Identifying Malaria Infection in Red Blood Cells using Optimized Step-Increase Convolutional Neural Network Model

Vikas Kashtriya, Amit Doegar, Varun Gupta, Poonam Kashtriya

Abstract*: A vast number of image processing and neural network approaches are currently being utilized in the analysis of various medical conditions. Malaria is a disease which can be diagnosed by examining blood smears. But when it is examined manually by the microscopist, the accuracy of diagnosis can be error-prone because it depends upon the quality of the smear and the expertise of microscopist in examining the smears. Among the various machine learning techniques, convolutional neural networks (CNN) promise relatively higher accuracy. We propose an Optimized Step-Increase CNN (OSICNN) model to classify red blood cell images taken from thin blood smear samples into infected and non-infected with the malaria parasite. The proposed OSICNN model consists of four convolutional layers and is showing comparable results when compared with other state of the art models. The accuracy of identifying parasite in RBC has been found to be 98.3% with the proposed model.

***Index Terms*: CNN, Deep Learning, Malaria, Machine Learning, Medical Diagnosis, Neural Networks, Image Classification.**

I. INTRODUCTION

Malaria is a parasitic disease which is transmitted mostly by female Anopheles mosquito's bite, which results in the individual being infected by a malaria parasite called Plasmodium. This parasite further has many species [1]. As per the World Health Organization (WHO) report, there were 219 million cases of malaria [2] and 435000 deaths due to malaria infection worldwide in 2017. The malaria infection, if detected at an early stage, can be cured and the infected person's life can be saved. Currently, the gold standard method for detection is considered to be light microscopy-based techniques. In such techniques, blood smears are analyzed visually by magnifying the image with the help of a microscope [3]. As it has been found that there are many types of malaria parasites [1], the blood smear sample needs to be analyzed thoroughly to check if multiple kinds of parasites are present in the sample. Moreover, there can be different stages of growth of the same type of parasite present in the same sample. Analyzing a smear sample with very high magnification factor such as 1000x needs a lot of time to traverse the whole sample and also it puts too much strain on the eyes of the examiner to examine just one sample. If a large number of individuals get infected by malaria in a particular region, diagnosing a large number of smear samples rapidly will not be possible by the pathologists and such delay in diagnosis results can be fatal for the malaria patients. Moreover, as there are many types of malaria parasites which differ in their appearance in smear samples, analyzing the samples also require certain expertise by the pathologists and any lack in observation can result in flawed results. This time-consuming process of diagnosis and need of high expertise in observational skills in analyzing smears samples have motivated the computer scientists all over the world to design systems to automatically analyze the smear samples and diagnose for the disease. These systems can greatly aid the pathologists in the various diagnosis processes. Till now a vast number of image processing and machine learning approaches have been proposed to accomplish such tasks. Such computer-aided diagnosis (CAD) softwares mostly are based upon image analysis where machine learning (ML) techniques are used with manually defined features to be analyzed [4]. But the manual defining of features requires expertise in analyzing various shapes, sizes and region of interest (ROI) within the image which is too complicated and also depends upon the expertise of the person doing it. This issue of devising features can be addressed by Deep Learning (DL) which is significantly successful in accomplishing this task [5]. In DL, there is a cascading of layers, where each layer works as a non-linear processing entity. Such design allows the DL to self-discover the features in the data. These DL models give an improved performance with larger data size. In the case of images, we can gather a lot of information from the spatial correlation of pixels/voxels. In the various DL models, there is a particular class known as convolutional neural networks (CNN). This CNN class can effectively exploit the information of spatial correlation.

Revised Manuscript Received on June 15, 2019.
Vikas Kashtriya, CSE Deparment, NITTTR, Chandigarh, India.
Amit Doegar, CSE Department, NITTTR, Chandigarh, India.
Varun Gupta, CSE Department, CCET, Chandigarh, India.
Poonam Kashtriya, CSE Department, NIT, Hamirpur, India.

II. RELATED WORK

To identify the infection of malaria parasite a sequence of operations must be followed which are acquisition of image, preprocessing the data, segmentation of RBC, extraction of various features and then finally classification [6]. In the phase of image acquisition, the blood smear images are collected. Preprocessing is the phase in which the undesirable noises present in the images of blood smears are removed for further analysis and better visualization [4]. In the phase of segmentation, the red blood cells (RBC) are isolated and the details which are not needed such as platelets and white blood cells are removed. The phase of feature extraction consists of extracting various aspects from the RBC such as texture, color, geometry and morphology. Then by utilizing the machine learning algorithms, RBC is classified as infected or non-infected. Usually, to identify the malaria infection, thick smear samples are used while to identify the particular species of the malaria parasite and its stage of maturity, the thin smear samples are used [1]. There have been a lot of approaches proposed for preprocessing images of blood smears. To reduce the impulse noise May et al. used Median filter [1]. Gaussian noise was effectively removed by applying Gaussian filter by Arco et al. [7]. In the case of microscopic images, Geometric mean filter was used by Das et al. [6]. Diaz et al. removed the high-frequency intensity with the help of low pass filter which averaged the pixels intensity [8]. With the application of Susan filter Soni et al. preserved image structure [9]. To smoothen the images Savkare et al. applied Laplacian filter [10]. By using Grey World Assumption Tek et al. corrected the illumination [11]. To preserve the contrast of images Surdhkar used adaptive local histogram equalization [12]. Soni et al. enhanced contrast of the image by applying partial contrast switching [8]. Abbas et al. attempted to normalize pixels intensity using histogram matching algorithm [13].

In the phase of segmentation, there are several aspects. To differentiate RBC from background image Suradkar used edge detection algorithm [12]. For finding overlapping cells Savkare et al. applied watershed algorithm [10]. Soni et al. used granulometry technique for detection of subject-of-interest objects [9]. For segmentation Khan et al. used K-means clustering [14]. Chayadevi et al. have used fuzzy logic approach for segmentation [15]. By analyzing the highest and lowest histogram values, Damahe et al. proposed Zack threshold for discernment of RBC [16].

Feature extraction is very important to recognize if a cell is infected with malaria or not. To find Haralick texture feature such as entropy, contrast, energy, correlation, standard deviation, mean, homogeneity, angular second movement and roughness, Das et al. applied Gray-Level Co-Occurrence Matrix [6]. Malihi et al. mainly focused on features of color histogram to detect infection in RBC [17]. Chavan and Sutkar also used histogram approach [3]. To feed the classifier with input Abu Seman et al. performed extraction of texture, shape and size of infected and non-infected erythrocyte [18]. Measurement of relative shape was proposed by Springl. He also proposed Flat texture features and Gradient to identify infected RBC [19]. Chayadevi et al. attempted to find features based on intensity using color channel intensity [15]. Features of highest significance which can be used to detect malaria parasite infection are color, texture, geometry and morphology respectively [6].

Currently, the most potent type of machine learning approaches in medical image processing are supervised learning methods. The multilayer perceptron network utilized by Abu Seman et al. showed 89.80% accuracy in classifying malaria parasites [18]. The neural network based upon morphological features used by Khot and Prasad achieved 73.57% accuracy [20]. The Naïve Bayes method used by Das et al. for classifying ring and stages of malaria parasites obtained 96.73% accuracy [6]. The Bayesian classifier used by Anggraini et al. achieved 93.3% accuracy [21]. Logistic regression approach used by Mandal et al. for detecting malaria parasite achieved 88.77% accuracy [22]. The gametocyte phase of the malaria parasite was classified with the help of multi-layer perceptron by Yunda with an accuracy of 77.19% [23]. Adaptive resonance theory was used by Chayadevi et al. to detect infected RBC with an accuracy of 94.45% [15]. An approach to detect infected parasite by using regional maxima and area suppression was used by Le et al. with an accuracy of 92.69% [24]. Otsu thresholding approach was used to classify four types of malaria parasite by Malihi et al. using K-Nearest Neighbor classifier and gained an accuracy of 91% [17]. The neural network introduced by Memeu to classify stages of parasite achieved an accuracy of 79.7% [25]. A morphological approach to detect infection of the parasite was applied by Prasad et al. and attained an accuracy of 96% [26]. A support vector machine used to identify parasitic infection stages proposed by Kumarasamy et al. obtained accuracy of 86% [27].

Automated malaria detection mechanisms mostly follow the three phases which act like a pipeline consisting of pre-processing, segmentation and feature extraction before the classification. But there are some drawbacks that need to be addressed in these phases. Error in any one phase can propagate to the next phase. An expert in the problem domain is required to hand-engineer the features and define the methods for pre-processing and segmentation suitable to that particular domain. To hand-engineer the features, expertise in the analysis of morphology, texture, color and size of region of interest is essential. CNN has been found to perform significantly well to overcome these drawbacks. CNN consists of multiple cascading layers which are able to automatically discover new features which reduce the requirement of expertise in the domain of malaria [28]. CNN is quite popular in deep learning and is used widely in the medical field because of its significant performance. Zhang et al. used a CNN consisting of nine layers to diagnose breast cancer with 94% accuracy [29].

III. PROPOSED APPROACH

A. Data Collection

The dataset used here has been taken from the work of Rajaraman et al. [30]. It consists of 27558 images of cells with an equal number of infected and non-infected cells. These cell images were acquired after segmenting images of 200 thin blood smear slides out of which 150 were from infected patients and 50 were from healthy patients. The dataset contained images of different sizes so to suit the needs of our customized CNN we re-sampled all images to 100 x 100. Figure 1 and figure 2 demonstrate typical instances of malaria-infected and normal RBCs.

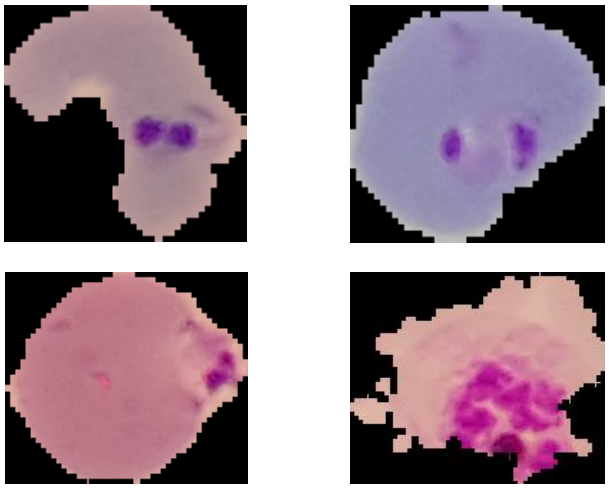

Figure 1: Infected RBCs

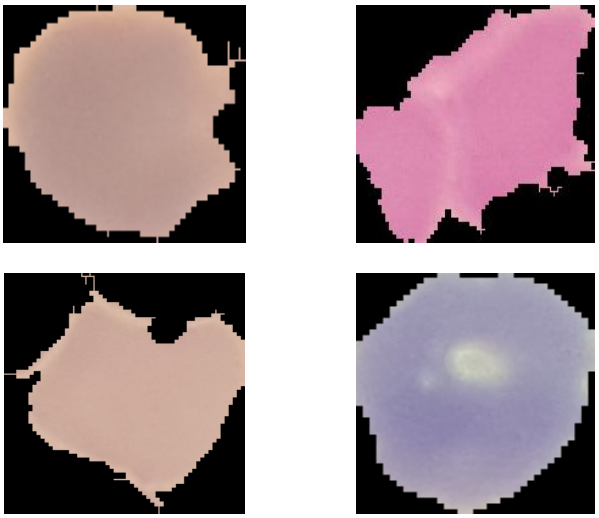

Figure 2: Normal RBCs

B. OSICNN Model

Our OSICNN model consists of four convolutional layers. Within every two cascading convolutional layers we used Cross Channel Normalization layer to perform normalization across channels, Leaky ReLU as the activation function and a Max-pooling layer to down-sample and thus reducing the spatial size of output representations of convolutional layers.

TABLE I. OSICNN ARCHITECTURE

Layer Type	Feature Size	Kernel Size	Padding	Stride
Input Image	100*100*3	-	0	-
Convolution 1	100*100*α	3*3	1	1*1
Cross Channel Normalization	-	-	-	-
Leaky ReLU	-	-	-	-
Max Pooling	50*50*α	2*2	0	2*2
Convolution 2	46*46*β	5*5	0	1*1
Cross Channel Normalization	-	-	-	-
Leaky ReLU	-	-	-	-
Max Pooling	23*23*β	2*2	0	2*2
Convolution 3	19*19*γ	5*5	0	1*1
Cross Channel Normalization	-	-	-	-
Leaky ReLU	-	-	-	-
Max Pooling	10*10*γ	2*2	1	2*2
Convolution 4	1*1*δ	10*10	0	1*1
Cross Channel Normalization	-	-	-	-
Leaky ReLU	-	-	-	-
Dropout (0.5)	-	-	-	-
Fully Connected	1*1*2	-	-	-
Softmax	-	-	-	-
Classification	-	-	-	-

We further have one fully connected layer and SoftMax layer for the classification of extracted features. And we used one Dropout layer before fully connected layer to prevent overfitting problems [31]. The dropout ratio used here is 0.5. Architecture of the proposed model is shown in detail in table I where α, β, γ and δ are number of filters on first, second, third and fourth convolutional layer respectively. Optimal values for α, β, γ and δ are adjusted gradually in each iteration to reach their optimal values. Starting from the predefined minimum values, these values are increased at each iteration, which has been called as step-increase. The increase in each step has been decided considering our current computational capabilities. After reaching some certain values if increasing further results in decreased performance, then the values are decreased a bit and those values are considered to be optimal. Figure 3 represents the pictorial representation of OSICNN.

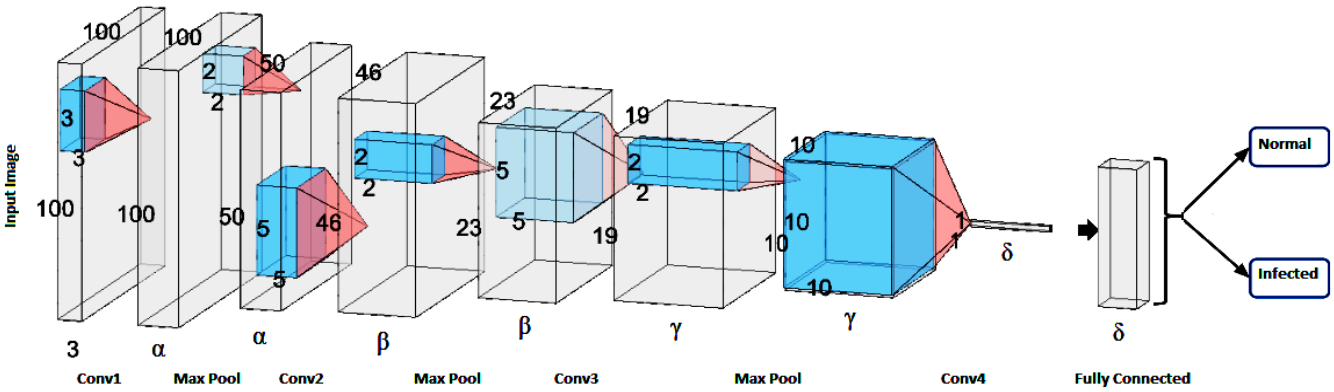

Figure 3: Pictorial representation of the proposed model

C. *Data Augmentation*

On the network with optimal configuration of α, β, γ and δ, the experimentation will be conducted using augmented dataset for better training of the OSICNN model. The various augmentation operations to be used are rotations by 90, 180, 270 degrees and reflections along X-axis and Y-axis. An instance of performing augmentation operations is shown in figure 4.

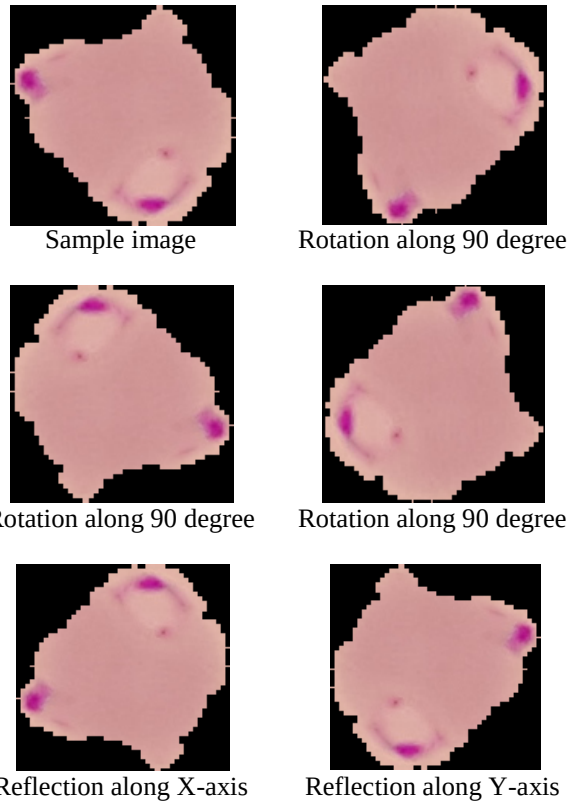

Figure 4: Augmentation operations on dataset.

IV. EXPERIMENT RESULTS AND DISCUSSION

Experimentation has been carried out in MATLAB version R2019a installed on windows 10. The hardware of the systemconsists of processor Intel i7, 16 GB RAM, 4 TB Hard Disk and 8 GB NVIDIA GTX 1080Ti. Optimization of hyperparameters like variance and initial learning rate wascarried out with the application of random search [32].Adam method has been used to optimize the network [33].

Configuration of each iteration in step-increase is evaluated by 5-fold cross-validation.

TABLE II. PERFORMANCE OF OSICNN ARCHITECTURE UNDER DIFFERENT CONFIGURATIONS

Configuration (α-β-γ-δ)	Accuracy	Sensitivity	Specificity	Precision	F1-Score	MCC
6-6-16-16	0.958273	0.963716	0.952830	0.953338	0.958499	0.961600
6-16-16-16	0.954282	0.941219	0.967344	0.966468	0.953676	0.940974
6-16-16-64	0.962627	0.950653	0.974601	0.973978	0.962174	0.950586
6-16-32-128	0.961538	0.955733	0.967344	0.966960	0.961314	0.955239
6-32-64-128	0.963716	0.959361	0.968070	0.967789	0.963557	0.958866
6-32-128-128	0.958636	0.948476	0.968795	0.968148	0.958211	0.948158
6-32-128-256	0.969521	0.955733	0.983309	0.982836	0.969095	0.955951
6-32-128-512	0.979318	0.976778	0.981858	0.981765	0.979265	0.976622
6-32-256-512	0.965530	0.957910	0.973149	0.971734	0.965265	0.957645
6-32-256-1024	0.960813	0.947025	0.974601	0.970881	0.960265	0.947044

Theperformance evaluation of the model under various numbers of filters on each step-increase is as shown in the table II.It was observed that by change in the number of filters on each convolutional layer, the performance of the network was varying significantly. So while designing a CNN, it is very important to choose an optimal number of filters on the convolutional layers for best performance. The performance of the network was tested under different configurations of different number of filters automatically by OSICNN system. Accuracy of 97.9% was observed with the number of filters 6, 32, 256 and 512 on first, second, third and fourth convolutional layer respectively. After applying data augmentation on the

training dataset, the accuracy of OSICNN further improved to 98.3 %.

TABLE III. COMPARISON WITH EXISTING MODELS

Approach	Accuracy
Rajaraman et al. [30]	0.986
Gopakumar et al. [34]	0.977
Bibin et al. [35]	0.963
Liang et al. [36]	0.973
Das et al. [6]	0.840
Ross et al. [37]	0.730
Vijayalakshmi et al. [38]	0.931
Proposed OSICNN Model	0.979
Proposed OSICNN Model (Augmented Training Dataset)	0.983

Except for the model of Rajaraman et al., the accuracy demonstrated by the proposed model proves itself to be better than all other existing models as shown in table III. But Considering the complexity and size of the model ofRajaraman et al. which consists of 50 convolutional layers and complex structure, our proposed model converges faster due to smaller size consisting of only 4 convolutional layers, while also showing comparable performance.

V. CONCLUSION

Malaria is a severe disease existing worldwide. If patient is correctly diagnosed at early stages, the medical treatment can effectively cure the patient. But if parasite of malaria grows into mature stages, it becomes difficult to treat the patient which puts the life of the patient at risk. The proposed model is showing an accuracy of 98.3% in identifying malaria parasite which is quite promising and good enough to be used by medical experts to identify malaria parasite in RBC. Medical experts can just take the high resolution image of blood smear and analyze the RBCs using the proposed model which will successfully indentify presence or absence of malaria infection with 98.3 % accuracy. The small size of the proposed model makes it convenient to be run at machines with low computational resources.

VI. FUTURE SCOPE

The proposed OSICNN model shows a good success in identifying malaria-infected cells. But this model is not able to differentiate among different species of the malaria parasite. This work can be further extended to identify malaria parasite species. Also, the performance of a CNN depends greatly on the size of training dataset so by acquiring a larger dataset, performance of the model can be enhanced.

REFERENCES

1. Z. May, S. S. A. M. Aziz, and R. Salamat, "Automated quantification and classification of malaria parasites in thin blood smears," *2013IEEE International Conference on Signal and Image Processing Applications*, 2013.
2. World Health Organization World Malaria Report – 2018. https://www.who.int/malaria/publications/world-malaria-report-2018/en/ Accessed May 2019.
3. S. Chavan and M. Nagmode, "Malaria Disease Identification and Analysis Using Image Processing," *IJLTET*, 2014.
4. M. Poostchi, K. Silamut, R. J. Maude, S. Jaeger, and G. R. Thoma, "Image analysis and machine learning for detecting malaria," *Transl. Res.*, vol. 194, 2018, pp. 36–55.
5. Y. LeCun, Y. Bengio, and G. Hinton, "Deep learning," *Nature*, vol. 521, no. 7553, 2015, pp. 436–444.
6. D. K. Das, A. K. Maiti, and C. Chakraborty, "Automated system for characterization and classification of malaria-infected stages using light microscopic images of thin blood smears," *J. Microsc.*, vol. 257, no. 3, 2015, pp. 238–252.
7. J. E. Arco, J. M. Górriz, J. Ramírez, I. Álvarez, and C. G. Puntonet, "Digital image analysis for automatic enumeration of malaria parasites using morphological operations," *Expert Syst. Appl.*, vol. 42, no. 6, 2015, pp. 3041–3047.
8. G. Díaz, F. A. González, and E. Romero, "A semi-automatic method for quantification and classification of erythrocytes infected with malaria parasites in microscopic images," *J. Biomed. Inform.*, vol. 42, no. 2, 2009, pp. 296–307.
9. J. Soni, N. Mishra, and C. Kamargaonkar, "Automatic difference between RBC and malaria parasites based on morphology with first order features using image processing,"*IJAET*, vol. 1, no. 5, 2011, pp. 290–297.
10. S. S. Savkare and S. P. Narote, "Automated system for malaria parasite identification," in 2015 I*nternational Conference on Communication, Information & Computing Technology (ICCICT)*,2015, pp. 1–4.
11. F. B. Tek, A. G. Dempster, and İ. Kale, "Parasite detection and identification for automated thin blood film malaria diagnosis," *Comput. Vis. Image Underst.*, vol. 114, no. 1, 2010, pp. 21–32.
12. Pallavi T. Suradkar, "detection of malarial parasite in blood using image processing,"*Int J Eng Inn Technol (IJEIT)* 2(10):124–126, 2013.
13. N. Abbas and D. Mohamad, "Microscopic rgb color images enhancement for blood cells segmentation in ycbcr color space for k-means clustering," *J. Theor. Appl. Inf. Technol.*, vol. 55, no. 1, 2013, pp. 117–125.
14. N. A. Khan, H. Pervaz, A. K. Latif, A. Musharraf, and Saniya, "Unsupervised identification of malaria parasites using computer vision," in *Computer Science and Software Engineering (JCSSE)*, 2014 11th International Joint Conference on,2014, pp. 263–267.
15. M. Chayadevi, G. Raju, "Usage of art for automatic malaria parasite identification based on fractal features,". *Int J Video Image Proc Netw Sec* 14(4), 2014, pp 7–15.
16. L. B. Damahe, R. K. Krishna, N. J. Janwe, and V. T. Nileshsingh, "Segmentation Based Approach to Detect Parasites and RBCs in Blood Cell Images,"*Int J Comput Sci Appl* 4(2), 2011, pp 71–81.
17. L. Malihi, K. Ansari-Asl, and A. Behbahani, "Malaria parasite detection in giemsa-stained blood cell images," in *2013 8th Iranian Conference on Machine Vision and Image Processing (MVIP)*, 2013, pp. 360–365.
18. N. A. Seman, N. A. M. Isa, L. C. Li, Z. Mohamed, U. K. Ngah, and K. Z. Zamli, "Classification Of Malaria Parasite Species Based On Thin Blood Smears Using Multilayer Perceptron Network," *Int. J. Comput. Internet Manag.*, vol. 16, no. 1, 2008, pp. 46–52.
19. V. Špringl, "Automatic malaria diagnosis through microscopy imaging," *Fac. Electr. Eng.*, vol. 128, 2009.
20. S. T. Khot and R. K. Prasad, "Optimal Computer Based Analysis for Detecting Malarial Parasites," *FICTA* (1), 2015, pp. 69–80.
21. D. Anggraini, A. S. Nugroho, C. Pratama, I. E. Rozi, V. Pragesjvara, and M. Gunawan, "Automated status identification of microscopic images obtained from malaria thin blood smears using bayes decision: A study case in plasmodium falciparum," in *2011 International Conference on Advanced Computer Science and Information Systems*, 2011, pp. 347–352.
22. S. Mandal, A. Kumar, J. Chatterjee, M. Manjunatha, and A. K. Ray, "Segmentation of blood smear images using normalized cuts for detection of malarial parasites," in *2010 Annual IEEE India Conference (INDICON)*, 2010, pp. 1–4.
23. L. Yunda, A. A. Ramirez, and J. Millán, "Automated image analysis method for p-vivax malaria parasite detection in thick film blood images," *Sist. y Telemática* Vol. 10 No. 20, vol. 10, no. 20, 2012, pp. 9–25.
24. M.T. Le, T. R. Bretschneider, C. Kuss, and P. R. Preiser, "A novel semi-automatic image processing approach to determine Plasmodium falciparum parasitemia in Giemsa-stained thin blood smears.," *BMC Cell Biol.*, vol. 9, no. 1, 2008, p. 15.

25. D. M. Memeu, "A Rapid Malaria Diagnostic Method Based On Automatic Detection And Classification Of Plasmodium Parasites In Stained Thin Blood Smear Images," 2014.
26. K. Prasad, J. Winter, U. M. Bhat, R. V Acharya, and G. K. Prabhu, "Image analysis approach for development of a decision support system for detection of malaria parasites in thin blood smear images," *J. Digit. Imaging*, vol. 25, no. 4, 2012, pp. 542–549.
27. S. K. Kumarasamy, S. H. Ong, and K. S. W. Tan, "Robust contour reconstruction of red blood cells and parasites in the automated identification of the stages of malarial infection," *Mach. Vis. Appl.*, vol. 22, no. 3, 2011, pp. 461–469.
28. D. S. Kermany et al., "Identifying medical diagnoses and treatable diseases by image-based deep learning," *Cell*, vol. 172, no. 5, 2018, pp. 1122–1131.
29. Y.D. Zhang, C. Pan, X. Chen, and F. Wang, "Abnormal breast identification by nine-layer convolutional neural network with parametric rectified linear unit and rank-based stochastic pooling," *J. Comput. Sci.*, vol. 27, 2018, pp. 57–68.
30. S. Rajaraman et al., "Pre-trained convolutional neural networks as feature extractors toward improved malaria parasite detection in thin blood smear images," *PeerJ*, vol. 6, , 2018, p. e4568.
31. B. Xu, N. Wang, T. Chen, and M. Li, "Empirical Evaluation of Rectified Activations in Convolutional Network," *Journal of Machine Learning Research*, 15(1), 1929–1958. 2015.
32. J. Bergstra and Y. Bengio, "Random search for hyper-parameter optimization," *J. Mach. Learn. Res.*, vol. 13, no. Feb. 2012, pp. 281–305.
33. D. P. Kingma and J. L. Ba, "Adam: A Method for Stochastic Optimization," *Int. Conf. Learn. Represent.*, 2015.
34. G. P. Gopakumar, M. Swetha, G. S. Siva, and G. R. K. S. Subrahmanyam, "Convolutional Neural Network-based malaria Diagnosis from Focus Stack of Blood Smear Images Acquired Using Custom-built Slide Scanner," J. *Biophotonics*, vol. 11, no. 3, 2018.
35. D. Bibin, M. S. Nair, and P. Punitha, "Malaria Parasite Detection From Peripheral Blood Smear Images Using Deep Belief Networks," *IEEE Access*, vol. 5, 2017, pp. 9099–9108.
36. Z. Liang et al., "CNN-based image analysis for malaria diagnosis," in *2016 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 2016, pp. 493–496.
37. N. E. Ross, C. J. Pritchard, D. M. Rubin, and A. G. Dusé, "Automated image processing method for the diagnosis and classification of malaria on thin blood smears.," *Med. Biol. Eng. Comput.*, vol. 44, no. 5, 2006, pp. 427–436.
38. A. Vijayalakshmi and B. Rajesh Kanna, "Deep learning approach to detect malaria from microscopic images," *Multimed. Tools Appl.*, 2019.

AUTHORS PROFILE

Vikas Kashtriya is currently a regular student of Master of Engineering in CSE Department of NITTTR, Chandigarh, India.

Amit Doegar is working as Assistant Professor in the Department of CSE in NITTTR, Chandigarh, India, He works in the field of image processing and virtual learning.

Varun Gupta is Associate Professor inCSE Department, CCET, Chandigarh, India. Before, he has worked as an information technology engineer in power sector.

Poonam Kashtriya is post graduate in M.Tech. (CSE) from Computer Science and Engineering Department, NIT, Hamirpur, India. His area of interest is machine learning.

Published By:
Blue Eyes Intelligence Engineering
& Sciences Publication