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Malaria Detection from Blood Cell Images using Convolutional Neural Network Model

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Abstract

There are various ensemble models used in healthcare domain for malaria detection but detection on the basis of presence of blood cell by using conventional neural network based models are very effective and useful. In this paper, we propose a model that is named as neural network model to detect the presence of malaria parasites in human blood cell pictures. In this paper an artificial intelligence based convolutional neural network (CNN) model has been developed to categorize the red blood cell into malaria infected and uninfected types of classes. Performance of the model has been evaluated using Standard evaluation measures against the public data set of malaria blood cell images obtained quantitative scores confirms its performance which outer forms the available state-of-the-art techniques. In the presented paper a CNN based model has been proposed which has least design cost and capable to achieve high performance in terms of various standard evaluation metrics.

Keywords—*Malaria parasite; Red Blood Cell; Computer-Added-Diagnosis; Medical Imaging; Deep Learning; Convolutional Neural Network*

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I. Introduction

Malaria is a life-threatening infection caused by the plasmodium parasite, which is spread via female anopheles mosquito bites. According to the WHO's World Malaria Report 2019, there were an estimated 405,000 malaria-related death in thethe previous year. The condition can be cured, but early discovery is crucial.Exsisting method known as Microscopic identification of infected cells is one method used to identify malaria in a Research Lab.

The model is both overpriced and monotonous. In 2018, the WHO African Region recorded 93 percent of all malaria cases worldwide. In addition, the region has one of the lowest per capita incomes in the world.

A quick, less expensive, and more reliable alternative to microscopic malaria testing has been proposed in this model. Malaria is a parasitic disease produced by the plasmodium parasite, which spreads throughout the human body via female anopheles bites, which can then be passed on to others by mosquitoes that bite malaria patients.

It cannot, however, pass from one person to another. Malaria can be transmitted from mother to foetus, but it can also be contracted through blood transfusions or sharing syringes. High fever, chills, septicemia, pneumonia, gastritis, enteritis, nausea, vomiting, and mortality are just some of the symptoms that an infected person may experience.

Malaria is commonly found in areas with hot, humid temperatures near natural water sources, which serve as the breeding ground for anopheles mosquitoes, which transmit dangerous diseases.In order to fulfill purpose of malaria detection,

This paper gives an overview of the use of different techniques and modals that can be used for malaria detection accurately and efficiently. Combination of various techniques and models has been used in various expert system. This paper also conveys information related to the efficiency of the model proposed by different researchers.

II. Literature Review

a. Using Image processing based approaches

Roy et al.[1] utilized traditional image processing based mechanism such as color based pixel discrimination method, segmentation process, watershed segmentation to detect malaria parasite from thin smear blood images [1].In this work author used image segmentation smoothing processing technique to find out malaria parasite in image obtain from giemsastained peripheral blood fragment. Additionally image processing in any other detection in blood sample had also been computed. Similarly padmapriya et al. had implemented K mean clustering technique for Discrimination based on race [2]. To extract the feature for classification, morphological procedures are used to the segmented material cell from K-means clustering.-6Using this method author get greater efficiency in the screening of the presence of malaria parasite. In addition to this the perimeter of the segmented parasite is computed and using the syntax region props other properties such as centroid eccentricity and area can also be identified.Dharpal et al.[3] proposed a technique for creating quick and moderate model of intestinal sickness analysis utilizing recolor thin blood spread image along with support vector machine (SVM) classifier. In order to find out the plasmodium parasite they are making use of image acquisition, image preprocessing, image segmentation, feature extraction, comparision and classification[3].Minakshi et al. introduced a smart phone-based system that allows anyone to take a picture of a still mosquito and labels it automatically. They combine image processing feature selection with supervised clustering and an SVM-based classification technique [4]. The existing manual procedure of detecting and recording species could be sped up. Image resizing, noise removal, background segmentation, feature extraction, dimensionally reduction, unsupervised clustering, and classification were among the methods they utilised. Punitha et al.[5]developed a different strategy for the diagnosis of plasmodium, a malaria parasite. The Exsisting system does not necessitate any technological expertise. As a result, people in remote areas with a low level of education can use it. It has the potential to reduce the likelihood of incorrect treatment as a result of a variety of factors.It has the potential to reduce the likelihood of incorrect treatment due to the lack of diagnosis systems in rural and economically depressed locations. The system was built in such a way that it is unaffected by extreme situations and has high sensitivity percentages. To achieve the maximum possible classification accuracy in two types of blood images: malaria and non-malarial [6]. To detect malaria, the author used the Q layer of the YIQ colour space. The research in [7] yielded a method based on Giemsa-stained thin smear image digital image processing.

These methods were created to help automate the enumeration and identification procedure. This method generates parasite clearance curves in a consistent and reliable manner. Knojiya et al.[8] developed a model capable of identifyingcells created from photographs of distinct cells in thin bloodsmears which categorise them as infected or uninfected on normal microscope slides using image processing as well as early and testing that is effective [8]. The author uses machine learning and cubic SVM to establish that he is the most accurate by having the greatest accuracy score.Usha D et al.[9] suggested an a formula to diagnose malaria is caused by a parasite in which images are obtainedthin blood smear slides stained with giemsa, the entrap colour images are transformed to gray-scale pictures, the noise abatement approach is used, and contrast stretching is used for image enhancement. The infected erythrocytes are separated into segments and differentiated by making use ofmachine that supports vectors for precise parasite perception and effective classification of positive as well as negative malaria cases.

Zheng[10] constructed an image processing pipeline for detecting malarial parasites within red blood cells, as well as describing its strengths and limits. Despite the fact that the pipeline has basic functionality, further work is needed to improve its resilience to the point where it can be put into practise to a large number of images. The existing pipeline provides a useful framework that may be strained and expanded to improve accuracy, image noise tolerance, and overall competence.

AUTHOR	METHODS	FEATURES/STRENGTH	CHALLENGE/LIMITATION	PERFORMANCE MEASURE	YEAR
Roy et al.[1]	. Watershed segmentation .HSV Segmentation	Limits the human error	Classification process are not introduced for accurate result.	HSV Seg.-70% WaterShed-85%	
Padmapriya et al.[2]	. k-mean clustering	Greater accuracy and efficiency	It didn’t prove to segment and classify the early stage of parasite.	Accuracy-86%	
Minakshi et al.[4]	.SVM Classifier	Latency and energy consumption are minimal	The data gathering technique is time-consuming, requiring months of trapping and tagging specimens.	Accuracy-87%	
Kanojia et al.[8]	.Morphological Segmentation .Cubic SVM	Easy and efficient	Inconsistencies among the images.	Recall-86.3% F Score-77.9%	
Shet et al.[6]	YIQ color space	It removes unwanted objects including platelets from the image efficiently	Digital slide preparation of malaria blood sample and diagnosing the details of diseases is one of the challenge.	Specificity-95% Accuracy-97.5%	

b. Using machine learning based approaches

By utilising image processing, Gomes et al[11] established a model that will be used for identification of cells from images of many cells in thin blood smears on conventional microscope slides and characterise them, whether infected or uninfected with early as well as effective testing. Also, using machine learning, do classification on the afflicted cell image. IT makes use of machine learning technology, and cubic SVM demonstrates its superiority by having the highest accuracy score. It resulted in a method that was extremely reliable. Kunwar et al.[12] presented a method for detecting malaria and built an algorithm for automated malaria detection and quantification. They also devised a machine-learning-based training technique that may be used to detect malaria in the presence of other parasites. They also devised a machine-learning-based training technique that may be applied to the detection of malaria caused by other parasites, and they discussed how to improve the prediction value of the results. According to the techniques employed for imaging, image preprocessing, parasite detection and cell segmentation, feature calculation, and automatic cell classification, Poostchi et al.[13] organise the diverse methodologies documented in the literature. Park et al.[14] describe an automated analysis method for detecting and staging red blood cells infected with plasmodium falciparum at the trophozoite or schizont stage of the malaria parasite.They used a variety of approaches, such as Linear Discriminant Classification (LDC), logistic regression (LR), and K-nearest Neighbour Classification (NNC), to create algorithms that incorporate all of the calculated physical properties to more efficiently identify cells. Sai prasath G et al.[15] use shallow machine learning algorithms, which have certain issues with sensitivity and specificity. They employed various machine learning techniques such as AdaBoost, Decision Tree, KNN, and Random Forest to divide the image into patches and analyse it depending on the presence or lack of parasites. Sharma et al.[16] devised a model in which the Root Mean Square Error (RMSE) and Receiver Operating Characteristic (ROC) are used to quantify the performance of two common data mining classification techniques, Support Vector Machine (SVM) and Artificial Neural Network (ANN).Aravinda et al.[17] proposed an advanced stage of technology based on Gabor Filters for computer based detection and identification of this malaria disease,XG-Boost classifier, support vector machine, and neural network classifier techniques are then contrasted as the best designs for identifying and categorising these malaria blood cells. Suratanee et al. [18] developed a framework for predicting human parasite protein associations using a machine learning approach based on a heterogeneous network structure, network topology features of proteins in the human PPI network and the P.vivax PPI network, and integrated protein sequence similarities.They also devised a method for calculating ranking scores in order to discover promising protein targets in humans for malaria treatment. Using several characteristics and machine learning models, Usha et al.[19] applied image processing and machine learning approaches. The proposed work is easy to use, and the strategies used resulted in improved presentation results. Machine learning for diagnosis was aided by automatic picture recognition technology [20]. A convolution neural network (CNN) was used to categorise single cells in thin blood smears using a machine learning approach. A collection of characteristics that support intensity are proposed.

AUTHOR	METHODS	FEATURES/STRENGTH	CHALLENGE/LIMITATION	PERFORMANCE MEASURE	YEAR
Sharma et al.[15]	.Support vector machine(SVM) .Artificial neural network(ANN)	The SVM model may forecast an outbreak 15-20 days ahead of time, allowing for early prevention and cure.	The model should be scaled up at country level.	ANN RMSE-0.47 ROC-0.77 SVM RMSE-0.12 ROC-0.89	
Arvinda et al.[16]	.SVM .XG-Boost .Neural network classifier	It slow down the complexity with less variance and obtain excellent result.	Image smoothing technique is little bit challenging noise is not properly removing.	SVM-94% XG-90% NNC-80%	
Saiprasath et al.[17]	.Ada Boost .Decision Tree .KNN .Random Forest	Other diagnostic tests, such as homoparasites worm infestations, may benefit from the classification scheme.	Shape of object in input patches is the main concern in plasmodium detection.	Random forest F_Score-0.645 Recall -0.553	
Usha et al.[19]	.SVM .ROC Curve	It is user friendly to use and provides better display result.	More detailed analysis of auspicious region is required.	Accuracy-97.93%	
Gomes et al.[11]	.Cosine KNN .Cubic SVM .Linear SVM	By removing noise and locating cell discontinuities, the system is able to solve the problem of cell overlapping.	Inconsistencies among the images.	Cubic SVM Accuracy- 86% F_Score-77.9%	

c. Using deep learning based approaches

KaustubhChakradeo et al.[21] provide a VGG-based model for recognising infected cells and compare it to previously produced models. In a variety of accuracy criteria, our model outperforms most previously developed models. The model benefits from the fact that it is made up of a modest number of layers. This cuts down on computing resources and processing time. Furthermore, we evaluate our model on two different datasets and suggest that current deep-learning-based approaches are ineffective at distinguishing between infected and polluted cells. A more detailed examination of questionable areas is required. It can be thought of as the first AI-based stage in determining whether a blood cell is very likely to carry a parasite, and it can do it faster and more correctly than manual testing.Tanzilur Rahman et al.[22] suggested acompletely automated Convolutional Neural Network (CNN) based 'ideas such as knowledge refining, data expansion,Autoencoder, feature drawing out by a CNN model and classification by Support Vector Machine (SVM) or K-Nearest Neighbors (KNN) are accomplished inside three strategical techniques named general mechanism, purification mechanism, and auto encoder mechanism to escalate as well asenhancing model performance and inference efficiency. S.Revathy et al.[23] introduced a new Convolutional Neural Network (CNN)-based machine learning model that automatically detects and predicts infectious cells in thin blood smears on conventional microscope slides. To grasp the cell parameter, it used a ten-fold cross-validation layer of a convolutional neural network using 27,558 single-cell images.To assess the accuracy and pick the precise accurate, we created three types of CNN models: Basic CNN, VGG-19 Frozen CNN, and VGG-19 Fine Tuned CNN. Then, by comparing the accuracy of the three types of CNN models - Basic CNN, VGG-19 Frozen CNN, and VGG-19 Fine Tuned CNN - you can choose the most exact one. Patnaik et al.[24]established a successful different-magnification deep residual neural network, which, at various magnifications, distinguishes between microscopic blood smear images that are contaminated and those that are not.On datasets from mobile devices, we put our technique to the test by utilising it to train more effective variants of multiple compact deep convolutional neural networks (CNN). According to GPU timings on the freely accessible photos of microscopic blood smears on phones, the MM-ResNet end-to-end framework exhibits comparable or greater accuracy than the baseline designs. This method is the first use of an MM- ResNet for the identification of malaria-diagonised erythrocytes in microscopic blood smear pictures.Mahendra et al.[25] proposed model has used a famous deep learning technique popularlyknown as Deep Convolutional Neural Network (DCNN).

The suggested technique examines images of microscopic blood samples (thin blood smear images) and determines whether or not malaria is present in those smears. This concept has the potential to aid in the early treatment of malaria. Artificial Intelligence-based disease diagnosis and healthcare applications could be a new step toward the present industrial revolution and digitization. Feng et al.[26] looked into the possibilities of using smartphones to detect malaria parasites in thick blood smears. There are two processing steps in this approach. First, apply an intensity-based Iterative Global Minimum Screening (IGMS), which performs a fast screening of a thick smear image to find parasite candidates. Then, a customized

Convolutional Neural Network (CNN) classifies each candidate as either parasite or background make dataset of 1819 images from 150 patients publicly available, as a service to the research community, which will mitigate the problem of lacking training data for automated malaria diagnosis in thick blood smears.Sivaramakrishnan et al.[27]presented cutting-edge computer-aided diagnosis (CADx) methods using machine learning (ML) methods, applied to microscopic images of smears using manually created characteristics (ROI). Deep learning (DL) models using convolutional neural networks (CNN), on the other hand, offer highly scalable and superior results for feature extraction and classification from start to finish. As a result, automated malaria screening utilising DL approaches could be a useful diagnostic tool.In order to improve disease screening, this work assesses the effectiveness of pre-trained CNN-based DL models as feature extractors for varying parasitized and decontaiminated cells.Microscopy has been advocated as the gold standard for malaria diagnosis by Kristofer et al[28]. When instances are in remote rural locations, this process gets more difficult because experts may not be available to provide such a diagnosis. This challenge could be solved by automating the use of an intelligent system in the diagnostic process that recognises malaria parasites. This research presents an intelligent system that can identify malaria parasites using photos of thin blood smears. In this study, we used a Convolutional Neural Network. Masud et al.[29] use a cyclical stochastic gradient descent (SGD) optimizer using an automatic learning rate finder to test the overall working of a custom CNN model with a high level degree of precision as well as sensitivity, In order to address issues with treatment dependability and a lack of medical competence, the author also makes malaria microscopy diagnosis accessible through a mobile application.Proposed improvedmodel showed better performance compared to the customizedand other CNN models (pretrained such as VGG-16 and

ResNet-50) with respect to accuracy.Faizullan et al.[30] suggested a completely automated model for diagnosing malaria from microscopic blood smear images based on Convolutional Neural Networks (CNN). Three training procedures—general training, distillation training, and auto encoder training—are employed to amend and enhance the model accuracy and inference performance.These techniques include knowledge purification, data accretion, Auto encoder, feature extraction by a CNN model, and classification by Support Vector Machine (SVM) or K-Nearest Neighbors (KNN).

AUTHOR	METHODS	FEATURES/STRENGTH	CHALLENGE/LIMITATION	PERFORMANCE MEASURE	YEAR
Rajaraman et al.[27]	.CNN Model	End-to-end feature extraction and categorization yields highly scalable and excellent outcomes.	CNN is not everytime optimal for drawing out the features from the underlying collective data.	PPV-0.944 Sensitivity-0.962 F_Score-0.952	
Feng Yeng et al.[21]	.IGMS .CNN	Fast screening Highest accuracy	Improve the parasite detection method's performance and run time on a smartphone by leveraging network ensemble techniques.	Accuracy-97.26%	
Shekar et al.[23]	.Basic CNN .VGG-19 Frozen CNN .VGG-19 Fine .Tuned CNN	High accuracy rate and low time duration.	It is not applicable to other disease detection methods, such as utilising CNN to detect pneumonia or planning to detect covid 19 smears in the lungs.	Accuracy-0.9989	
Fuhad et al.[30]	.CNN .SVM .KNN	In all the modes I,e offline (smartphone only) and online (web application) mode, the model can develop inference in under 1 second per sample.	Inconsistency among data and cost is high as compare to others.	Accuracy-99.23%	
Chakradeo et al.[26]	.VGG based model	It's made up of a relatively limited number of layers.	More detailed analysis of a suspicious region by a new deep learning method is required.	Accuracy-97.90%	

III. Dataset

The research that focuses on inferring extremely beneficial & valuable knowledge in any increasing as well as demanding subject necessitates a large database that delivers a large number of different outputs based on the algorithm used in the intended scope. Different phases have been considered in this work, and this assessment reveals that the author primarily uses public datasets for their adopted methodologies. However, in other cases, authors may have also produced private data for the purposes of using their recommended methodology. A summary of several types of datasets for the intelligent vehicle system's several stages is offered in this section.

Approximately 10 public datasets were considered in the Road Detection phase, withthe KITTI datasets are the ones that authors make available the most.The lane detection process utilised about eight public datasets, with the Caltech dataset being the most popular. During the pedestrian detection phase, about 13 datasets were cited, with Caltech being the most popular among the authors. However, INRIA and DAIMLER were identified as the second and third most often utilised datasets, respectively. PASCAL VOC and KITTI datasets have also been used in Vehicle Detection datasets. Depending on local customs and laws, additional datasets have also been used for the Traffic Light / Signal / Gesture identification phase.

All of the mentioned datasets have been found to be among the most appropriate and successfully accessible, as well as validated in numerous articles. In multiple literatures, authors prepared and used their own private datasets to establish their usefulness, traits, and capacities in various phases of intelligent vehicle systems. However, in other phases, such as pothole detection and gesture detection, standard or benchmark public datasets still have limitations and are required for the validation of the technique in these phases.

In Table 7, the size, list of publicly available datasets that have been used includes the quantity of images or sequences and the available object types. and used in numerous differing various writers' phases of intelligent vehicle systems are discussed. In addition, a graphical depiction is provided to demonstrate the benefit and application of dataset size and sample sizes for the data in each phase for every current as well as analysed datasets.

<u>List of public dataset accessed in Literature</u>

Phase	Dataset	Overall Size	Number of Images	Class of Objects	References (Accessed By)
Malaria Detection	Publically available	-	13000	2	Yang et al 2017 K. Torres et al 2018 Rajaraman et al 2018
	NIH (National Institute	-	27,558	-	S.K Antanietal 2018

	of Health)				Vijayalakshmi et al 2019
	KAGGLE	-	27,558	-	Arunava 2018 Dec5 Malaria Cell Images Data Set
	National Vector Borne Diseases Control Program Pune	-	1680	-	-
	employing a 1000x magnification, 133 people's oil immersion objective lenses	-	2703	-	Quinn et al 2014 Mekenziectal 2003
	WHO website	-	27,203	-	WHO “fact sheet” world Malaria Report 2016
	Chitta gong Medical College Hospital Mahidol Oxford Tropical Medicine Research unit	-	27,558	-	Rajaraman at al 2018 Malaria Data Google Drive 2019 poostchi et al 2018
	Galaxy G5 Smart phone in three visually distinct background 16 MP Sensor Resolution	-	303 images spread across nine species		Anita Dixit &Nagaratna P Hedge 2012 Shanmugain at al
	Vector Borne Disease research & Training center (VBDRTC) Hetavda Epidemiology &Discase ctrl Division	-	More than 40 images	-	-
	Kaggle.com National Medical Science Organisation		27,558	-	MadhuKeerthance et al (2016) S. Revathy et al(2019)
	150 p. falciparum& 50 healthy patients from Chittagong Medical College Hospital	-	27,558	-	Poostchie et al 2018 Rajaraman et al 2018
	National Institute of Health, 150 p.faliparum& 50 healthy patients collected from Chittagong Medical College Hospital	-	27,558	-	Rajaraman Sivaramakrishna et al (2018)

IV. Conclusion

Malaria is a devastating disease that has claimed the lives of countless people and is on the danger of taking far more. It impacts a wide range of creatures, not just humans. Even the World Health Organization is concerned about this form of sickness. Malaria must be detected early in order to save a person's life. The suggested model makes use of the Deep Convolutional Neural Network, a well-known deep learning technique. This concept has the potential to aid in the early treatment of malaria. This approach of disease identification and healthcare applications could be a major step forward in the present industrial revolution and digitization.When combined with standards for the improvement of our society, AI techniques have the potential to help with some of the most difficult situations. Deep learning is one of the most recent AI-based techniques that helps to construct robust, accessible, and operative solutions that can also be applied to the Malaria detection challenge in blood cells. A convolutional neural network (CNN)-based model has been used in this proposed strategy, which not only successfully classifies parasitized and uninfected images, but also drives the implementation of other disease classification or detection in the same domain.

This study provides an overview of the various strategies and modals that can be utilised to correctly and efficiently detect malaria. In the numerous expert systems, a combination of various methodologies and models has been applied. This publication also includes information on the efficacy of the models proposed by other researchers, as well as a faster, less expensive, and more reliable alternative to microscopic malaria detection.

Various methodologies are studied and comprehended as part of the survey. Machine Learning, Image Processing, and Deep Learning are examples of these methods. Deep Learning is one of the most effective techniques for achieving cost efficiency and data accuracy.

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