating impact, A number of initiatives and regulations have been implemented, including the Sustainable Development Goals (SDGs) and Elimination 8. These programs aim to eradicate malaria while also focusing on the most vulnerable societies. The year 2030 is set as the target to achieve these goals [4] [5].

Every year, Expert pathologists painstakingly examine millions of blood smear films, and identifying malaria involves a large financial and human effort. Additionally, accurate disease diagnosis and grading depend on reliable parasite counts from blood films. For instance, if a patient did not have malaria cells but the doctor mistakenly gave medications, the patient would unnecessarily experience nausea or abdominal pain. Malaria diagnosis needs to be accurate and sensitive (few false negatives) To acquire parasites over the entire disease life cycle. For the treatment of malaria in endemic areas with a dearth of specialist pathologists and a heavy workload of screening blood films, an early and accurate diagnosis can be beneficial.

Traditional approaches to automating the identification of malaria entail sophisticated image-processing methods with manually crafted features, such as form, colour, intensity, size, and texture. These techniques use several segmentation algorithms to identify red blood cells from microscopic pictures. Following Segmentation photos are split into classes of infected and uninfected images using a computed set of features that are appropriate for red blood cells. Morphologically based techniques are used to segment cell images with structuring features, which improves the qualities of red blood cells, such as the roundness of the cells. This improves classification accuracy. Numerous strategies are employed for the segmentation, feature extraction, and classification of malaria diagnosis. It is evident from contrasting conventional and contemporary malaria detection methods that model accuracy and computing complexity must be traded off, as model accuracy rises, so does computational complexity. For instance, a deep neural network is discovered to have superior accuracy than a support vector machine (SVM), despite the latter having a faster computation time for classification.

Granulometry uses the intensity of picture pixels to gather important data. Bayesian learning and Support vector machine (SVM) are used to categorize malaria cells using the discriminative feature set.

Deep learning (DL) techniques have recently been used to diagnose malaria automatically with decent rates of detection. Because the hidden layers of deep learning models automatically extract features from the data, they do not require the computation of manually produced features. Large datasets are needed for deep learning models in order to train neural networks and increase model accuracy. However, there are just a few tiny datasets available for medical applications like diagnosing malaria. This is due to the fact that creating pathologists' input is necessary for an annotated dataset, although this is not always possible.. Deep learning models newly presented picture augmentation approaches enable greater To get beyond the dataset's scarcity, limit overfitting and increase generalization. By employing methods like rotation, shear, and translation to divide the original image into many images, image augmentation expands the dataset and helps the model attain higher accuracy. The use of machine learning techniques to predict malaria outbreaks involves employing algorithms that analyse and learn from data to make forecasts about the likelihood of malaria outbreaks occurring in a specific area. This can be achieved by utilizing decision trees, random forests, and neural networks are only a few examples of the various machine learning methods[6] [7]. The aforementioned algorithms have the ability to handle vast amounts of data, which can include various parameters such as weather conditions, population density, and past occurrences of malaria. By analyzing this data, the algorithms can predict the probability of future malaria outbreaks occurring[8] .The objective is to offer timely notifications to public health authorities, enabling them to take necessary preventive actions and minimize the spread of the disease.

Each year, a significant number of blood films are analyzed under a microscope for the purpose of diagnosing malaria [9].Although the method of examining films under a microscope is widely used, it is prone to errors and can be time-consuming. Hence, numerous studies have proposed computer-aided systems to detect malaria [10].

Additionally, recent research has demonstrated that deep learning architectures for malaria diagnosis greatly outperformed by models based on traditional classifiers. ZahidAlam Khan et al. [11] the utilization of deep learning-based algorithms, such as Deep Deterministic Policy Gradient (DDPG), has demonstrated better performance in managing the transmission of diseases and their impact on human health within a population, compared to traditional algorithms like Q-Learning or SARSA.

Masud, Mehedi [12] demonstrated the effectiveness and accuracy of deep learning architecture, specifically the convolutional neural network (CNN), in real-time malaria detection using input images. The goal is to minimize manual labor through the integration of a mobile application. The study involves the assessment of a customized CNN model employing a cyclical stochastic gradient descent (SGD) optimizer equipped with an automatic learning rate finder. The results showcase an impressive 97.30% accuracy in distinguishing between healthy and infected cell images, characterized by both high precision and sensitivity.

Anupama Raskar et.al [13] convolutional neural networks (CNNs) have been employed to identify malaria and dengue in under 60 seconds, as opposed to traditional diagnostic methods.

Ren Qi et.al [14]showcased a comprehensive evaluation and recommended a gene cluster analysis and classification by assessing the pros and cons of various techniques utilizing updated variations of clustering and classification frameworks, including both linear and non-linear approaches. The study further integrated and provided an RNA-seq clustering and classification, as well as dimension reduction methodologies for short conditional RNA-seq (scRNA-seq) data.

Qiong Cai et al. [15]conducted a thorough examination of the techniques employed in smart healthcare systems, with a particular emphasis on decision-making processes that employ multimodal association mining and fine-grained data semantics. Michelle Viscaino et al. [16]used SVM, KNN, DT, and SVM to suggest a multi-classification model with 93.9% accuracy for identifying external and middle ear conditions.

S. Sharma et al. [17]proposed a dataset of histopathological image data, a CNN model for multiclass classification of breast cancer. Using the suggested CNN approach, 80.47% accuracy was attained.

Jinzhu Lu et al [18]analyzed the most recent CNN networks relevant to the classification of plant leaf diseases and outlined the Basic concepts used to classify plant diseases. Also, outlined CNN's primary issues and their associated fixes for classifying plant diseases. Also, the direction of future development for plant disease classification was explored.

Teja Kattenborn et. al. [19] expounded upon the guiding principles of CNN and explained why vegetation remote sensing is a suitable application for them. The main section provided an overview of the latest trends and developments, considering factors such as spectral resolution, spatial grain, various sensor types, methods for generating reference data, existing sources of reference data, and various CNN techniques and architectures. Elliot Mbunge et al. [20]

employed decision trees, support vector machines, random forests, and logistic regression to predict malaria; the study shows that, with 83% accuracy, 82% precision, and 90% F1-score, logistic regression surpasses alternative machine learning classifiers.

G.Hanitha et al. [21] processed the slide images for the blood cells that were both disease-infected and uninfected, and this process was done without the involvement of any humans. By using the technique, the pathologist will obtain better outcomes, aid in the decision-support system for doctors, provide correct results, and complete the inspection fast or in a shorter amount of time.

In this study, we apply deep learning to identify parasite-infected white blood cells in smears on conventional microscope slides by using a deep learning model called the convolutional neural network (CNN). All existing deep learning models are outperformed by the suggested customized CNN-based algorithm. This study makes a contribution by suggesting a custom CNN model that performs better than every deep learning method currently available. Bilateral filtering and picture enhancement techniques are used to highlight white blood cell properties before training the model. The tailored CNN model is generalized and prevents over-fitting thanks to image augmentation methods [22]. Malaria Dataset is used for all experimental evaluations, and the results demonstrate that when recognizing malaria from microscopic blood smears, the suggested approach is 94.63% accurate. The rest of this paper is ordered as; Sect. II will introduce the Materials and methods (data set, system design and architecture) followed by Sect. III which clarify the results and discussion and conclusion included in the final section.

2. Malaria Classification System

The conventional pipeline for automating the diagnosis of malaria : Feature selection, cell segmentation, image pre-processing, and classification of malaria-infected and -uninfected cells. In the literature, various methods are suggested for each phase Figure 1 illustrates the four processes that make up [23].

2.1. Image pre-processing

In order to increase the accuracy of subsequent processing procedures including feature extraction, cell segmentation, and classification, approaches are used to improve images showing blood smear quality [24]. Any type of impurity in the images has the potential to degrade the effectiveness of the subsequent processing steps could leave malaria cells vulnerable to incorrect diagnosis. Several smoothing filters, including Gaussian, median, and geometric mean filters, are used to lessen noise in microscopic images, are frequently utilized. Additionally, morphological operators have been employed to control noise by filling gaps and removing contaminants by enhancing cell outlines. Adaptive threshold and histogram equalization are also used to enhance the photographs' quality and contrast. Some malaria detection methods aim to reduce the variation in cell illumination, such as HSV colour space and grayscale colour normalization, was applied [25]. Low-pass filters have also been employed to remove noise-related frequency components from the microscopic images. The Laplacian filter was employed in several approaches to increase the red blood cell (RBC) borders and sharpen edges in images .

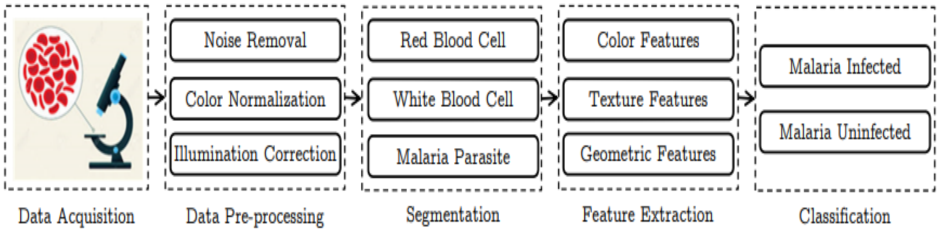


Fig 1. Traditional automated pipeline for detecting malaria

2.2 . Cell Segmentation

Red blood cells (RBC), white blood cells (WBC), malaria parasites, and other artefacts are separated from pre-processed microscopic images into small, non-overlapping sections. This is the most crucial step in any automated malaria identification approach. Unsupervised cell segmentation is often done using image-based techniques like Chan-Vese segmentation, holefilling algorithms, and histogram-based techniques. In low-contrast pictures, cells are segmented using the RGB image's green channel. In order to separate RBCs from improved pictures, we apply the Otsu threshold. To separate cells from microscopic images, The S and V channels of the Hue-Saturation-Value (HSV) colour space employ thresholding algorithms. For cell segmentation, the fuzzy divergence technique is employed [26]. The fuzzy rule-based segmentation approach separates malaria cells from images using three different colour schemes. To identify regional extrema and divide cells, morphological-based approaches employ grayscale granulometry. Cells are separated from unlabeled data using K-means clustering, and RBCs are identified using the Hough transform depending on the morphology of the RBC. To remove the overlapping cells that obstruct segmentation, use a marker-controlled watershed method [27].

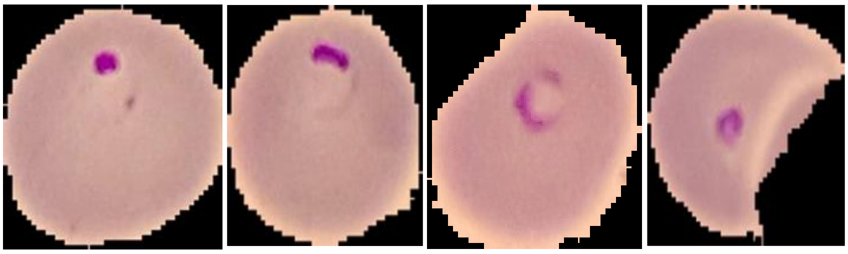
2.3. Feature Selection

Red blood cells' dimensions, hue, and texture are used to create cell images. The HSV colour space and the green channel of the RGB colour space are preferred for feature extraction since colour characteristics are prominent in stained blood pictures. Haralick's texture features, local binary patterns, the histogram of oriented gradients (HOG) features, and other feature-selection methods have all been used to extract features from cell images [28]. Using the colour and shape details in cell images, different types of parasites can be recognized. Morphological transformations like grayscale and thinning to find malaria cells in blood smear images, the malaria detection technique employs a Poisson distribution-based linear Euclidean distance classifier with a Gabor filter. To identify different malaria infection species, an adaptable neuro-fuzzy interface system (ANFIS) employed to identify cells that have been infected with malaria, Also employed is a genetic strategy based on chromosome-encoding techniques and mutation tactics [29]. For the unsupervised detection of cells harbouring malaria, K-means clustering is employed. SVM and artificial neural networks (ANN) use the information of normalized red, green, and blue, as well as the textural characteristics that are invariant to staining fluctuations, to identify the malaria parasite.

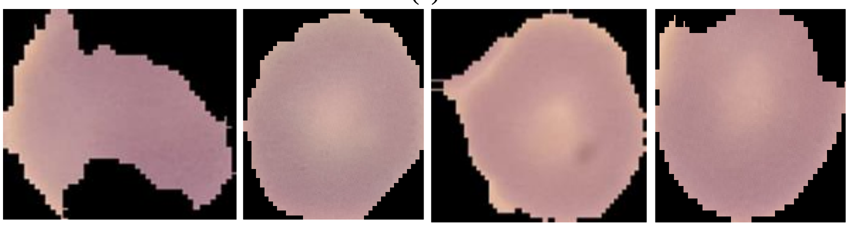
3. MATERIALS AND METHODS

3.1. Data Set

In this paper, the dataset contains blood smear images from 150 malaria cases, with an average of 12 images per patient. The dataset contain 13780 images for each parasitized and un infected. The data were obtained from National Library of Medicine, National Institutes of Health, Bethesda, MD, USA[30] . Fig. (2) data samples from the categories of parasitized and non-parasitized people should be displayed.



(a)



(b)

Fig.2. Samples from Malaria dataset: (a) Parasitized white blood Cell Images and (b) uninfected white blood Cell Images.

3.2. Data Analysis

Biomedical images can vary greatly various clinical interactions, both between individuals and even within the same person, due to factors such as lighting conditions, different marker stains used in pathological tests, variations in the image extraction process, and differences in image dimensions. To ensure consistency and eliminate irrelevant noise in research, image preprocessing is used to standardize the images to a common format. In this study, all images were scaled to a dimension of (64,64) and padded by repeating the same pixel, provides input to train the customized model, with an RGB scale. Only RGB channel photos were permitted during the pre-processing step of resizing. To increase generality in the dataset and reduce overfitting, data augmentation was done using the Kerass Image Data Generator. A method for changing an existing dataset to generate new data is called data augmentation. Expanding the collection and introducing heterogeneity is beneficial since it offers researchers access to more images. The dataset's high level of randomization also helps to reduce overfitting. A few of the data augmentation methods used were rotation, shearing, zooming, horizontal flipping, feature-wise normalization, and width and height shifts. The data became more diverse as a result of the addition of shifts and rotations.

3.3. Data Split

Once the picture enhancement and data processing are finished. The training set used to train the model and the validation set to verify it. The dataset is split into three sets: a training set, a validation set, and a test set with an 80:20 split to allow deep learning systems to recognize all of the underlying visual patterns and representations. In particular, 80% of the data are in the training set, while 20% of the data are split between the validation set and test set.

3.4. System Architecture and Design

All models and tests will be based on convolution neural networks (CNNs). An array of pixel values represents an image in its raw form. The highly connected neighboring pixels serve as the foundation for feature extraction most of the time. CNNs use techniques to deepen the overall architecture, such as local receptive fields, weight sharing, pooling, and the use of many layers take advantage of this correlation [31] [32].

3.4.1. Transfer Learning

In essence, CNNs are feature extractors that are trained to understand how to represent an image [33]. Modern CNN models have mastered the art of extracting information from millions of photos Transfer learning is the process of using these models' abilities to address a similar issue [34]. The absence of appropriate structured data and computational resources are the key justifications for leveraging the previously trained models' information. Deep learning is being used in the field of digital pathology, transfer learning is crucial because there aren't enough properly labeled bio-medical images.

A CNN's early layers collect generic features (corners and edges), whereas it's later layers aggregate these generic features to extract abstract features.edges, while the final few layers are used to categorize photos using the retrieved characteristics.

The pre-trained models' last layers could not be helpful in categorizing the ill images and might be eliminated. To make sure that all of the prior data from the base model is remembered and used, a slower learning rate is used. Inception-v3, Xception, InceptionResNet-V2, ResNet50-V2, DenseNet121, Inception-v3, and EfficientNet are examples of contemporary architectures will be used for transfer learning because they have been trained on millions of images and have obtained the best performance [35] [36] . Only 13780 images from each category are included in the collection. Massive amounts of data are needed for deep learning algorithms to learn every potential representation and function at their best in real-world settings.

3.4.2. Custom Model

Input and output layers, two convolutional layers, a layer for global average pooling, two max-pooling layers, and 64 filter units make up the total of 15 layers in the custom model. Batch normalization is used to activate the ReLU of each convolutional unit. The input is convolved using filters of size (2x2) with padding set to "same." The pool window for the Max Pool layers is (2x2). The dense layer is made up of one unit and sigmoid activation,the top layer of classification. The model design is shown in Fig. (3).

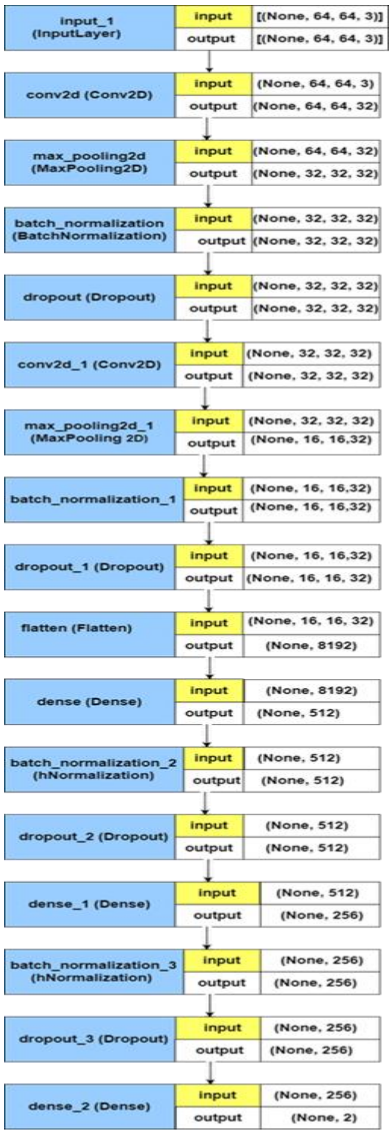


Fig. 3. Custom model design

3.4.3. Hyperparameters & Callbacks

The hyperparameters and callbacks listed in Table 1 will be used for all model experiments.

Table 1. Model Training Tarameters.

Hyperparameters	**Value**
Activation Function	ReLU, Sigmoid
Cost Function	Categorical Cross Entropy

Optimizer	Adam
Epochs	7
Dropout Ratio	0.2
Batch Size	64

Loss Function A function or parameter that is frequently used to gauge the model's effectiveness in terms of loss is the cross-entropy loss function. The binary cross-entropy loss function is used for problems whose output is binary labels (often referred to as binary classification). The categorical cross-entropy. Loss function is used for a multiclass problem with multiple labels as its output (commonly referred to as multiclass classification). Given that the dataset utilized includes two labels and that binary classification is the problem at hand, we employed the binary cross-entropy loss function in the suggested model [37].

Activation function It is thought of as a gateway between the input layer and its output layer, the activation function. It is a type of function, in other words, that restricts the output signals to a finite value. Therefore, it is crucial to include an activation function in order to limit the output value to a particular finite value. The input and hidden layers of the proposed model used a Rectified Linear Unit (ReLU) as an activation function. Given that our data includes a binary label, the sigmoid function is utilized as the activation function in the output layers [38].

Optimizer Optimizers are regarded as a collection of specific algorithms that are used to modify neural network properties like weights and learning rates in order to minimize loss. There are several different optimizers, including SGD, RMSprop, Adam, and Adamax. We have selected the Adam optimizer for our model out of all of these optimizers. The Adam optimizer can be viewed as a hybrid of momentum-based stochastic gradient descent and RMSprop [39].

Validation and Testing the verification of model using random batches of 7 samples after training it in each epoch. After each epoch's training is complete, this validation takes place. By selecting random photos from the test set after the model has been validated, we are evaluating our model, and the testing accuracy after thorough analysis comes out to be 94.63%.

4. RESULTS AND DISSCUSION

Several CNN models are utilized as pre-trained models to address the unique applications. Choosing the ideal CNN network depends on how well you can categorize the target dataset.

The dataset is divided into three subsets: a training set, and a test set, following an 80 % for training and 20 % for testing distribution. This division facilitates comprehensive recognition of underlying visual patterns and representations by deep learning systems.

The customized model is set up to train for 7 epochs and then stop early. The evolution of certification and verification is seen in Fig. (3). Sufficient convergence is achieved by the model on the training and validation data. A test dataset was used to evaluate the model after training for 7 epochs, resulting in an accuracy of 94.63% and demonstrating overall good performance.

The graphs indicate a gradual increase in both training and testing accuracy over time, indicating effective learning by the model. Additionally, a decrease in loss is observed in the model.

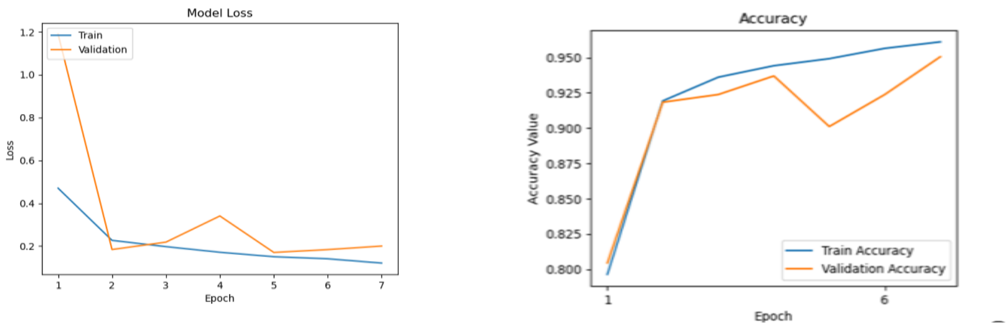


Fig. 4. CNN performance.

The model is being assessed based on several critical parameters for result analysis. It is important to note that accuracy alone is not always the best metric for evaluating a classifier's performance. Other metrics, such as precision, and recall, should also be considered to ensure that the model is performing well on all aspects of the data. Precision denotes a classification model's competence in singling out only the relevant data components. In mathematical terms, precision is computed by dividing the total count of true positives by the sum of true positives and false positives. Recall denotes a model's ability to identify all relevant occurrences within a dataset. Mathematically, recall is determined by multiplying the count of true positives by the reciprocal of the sum of true positives and false negatives. Table 2 indicate the proposed model metrics.

Table 2: Performance metrics for the base model.

	accuracy	recall	precision
Proposed model	94.63%	96%	95%

The recall of the model is also high for both classe. This means that the model correctly identified of all negative samples and of all positive samples in the test set. The precision of the proposed model is high. This means that when the model predicts a sample to be in a certain class.

5. CONCLUSION

The most fatal infections, especially in tropical or warm climates, are malaria. A pathologist uses a microscope primarily to use to diagnose the disease. Nevertheless, this is not just a time-consuming operation; it also directly depends on the pathologist's knowledge and the available machinery and software, which are extremely scarce, particularly in rural regions. With the use of advanced algorithms and electronic systems, an automated approach for diagnosing diseases has become more and more popular in recent years.

This study developed a deep learning algorithm that uses thin blood smear full slide images to diagnose malaria. The algorithm was built through several experiments and utilized transfer learning, which is a useful approach for creating high-performance models in healthcare, where there is often a shortage of accurately labelled data. The study achieved an accuracy of 94.63% in detecting malaria using medical imaging.

The suggested approach may be expanded in the future to include classification of more malaria parasite types. Moreover, the performance of the suggested technique may be enhanced by creating a fresh CNN model and adding more photos to the malaria corpus. Because the strength of deep learning is strongly correlated with the number of samples in the training set, future study will try to train the system with a large data collection. Moreover, the utilization of parallel computing tools like Graphics Processor Units and/or multi-core computers is intended to cut down on training time. Lastly, establishing settings properly might lead to improved accuracy.

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