EAI Endorsed Transactions
on Pervasive Health and Technology
Research Article **EAI.EU**

Detection of Female Anopheles Mosquito-Infected Cells: Exploring CNN, ReLU, and Sigmoid Activation Methods

A. L. Leena Jenifer[1,*], B. K. Indumathi[2] and C. P. Mahalakshmi[3]

[1] Department of Information Technology, Rajalakshmi Engineering College, Thandalam, Chennai, India
[2] Department of Information Technology, Rajalakshmi Engineering College, Thandalam, Chennai, India
[3] Department of Information Technology, Rajalakshmi Engineering College, Thandalam, Chennai, India

Abstract

INTRODUCTION: Deep learning uses multi-layer neural networks where the algorithm decides for itself whether aspects are essential for analysis based on the raw input. In general, deep learning networks get better as more data is used to train them. For a variety of applications, convolutional neural networks are frequently used to analyse, categorize, and detect images.
OBJECTIVES: The proposed system technique is used for automated analysis of malaria-detecting frameworks. A female Anopheles mosquito bite is the primary method of transmission of the blood disease malaria. It is still common to manually count and identify parasitized cells during microscopic examination of either thick or thin layers of haemoglobin, which takes time for disease prognosis.
METHODS: The current research uses a neural network based on convolution to catalogue images of cells with and without malaria infection. This method improves the precision of classification for the datasets under study. The ReLu activation function used by this model enables it to learn more quickly and perform more effectively.
RESULTS: The prediction of infected and healthy cells was done accurately by the proposed model, which uses only 3 layers of convolution, and this was the idea behind the implementation. The model achieved an improved accuracy of 99.77% across 12 iterations (epochs).
CONCLUSION: The proposed model is straightforward and successful in differentiating between malaria-infected and uninfected cells.

Keywords: ReLU, CNN, Sigmoid activation layer, Image classification

Received on 02 December 2023, accepted on 24 February 2024, published on 01 March 2024

Copyright © 2024 A. L. Leena Jennifer *et al.*, licensed to EAI. This is an open access article distributed under the terms of the CC BY-NC-SA 4.0, which permits copying, redistributing, remixing, transformation, and building upon the material in any medium so long as the original work is properly cited.

doi: 10.4108/eetpht.10.5269

---

[*] Corresponding author. Email: leenajenifer.l@rajalakshmi.edu.in

1. Introduction

Deep learning is a significant area of research currently since it makes use of a lot of facts, numerous machines, and several methods. Deep learning techniques are applied in the prediction and development of illness based on locomotion, speech, information about facial expressions, cell pictures, and other factors [1]. The structure and operation of the human brain have an impact on deep learning. In order for us to comprehend the information we encounter; the human brain structure is made up of an immense number of nerves that are connected, exchange information, and communicate with one another. In order to distinguish and categorise various objects or properties in images, intensively programmed neural networks, like neural networks in biology, comprise neurons with changeable weights and biases [2]. It is necessary to have a suitable archive for preserving the image data because the number of pictures and video recordings recorded at various events is increasing. Due to the vast amount of data and diversity of the visual content, it is challenging for a computer to comprehend and analyse an image. To extract a picture from an image collection, automatic retrieval of images and classification are necessary.

The medical field has been profoundly affected by deep learning as a result of its pivotal role in the development of medical image processing. Recently, several X-ray-based pneumonia classification methods have been developed. One important drawback is the development of lightweight models that require less processing and are more efficient. It has been shown that modern algorithms can fulfil efficiency demands, while the ensemble method can boost accuracy [3].

From a scientific point of view, new prognostic markers that focus on lifetime outcomes rather than mortality risk are preferred. There is a need for in-depth research into several of the strongest life expectancy indexes to ascertain their treatment efficacy. Life expectancy forecasts can be made in real time using data pieces that are readily available and observable in the electronic health record, making it an ideal candidate for use in developing a new prognostic index. Given the importance of prognosis in guiding clinical decisions, we cannot afford to wait for the ideal index to be developed, validated, and rigorously evaluated. These computations may be simplified by using an electronic medical record or other electronic device [4].

Malaria is a serious parasitical infection of the blood vessels brought on by Plasmodium parasites, which are spread via bites from mosquitoes. The Red Blood Cells (RBCs), which can cause deadly symptoms, are infected once the parasites enter the bloodstream from the liver. Over 200 million incidents occur every year, and over 400,000 people die as a result [5]. Medical diagnoses and assessments of parasite infections sometimes involve microscopic examination of thin and thick blood samples. The quality of the smear and the examiner's skill in distinguishing between parasitized and healthy cells affect how precise their findings will be. Inter- and intra-observer heterogeneity has a negative impact on diagnostic accuracy, especially in circumstances involving extensive screening with few resources. When a mosquito bites an individual who has malaria, it becomes infected. In the future, anyone who gets bit by a mosquito that is infected could develop parasites that cause malaria. Depending on the species, the parasite goes to the liver after entering the human body and may remain there for an extended period of time. Upon reaching adulthood, these parasites exit the liver and proceed to infect the blood vessels. People are currently experiencing malaria symptoms such as a high body temperature, diarrhoea, lethargy, coughing, rapid breathing issues, etc. Blood transfusions, sharing of drug-injected needles, and transfer from an infected mother to the foetus are possible additional modes of transmission. Infants, young children, and adults with relatively poor immunity are all susceptible to malaria.

Malaria is an infectious illness that is multifaceted in its development and transmission and extremely challenging to treat. The difficulty in detecting malaria is distinguishing between cells that are parasite-infected with a minimum of labour, resources, and time. Pattanaik et al. has proposed a whole Computer-Aided Diagnosis method for detecting malaria parasites in blood vessel smear pictures [6]. To create a model utilising various machine learning techniques that are able to be trained using huge amounts of data, low-level characteristics must be combined to generate deeper, more conceptual graphical feature information. To improve classification and prediction accuracy, the distribution of various data representations is provided in order to categorise and forecast outcomes [7].

CNNs, which have been used to apply in the proposed model to find parasite-infected cells that lead to malaria, a fatal and contagious disease, are improved by deep learning. Image classification is believed to be one of the most effective techniques for identifying malaria infected cells. CNNs, which are explored in detail in section 3, are heavily utilised in the field of image classification, which is regarded as the suggested technique in the proposed model.

2. Related works

Using machine learning methods, parasitaemia may be found in blood smear pictures. In the early stages, RBCs were improperly classified as contaminated or sterile by automated and qualitative identification of parasitaemia. The model uses a Convolutional Neural Network with an Alex-net architecture to do picture recognition [8]. The programme uses a CNN with 17 layers to classify malaria blood smears. Using 90% training photos and 10% testing images for ten-fold cross-validation. Accuracy was 97.37% and 91.99% of what is learned is retained. Despite being trained using 27,000 pictures, the quantity of training data and the structure still have an impact on performance [9]. It is suitable for classifying blood smears.

Every year, almost 240 million new cases of parasitic infections are reported, putting around 40 percent of the world's population at risk. Manual inspection could result in delayed or erroneous analysis. In order to distinguish between parasite and non-parasitic cells during screening, the author deployed an optimised CNN-based deep learning model. To increase accuracy, features including size, hue, cell number, and shape are chosen for the analysis procedure. By randomly dividing the photos into a set to be trained and a testing set, data preparation is done. 10% of the data that was originally collected is used to train the model to prevent overfitting. All labels are converted into two distinct categories using Keras to obtain categorical classification once the image has been resized and normalised. One benefit of this model is that Resnet-50 was trained on a billion photos. Nearly which 41,337 segmented cell images consisting of infected and non-parasite cells, was donated by the Lister Hill National Centre. Here, six folds are employed for good accuracy. The ResNet model provided reliable results in the classification of images. The model employs a confusion matrix to categorise the photos, and the data accuracy is about 93.87% [10].

CNN follows controlled learning that utilises text, sound, and image data and can be used to detect the intersection of malaria and malaria illness because deep learning has the capacity to acquire beneficial characteristics and does not require any manual extraction [11]. The majority of object recognition algorithms used today have focused on a select few widely used purposes, such as faces, cars, and people. This is mostly caused by the large number of images in the aforementioned groups [12].

The most suitable values for the particular CNN's variables and hyperparameter values were determined using the Talos optimisation tool [13]. In order to optimise kernel functions, spare representations are incorporated into the machine learning architecture. A method for classifying images is used to increase accuracy and is appropriate for many different picture databases. In order to create a precise dataset for ImageNet construction, candidate images for each synset are first acquired, and then every suggested image is cleaned.

Activation functions are becoming increasingly fundamental and involved in deep Convolutional Neural Networks. Issues with conventional activation functions consist of output offset and gradient vanishing. In order to reduce network runtime and increase speed, a new activation function called Fast Exponentially Linear Units has been developed. The FELU boosts accuracy and speed by integrating features from the Rectified Linear Unit (ReLU) and the Exponential Linear Unit [14]. Hassairi, S et al. built a deep neural network using several auto-encoders. The network has been stacked after being trained with a linear classifier. The model undergoes significant revisions. When building a deep convolutional neural network, we use a smart pooling technique and local normalisation. CNNs with a deep layer are constructed by combining an intelligent pooling method and a local normalisation strategy. Based on the evaluation results, we decide to concentrate on CNNs, which are among the top approaches for image categorization [15,16].

A clean dataset must be provided at every level of the WordNet structure. At all ImageNet levels, it is challenging to achieve high precision because a synset's classification difficulty increases with its hierarchical position. The goal of image net is to allow objects in photos to adapt changeable looks with accuracy in tree depth and placements, using an illustration of a Siamese cat against Burmese cat diversity. An independent group of objects verified the veracity of the photograph. A standard precision of 99.7% is attained for each synset. An Artificial Neural Network (ANN) connection is used to pretrain the parameters, and then a spare layered auto encoder is used to refine the results. Using 10-fold cross-validation, this method operates more quickly and produces findings with higher precision. It is still necessary to classify various malaria plasma strains better. A method to find malaria parasites using standard light microscopes has been proposed by Tek et al. [17]. To keep illumination and consistency consistent, colour normalisation is utilised. Bayesian classification is used for strain extraction. To determine the accuracy of the diagnosis, more tests must be done. The approaches mentioned above employ a variety of techniques to find cells that are infected with malaria. Malaria-infected cell classification and image clustering were both enhanced by the application of the ReLU activation function and a set of convolutional neural networks in this investigation.

3. Proposed work

A Deep Neural Network (DNN) is a type of ANN that combines features from both CNN and a Recurrent Neural Network (RNN). A deep neural network was utilised to classify and forecast the content of photographs. CNNs were used to identify images and extract features. These days, we simulate time sequences, events, and other phenomena using Recurrent Neural Networks [18]. Between the input and output layers of a CNN, there are several hidden layers. CNN, a leading deep learning algorithm, just won first place at the ILSVRC. The impact of CNNs on automatic labelling and recognition of images is significant. Using neural networks with many processing layers (input, hidden, and output), deep learning is a subfield of machine learning. Layer sharing reduces the need for as many parameters and computations in the network. It prevents overfitting by reducing the network's coverage area. Most malaria detection approaches need human feature extraction of dataset-specific algorithms that have been trained to account for machine, perspective, dimension, and geographical changes. Classification of parasite and healthy cells is evaluated using both the enhanced CNN and pretrained models.

3.1. Datasets collection

The plasmodium dataset includes 2,000 cell pictures that are split into two groups: parasitized cells and cells that are uninfected. Every cell has an equal number of instances in each category. The malaria parasites dataset includes a variety of different parasite species, including Falciparum, Malariae, Ovale, and Vivax. Each species goes through four distinct stages of development: the ring stage, the trophozoite stage, the schizont stage, and the gametocyte stage. Expert pathologists have provided and labelled a mask for each original image. In order to train a model and determine its overfitting, robustness, and generalizability, it is crucial to collect publicly available protozoan parasite datasets.

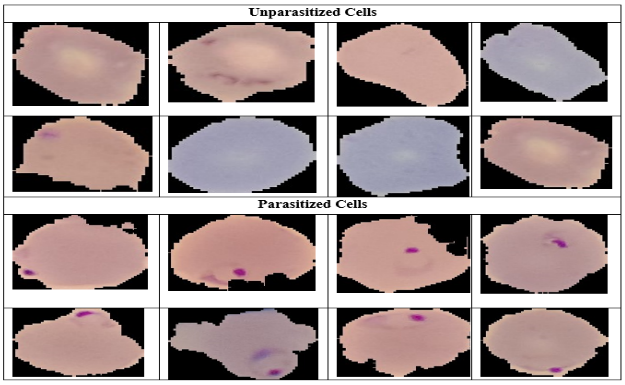

Figure 1. Malarial unparasitized and parasitized cell images.

Figure 1 represents some of the uninfected and parasitized cells available in the dataset used for predicting the results. The Kaggle websites provide clinical access to the datasets cell pictures. For the validation procedure, 200 photos are exposed. The categorization performance dramatically increased after training with 1100 infected and 1100 uninfected pictures. The suggested model was trained and tested using pictures of malaria-infected and uninfected cells.

3.2 Pre-processing

Big data has a vast amount of data, which makes deep learning extremely significant. In computer vision, picture categorization and recognition of images have grown in importance. Applications such as handwritten character identification, medical imaging, crop or seedling disease acknowledgment, digital fingerprint recognition, etc., all require image categorization. A suitable technique to suggest for classifying blood smears can be Convolution Neural Networks. The collected images are pre-processed by resizing them to a consistent size and a normal pixel value between 0 and 1. Augmentation is done if the training sample needs to be increased. The model optimises the results of transfer learning as well as related research. As illustrated in Figure 1, the model was trained using 20,000 pictures from the parasitized and uninfected classes. Images of parasitic cells and infected cells categorization are shown in Figures 2 and 3.

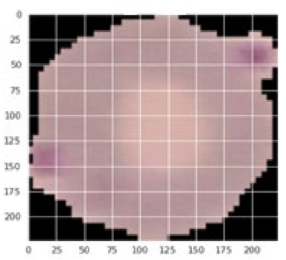

Figure 2. Parasitic cell categorization in image

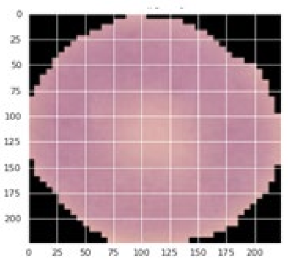

Figure 3. Uninfected cell categorization in images

3.3 Training

The gathered images are then divided into 90% training data and 10% test data. The loss function for binary classification can be identified using binary cross entropy. The CNN employs a base kernel of size 3 and 6464, 32 stride 2, and 12 maximum pooling layer filters. The CNN accepts the cell image as input. The CNN's convolutional layers examine the image and discover numerous patterns and attributes useful for identifying malaria infections.

After each convolutional layer, the model is given a non-linear boost via ReLU activation so that it can learn more complex patterns. Pooling layers minimise the feature maps across convolutional layers, easing the computational load and supplying translational invariance. In the last layers of the CNN, which tend to be fully connected layers, the features extracted are combined to provide the final judgement. In the last layer, the Sigmoid activation function is used to transfer the model's output to a probability score that represents the cell's likelihood of becoming infected. On the basis of the probability score acquired from the Sigmoid activation, the model makes a prediction about whether the outcome will be infected or not. A powerful model for malaria cell detection is produced by this combination technique, which uses the CNN's capacity to learn multilayer features, ReLU's incorporation of non-linearity, and Sigmoid's provision of a probabilistic output.

The function known as activation, which is linked to neural networks, has the function of understanding and learning complex designs. The activation function keeps the "active neuronal features," expands with nonlinear variables that get rid of extraneous information and connects these patterns through nonlinear functions. Subsequently, it converts the signal coming in to the output signal for the artificial neural network. The output shifts linearly whenever the input is larger than zero. The network's sparseness is increased, and parameter dependence is decreased by limiting the output to zero. It successfully resolves the problem of parameter overfitting. Because it does not require power operation, the ReLU function reduces the computation quantity and shortens the network's training duration. The two functions, such as sigmoid (S-shaped), are monotonically rising on their relative domain and are frame worked, for example, between 0 and 1. Sigmoid functions are important in many relevant fields, including the life sciences.

Sigmoid functions resemble step functions with a step greater than the centre because they have a steep slope close to the centre. It is done to determine how similar a sigmoid function and a related step function are to one another [19]. Figure 4 explains how the proposed model works, and Table 1 provides an overview of the model and the proposed system.

Table 1. Model summary

Parameters	Range
Convolutional dropout	[None,62,62,32]
Optimizer	[Adam]
Activation	[Rectified Linear Unit, Sigmoid]
Dense dropout	[0.29, 0.58]

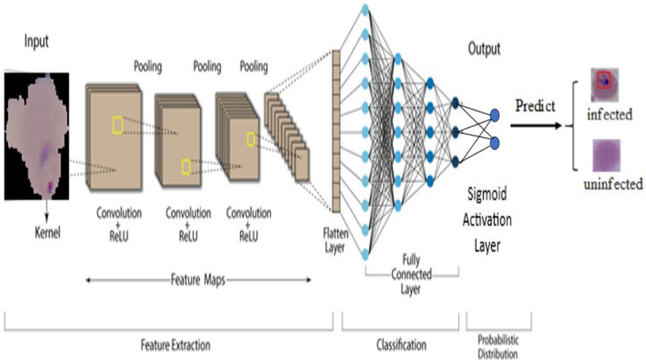

Figure 4. Architecture of the proposed model to classify and to detect malaria-infected cells

4. Results and Discussions

Accuracy, sensitivity, specificity, F1-score, and precision [28-30] are all higher for the proposed model at the 12th iteration than they are for any of the alternatives listed in Table 2. The performance comparison of the methods indicated in Table 2 is depicted graphically in Figure 5. Figures 6 a. and 6 b. depict the evaluation's accuracy and loss during training and validation, respectively.

Table 2. Performance comparison of various existing methods

Author and references	Accuracy %	Specificity%	F1 Score%	Precision%	Sensitivity%
Ross et al., [20]	73	-	-	-	85
Das et al., [21]	84	68.9	-	-	98.1
SS. Devi et al., [22]	96.32	96.79	85.31	-	92.87
Zhaohuiet al., [23]	97.37	97.75	97.36	97.36	96.99
Bibin et al., [24]	96.3	98.5	-	-	97.6
Gopakumar et al., [25]	97.77	98.5	-	-	97.3
S. Rajaraman et al., [26]	99.5	98.5	-	-	97.1
Fuhad KM et al., [27]	99.23	99.1	99.922	-	99.52
Proposed Method	99.77	99.6	99.712	98.73	99.79

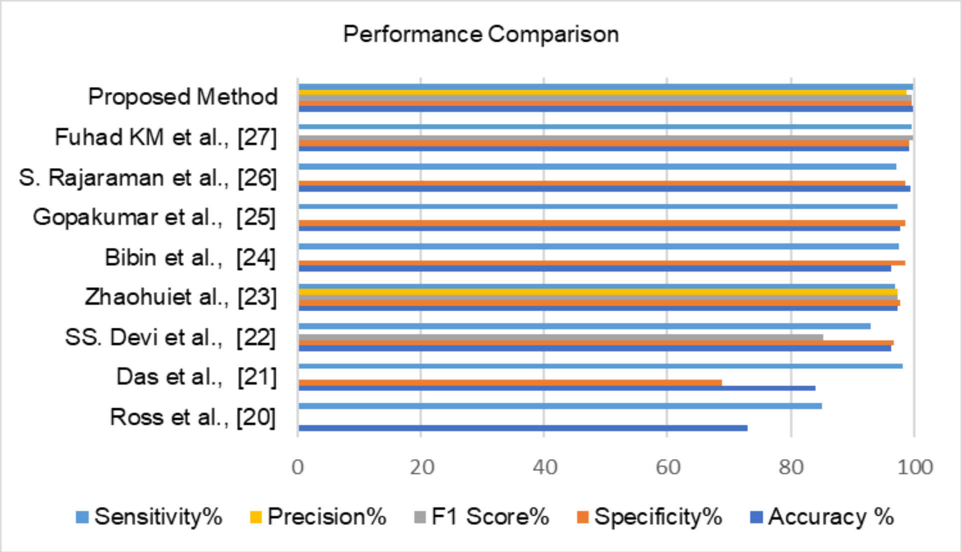

Figure 5. Performance comparison of the techniques for detecting malaria-infected cells

Figure 6a. Accuracy after validation and training

Figure 6b. Loss after validation and training

5. Conclusion

The proposed model that was created is straightforward and successful in differentiating between malaria-infected and uninfected cells. The activation functions of ReLU and sigmoid are employed in the model. Numerous activation functions, including Sigmoid, ReLU, tanh can be employed to solve challenging nonlinear issues. In the proposed image classification technique, ReLU and sigmoid activation functions are employed. The ReLU activation function, which was used in neural networks, successfully addresses the gradient disappearing and extended training time difficulties related to S-type saturated activation processes. To prevent the overfitting issue, dropout layers are employed before flattening layers. By randomly choosing the photos from the individual cell image collections, the loss of validation was also minimised. The prediction of infected and healthy cells was done accurately by the proposed model, which uses only 3 layers of convolution, and this was the idea behind the implementation. The model achieved an improved accuracy of 99.77% across 12 iterations (epochs).

References

[1] Skaramagkas, V, Pentari, A, Kefalopoulou, Z, Tsiknakis, M. Multi-modal Deep Learning Diagnosis of Parkinson's Disease-A Systematic Review. IEEE Transactions on Neural Systems and Rehabilitation Engineering. 2023; 31: pp. 2399 - 2423.

[2] Tripathi S. Image classification using small convolutional neural network. In: Proceedings of the 9th International Conference on Cloud Computing, Data Science & Engineering (Confluence); 10-11 January 2019; Noida, India. IEEE Xplore: IEEE; 2019. p. 483-487.

[3] Sriram, G.K. Deep Learning Approaches for Pneumonia Classification in Healthcare. In: Proceedings of the 3rd International Conference on Innovative Practices in Technology and Management; 22-24 February 2023; Uttar Pradesh, India. IEEE Xplore : IEEE; 2023. p.1-6.

[4] Devi Padma, K. Exploring The Potential of Machine Learning for Early Diagnosis of Parkinson's Disease: A Comparative Study. In: Proceedings of the 4th International Conference on Intelligent Engineering and Management. 9-11 May 2023; London, United Kingdom; IEEE Xplore; 2023. p. 1-6.

[5] Poostchi, M, Silamut, K, Maude, R.J, Jaeger, S. Image analysis and machine learning for detecting malaria. Translational Research. 2018; 194: pp.36-55.

[6] Pattanaik, P,A, Mittal, M, and Khan, M,Z. Unsupervised deep learning cad scheme for the detection of malaria in blood smear microscopic images. IEEE Access. 2020; 8: pp.94936-94946.

[7] Lin G, Shen W. Research on convolutional neural network based on improved ReLU piecewise activation function. Procedia computer science. 2018; 131: pp. 977-84.

[8] He, K. Deep residual learning for image recognition. In Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition (CVPR); 27-30 June 2016; Las Vegas, NV, USA. IEEE Xplore: IEEE; 2016. p. 770-778.

[9] Liang, Z. CNN-based image analysis for malaria diagnosis. In: Proceedings of IEEE International Conference on Bioinformatics and Biomedicine. 15-18 December 2016; Shenzhen, China; IEEE Xplore: IEEE; 2016. p. 493-496.

[10] Jaspreet Singh, C, Abhishek, S, Karan, S, Rekha, R. Malaria Cell Image Classification using Deep Learning. International Journal of Recent Technology and Engineering. 2020; 8: pp. 1-7.

[11] Patil, GG. Techniques of Deep Learning for Image Recognition. In: Proceedings of IEEE 5th International Conference for Convergence in Technology; 29-31 March 2019; Bombay , India. IEEE Xplore: IEEE; 2019; p. 1-5 .

[12] Deng, J. Imagenet: A large-scale hierarchical image database. In: Proceedings of IEEE conference on computer vision and pattern recognition; 20-25 June 2009; Miami, FL, USA. IEEE Xplore: IEEE; 2009. p. 248-255.

[13] Rajaraman, S, Antani, S.K, Poostchi, M, Silamut, K. Pre-trained convolutional neural networks as feature extractors toward improved malaria parasite detection in thin blood smear images. PeerJ. 2018; 6: pp. 1-17.

[14] Qiumei, Z, Dan, T, Fenghua, W. Improved convolutional neural network based on fast exponentially linear unit activation function. IEEE Access. 2019; 7: pp.151359-151367.

[15] Hassairi, S. Supervised image classification using deep convolutional wavelets network. Proceedings of International Conference on Tools with Artificial Intelligence; 09-11 November 2015; Vietri sul Mare, Italy. IEEE Xplore: IEEE; 2015. p. 265-271.

[16] Vijay, K. Survey on chaos RNN–A root cause analysis and anomaly detection. In: V.D. Ambeth Kumar, editor. AIP Conference Proceedings. Proceedings of the 5th International Conference on Intelligent Computing (IConIC 2k22); 25–26 March 2022; Chennai, India. AIP Publishing; 2023. p. 1-8.

[17] Tek, F.B, Dempster, A.G, and Kale, I.: Malaria parasite detection in peripheral blood images. BMVA.2006; 1: pp. 347-356.

[18] Babu, R, Jayashree, K, Viswanathan, K,B ,Vijay K. An Efficient Spam Detector Model for Accurate Categorization of Spam Tweets Using Quantum Chaotic Optimization-Based Stacked Recurrent Network. Nonlinear Dynamics. 2023; 111: pp. 18523–40.

[19] Iliev, A, Kyurkchiev, N, Markov S. On the approximation of the step function by some sigmoid functions. Journal of Mathematics & Computers in Simulation. 2017;133:pp 223-234.

[20] Ross, N, E, Pritchard, C, J, Rubin, D, M, Duse, A, G. Automated image processing method for the diagnosis and classification of malaria on thin blood smears. Medical and Biological Engineering and Computing. 2006; 44: pp 427–436.

[21] Das, D, K, Ghosh, M, Pal, M, Maiti, A, K, Chakraborty, C. Machine learning approach for automated screening of malaria parasite using light microscopic images. Micron. 2013; 45: pp 97–106.

[22] Devi, S.S, Sheikh, S.A, Talukdar, A, Laskar, R.H. Malaria infected erythrocyte classification based on the histogram features using microscopic images of thin blood smear. Indian Journal of Science and Technology. 2016; 9: pp. 1-10.

[23] Liang, Z. CNN -based image analysis for malaria diagnosis. In: Proceedings of IEEE International Conference on Bioinformatics and Biomedicine (BIBM); 15-18 December 2016; Shenzhen, China. IEEE Xplore: IEEE; 2016. p. 493–496.

[24] Bibin, D, Nair, M.S, Punitha, P. Malaria parasite detection from peripheral blood smear images using deep belief networks. IEEE Access. 2017; 5:pp. 9099–9108.

[25] Gopakumar, G,P, Swetha, M, Sai Siva, G, SaiSubrahmanyam, G,R,K. Convolutional Neural Network based malaria diagnosis from focus stack of blood smear images acquired using custom-built slide scanner. Journal of Biophotonics. 2018; 11: pp. 111- 123.

[26] Rajaraman, S, Jaeger, S, Antani, S.K. Performance evaluation of deep neural ensembles toward malaria parasite detection in thin-blood smear images. PeerJ. 2019;7: pp. 1-16.

[27] Fuhad, K,M, Tuba, JF, Sarker, M,R, Momen S, Mohammed, N, Rahman, T.: Deep learning based automatic malaria parasite detection from blood smear

and its smartphone based application. Diagnostics. 2020; 10: pp. 329- 348.

[28] Braveen, M, Nachiyappan, S, Seetha, R, Anusha, K, ALBAE feature extraction based lung pneumonia and cancer classification. Soft Computing. 2023; 27: pp. 1-14.

[29] Jayachitra, S. Hierarchical-Based Binary Moth Flame Optimization for Feature Extraction in Biomedical Application. In: Nilay Khare, editor. Machine Learning, Image Processing, Network Security and Data sciences. Proceedings of the 4th International Conference on Machine Learning, Image Processing, Network Security and Data 21 Dec 2022; Springer Link: Springer Nature Switzerland; 2023. p. 27-38.

[30] Sekar, J, Aruchamy, P. An Efficient Clinical Support System For Heart Disease Prediction Using TANFIS Classifier, Computational Intelligence. 2022; 38: pp. 610-640.