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A Novel Approach to Detect Malaria using Deep Learning

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Abstract: Mosquitoes, though seeming to be tiny and fragile, transmit numerous diseases and are responsible for threatening the health of billions of people around the world. Combating these insects is becoming increasingly difficult as they are developing resistance to available insecticides. Malaria, one of the diseases transmitted through infected mosquitoes, is life-threatening in various parts of the developing world. However, early detection of this disease is propitious for proper diagnosis and effective cure. Automating the task of detecting malarial parasite from cell images using Mathematical techniques, like Machine learning algorithms or Neural Networks for deep learning, can help with the accurate diagnosis as well as funnelling resources on other important aspects of the treatment in resource-scarce areas.

Keywords: Malaria, Early detection, Machine Learning, Deep Learning, Neural Networks

I. INTRODUCTION

Malaria, spread by mosquitoes, has been a notoriously life-threatening disease. This situation is because, during the initial stages, the symptoms can be mistaken easily for fever, flu, or the common cold. But, in the advanced stages, it could wreak havoc by infecting and rupturing the cell structure, which could be potentially fatal. And if left untreated, it could even result in death. Although most researchers believe that the disease has originated from the African continent, the origin of this disease is debatable. Due to their tropical climate, which acts as a catalyst and breeding ground for an infected female mosquito of the genus Anopheles which carries the plasmodium parasites, South American countries, the African countries, and the Indian sub-continent are at a high risk of infection.

According to the World Health Organisation [1], close to 405000 people have died from cerebral malaria in 2018, mainly children aged under five, despite the extensive availability of both preventive and therapeutic drugs to treat this disease. These deaths resulted from almost 228 Million infections in 2018 alone. In most of the infection cases, the only available method of diagnosing this disease is through the manual examination of the microscopic image of the infected cells. This method has the following problems: the manual examination requires extensive training and experience, but unfortunately, such specialized personnel is often in inadequate numbers in rural areas where the disease is widely prevalent. Also, this method is subjective and majorly suffers from a lack of standardization.

Advancements in electronic medical records have been remarkable, but the information these devices provide is not much better than that of the old paper charts they replaced. The information these devices provide to doctors can be enhanced using analytics and machine learning. In the case of malaria, Early detection is essential for ensuring proper diagnosis and improving the chances of cure. Using the latest technological advancements, we can advance more information to the clinicians so they can make better decisions about the diagnosis and the treatment options while understanding the possible outcomes and costs for each one. To achieve this, the process of diagnosis can be automated using machine-learning and deep-learning algorithms. Machine learning can offer an objective opinion to improve accuracy, reliability, and efficiency. Therefore, this research addresses the area of a computer-aided malaria detection system using a deep learning architecture.

II. LITERATURE REVIEW

A. Current System

In the present times, malaria diagnosis is made by using manual techniques like Rapid diagnostic test, Molecular test, Antibody test etc. Here, the pathologists, using past domain knowledge, analyze the blood sample in a laboratory setting to study the variations in shape, size, and colour characteristics of RBCs to conclude the presence of plasmodium parasite. These tests are time taking considering the amount of time being spent on a single patient and also erroneous due to subjectivity. Consequently, conventional microscopy diagnosis cannot be recommended as a safe testing strategy [2].

B. Limitations of the Current System

1) Manually diagnosing patients for the presence of plasmodium parasite is time-consuming and particularly inefficient in resource-scarce areas.
2) Furthermore, recent studies have revealed that the concurrence rates among pathologists for the identification of this epidemic have alarmingly decreased.

C. Current Research

A considerable amount of research in the field of computer vision has been done on automated malaria parasite detection. Tek et al. [3] proposed a colour histogram-based stained object detection method and later suggested a method which adopts the K-nearest neighbour method [4] for binary classification. Later, Diaz et al. [5] proposed a method for classifying Plasmodium-parasite-infected peripheral blood smears. In [6], Raviraja et al. have used a statistical approach for detecting malarial parasite. A supervised-learning based method to detect malaria infection was put forward by [7]. In [8], a malaria parasite identification system was proposed based on the histogram-based feature set, and different statistical classifiers such as ANN, SVM, K-NN and naive Bayes were used in which ANN gave the highest detection accuracy.

III. PROPOSED SYSTEM

A. The Proposal

The main objective of the study is to develop a computerized framework for malaria detection that replicates the conventional standard in the diagnosis of malaria to identify malaria parasites in blood smear images. Such a system can be of immense help to the clinicians in the diagnostic process. Recent studies have proven that classification models based on the deep learning paradigm can outperform the conventional classifiers [9][10][11][12]. None of the aforementioned research has attempted to explore the power of deep learning architecture. The proposed system will utilize the capabilities of Convolution Neural Network (CNN) to learn the features of the dataset [13]. The dataset has been taken from Lister Hill National Center for Biomedical Communications, National Library of Medicine. The given dataset doesn't contain images of equal dimension; for the sake of performance, the images have been resized to 128x128 pixels with three channels. The resized images are then converted into tensors and are used for training the CNN model. The trained CNN model will differentiate the cell-images as 'Parasitized' and 'Uninfected'.

B. Benefits of The Proposed System

1) The proposed system will diagnose infected cells more efficiently.
2) The proposed system can be made available on the cloud so that it can be accessible in remote areas.
3) The time taken to arrive at a conclusion of illness is substantially reduced.

IV. PRELIMINARIES

This section briefly explains about the theory of each component used in the study. It illustrates the concept of Artificial Neural Network to provide a base to understand it's variant Convolution Neural Network. It further delves into ReLU activation function and Max-Pooling.

A. Artificial Neural Network

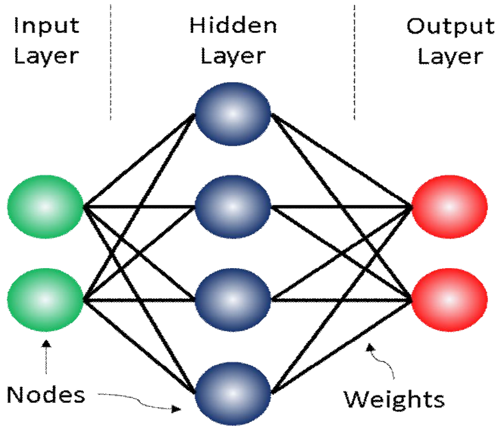


Fig. 1: A simple 2-layer NN with two features in the input layer, four nodes in the hidden layer and two nodes in the output layer

Above figure shows some input node, connected to some output node via an intermediate node in what is called a 'hidden layer' - 'hidden' because, in the use of NN only the input and output is of concern to the user, they are not directly observable from the inputs and outputs of the system.

In real, high-performing NN, there are usually more hidden layers. When we train our network, each node in the hidden layer performs a calculation using the values from the input nodes. The output of this is passed on to the nodes of the next layer. When the output hits the final layer, the 'output layer', the results are compared to the real, known outputs, and some tweaking of the network is done to make the output more similar to the real results. This is done with an algorithm called backpropagation.

B. Convolutional Neural Network

Convolutional networks, also known as convolutional neural networks, or CNNs, are a specialized kind of neural network for processing data that has a known grid-like topology. They were inspired by the biological processes [14][15][16], i.e. the connectivity pattern between the neurons are similar to that of the organization of the animal visual cortex. Examples include time-series data, which can be thought of as a 1-D grid taking samples at regular time intervals, and image data, generally perceived as a 2-D grid of pixels arranged in columns and rows.

Convolutional networks have been tremendously successful in practical applications. The name "convolutional neural network" indicates that the network employs a mathematical operation called "Convolution". Convolution is a specialized kind of linear operation. Convolutional networks are neural networks that use convolution in place of general matrix multiplication in at least one of their layers.

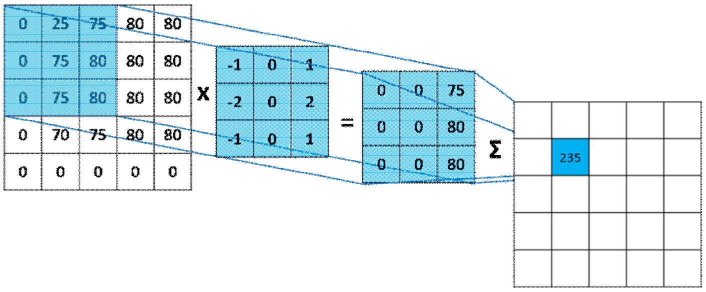


Fig. 2: A step in the convolution process

A kernel is placed on the top-left corner of the matrix. The pixel values covered by the kernel are multiplied with the corresponding kernel values, and the products are summated. The result is placed in the new image at the point corresponding to the centre of the kernel. An example of this first step is shown in the diagram above.

The kernel is moved over by one pixel, and this process is repeated until all of the possible locations in the matrix are filtered as below. Notice that there is a border of empty values around the convolved image. This is because the result of convolution is placed at the centre of the kernel. To deal with this, a process called 'padding' or more commonly 'zero-padding' is used. This means that a border of zeros is placed around the original image to make it a pixel wider all around. The convolution is then done as normal, but the convolution result will now produce a matrix that is of equal size as that of the original.

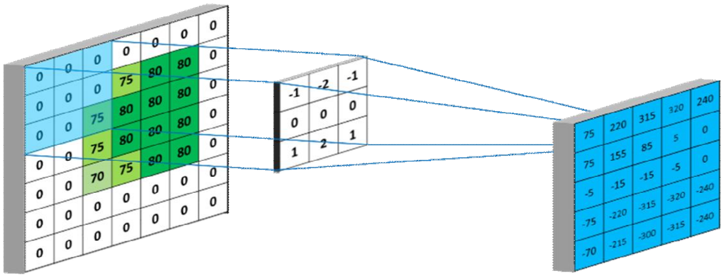


Fig. 3: Completed Convolution Operation

C. Rectified Linear Unit – Activation Function

Given an input set, an activation function decides the output of that node. In simpler terms, the activation function is used to introduce non-linearity into the output of a neuron.

Rectified Linear Unit, famously referred to as ReLU, is an activation function which is defined as the positive part of the integral, i.e. $f(x) = \max(0, x)$. It was first introduced in 2001 by Hahnloser et al. [17] with strong mathematical justifications and biological motivations.

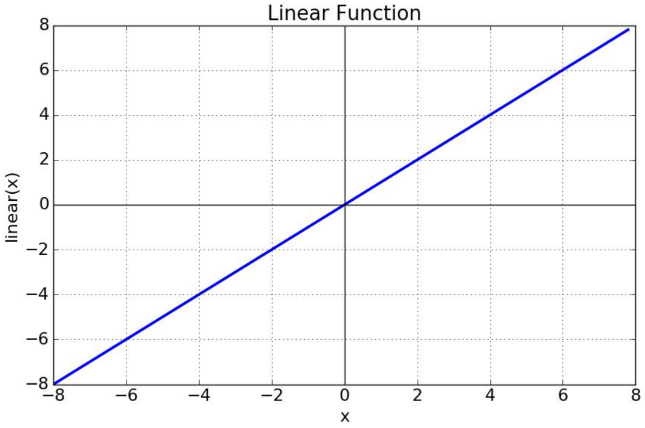


Fig. 4: Linear Function

The ReLU activation function has demonstrated to enable better training of deeper networks [18] compared to other widely used activation functions, i.e. it learns much faster than Sigmoid and Tanh activation function.

D. Max Pooling Layer

Pooling, an important concept of Convolutional Neural Networks, is a form of non-linear down-sampling. Max Pooling is the most commonly used non-linear function to implement pooling. It serves to reduce the spatial size of the representation, the memory footprint and also the number of computations in the network. Hence, it also controls the overfitting of the network. It is not uncommon to periodically insert a pooling layer between successive convolutional layers and following it by a ReLU layer.

It is worth noting that there are only two commonly seen variations of the max-pooling layer found in practice: a pooling layer with F=3, S=2 (also called overlapping pooling), and more commonly F=2, S=2, here 'F' refers to 'Spatial extent' and 'S' refers to the 'Stride'. Pooling sizes with larger receptive fields are too destructive.

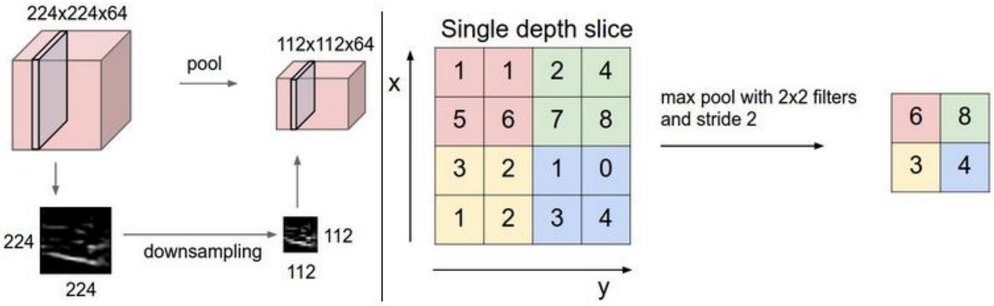


Fig. 5: Max Pooling Operation

V. IMPLEMENTATION

A. Exploratory Data Analysis

In this section, different aspects of the dataset are analyzed to understand the data in context. The dataset is an Image dataset which contains 27558 samples of cell images. The images are equally divided into two classes, "Parasitized" and "Uninfected". As mentioned earlier, each image of the dataset is resized to 128*128 for dealing with the problem of images with different dimensions. The batch size for the experiment of training the deep learning model is assumed as 128 images. Some sample images from the dataset are presented.

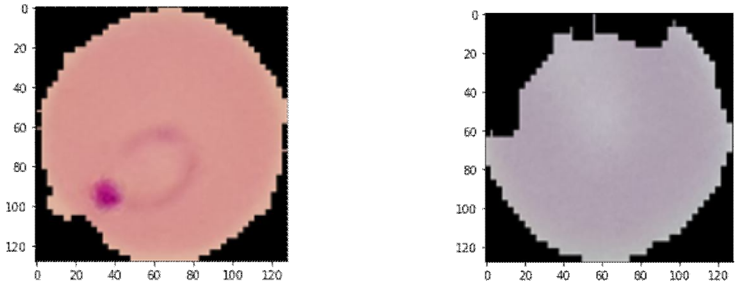


Fig. 6: Samples of "Parasitised" and "Uninfected" classes

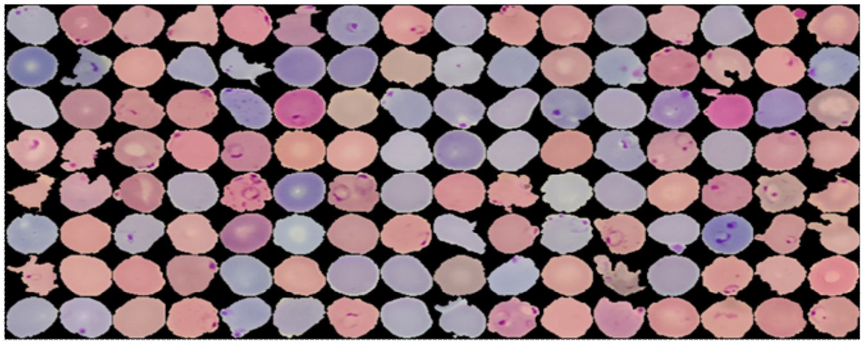


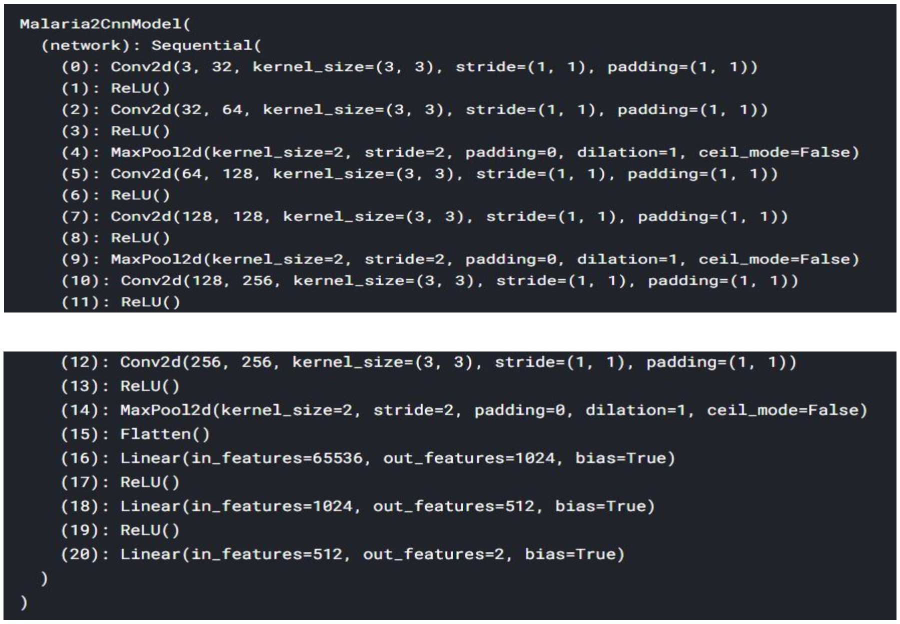
Fig. 7: Batch of 128 Images from the Dataset

B. Deep Learning Model

CNN's are generally used for image classification problems in which images are taken as an n-dimensional matrix of RGB values. In addition to this, CNN's can also be used indirectly in any other applications which have the input data in n-dimensional matrix values.

An object-oriented principle has been adopted for designing the inference model. Cross-Entropy has been used as the cost-function to calculate the loss while Adam Optimiser is used to update the attributes of the neural network.

The model consists of a set of 2 Dimensional Convolutional layers to detect features within each image, ReLU activation function and Max Pooling layers. The architecture of the model as an object is presented.



```
Malaria2CnnModel(
  (network): Sequential(
    (0): Conv2d(3, 32, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (1): ReLU()
    (2): Conv2d(32, 64, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (3): ReLU()
    (4): MaxPool2d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
    (5): Conv2d(64, 128, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (6): ReLU()
    (7): Conv2d(128, 128, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (8): ReLU()
    (9): MaxPool2d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
    (10): Conv2d(128, 256, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (11): ReLU()
```

```
    (12): Conv2d(256, 256, kernel_size=(3, 3), stride=(1, 1), padding=(1, 1))
    (13): ReLU()
    (14): MaxPool2d(kernel_size=2, stride=2, padding=0, dilation=1, ceil_mode=False)
    (15): Flatten()
    (16): Linear(in_features=65536, out_features=1024, bias=True)
    (17): ReLU()
    (18): Linear(in_features=1024, out_features=512, bias=True)
    (19): ReLU()
    (20): Linear(in_features=512, out_features=2, bias=True)
  )
)
```

Fig. 8: Model Architecture

The model has been trained on 16000 images while being validated on 6000 images. The validation accuracy of 95.6% has been attained at the end of 10 epochs. The model has been tested on the remaining 5558 images of the data set. The overall accuracy on the test data is 96%.

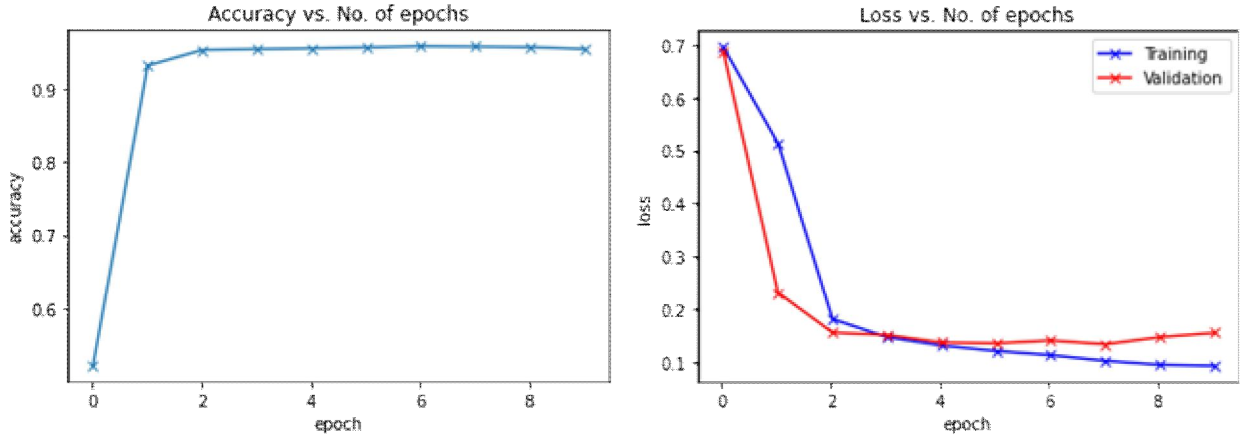


Fig. 7: Visualizations of Accuracy vs No. of epochs **&** Loss vs No. of epochs

C. Tools Used

1) *PyTorch:* PyTorch is an open-source ML library based on the famous Torch library, used for developing applications such as computer vision and natural language processing, primarily developed by Facebook's AI Research lab. It is free and open-source software released under the Modified BSD license.
2) *Kaggle:* Kaggle is an online platform for data scientists and ML practitioners. It allows users to discover and publish data sets on its platform and also build machine learning models in a web-based development environment.
3) *TorchVision:* The TorchVision package includes popular computer vision datasets, model architectures and commonly used image transformations.

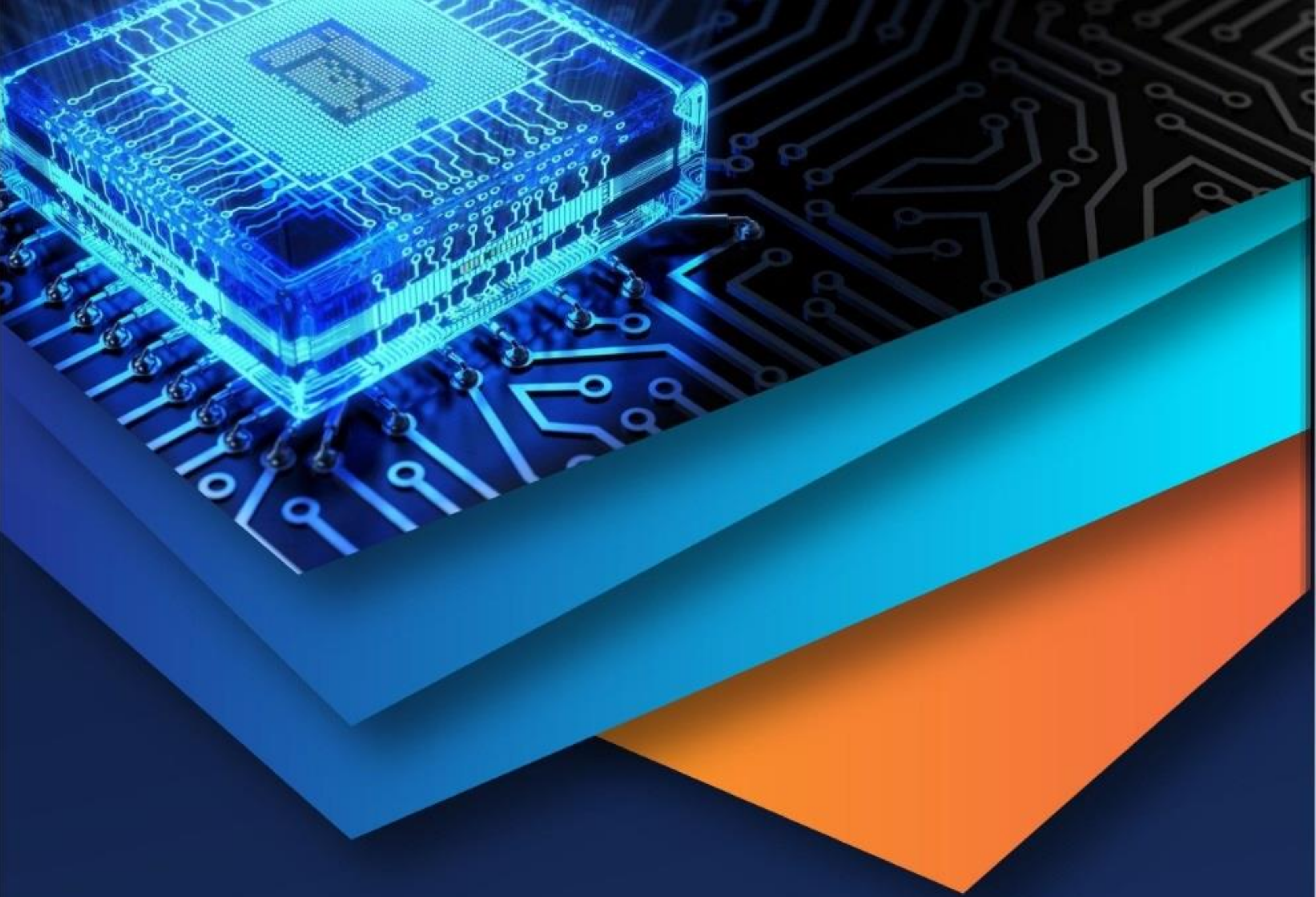
VI. CONCLUSION

This work proposes an effective automated decision support system using a deep learning architecture to identify malaria parasites. This study will help practitioners of medicine in detecting malaria from blood cell images. This work implements a unique deep-learning-based binary classifier that provides a significantly higher sensitivity and specificity compared to existing studies in this area. As per the methods already reported in the literature, the work presented in this paper is the first application of deep-learning for malaria disease identification using cell images. Since this study has used generic pattern recognition and deep learning architecture, it could easily be leveraged for the diagnosis of a variety of other related abnormalities.

REFERENCES

[1] World malaria report 2019. Geneva: World Health Organization; 2019. Licence: CC BY-NC-SA 3.0 IGO.
[2] K. Mitiku, G. Mengistu and B. Gelaw, "The reliability of blood film examination for malaria at the peripheral health unit", Ethiopian J. Health Develop., vol. 17, pp. 197-204, 2004.
[3] F. B. Tek, A. G. Dempester and I. Kale, "Malaria parasite detection in peripheral blood images", Proc. Brit. Mach. Vis. Conf., pp. 347-356, 2006.
[4] F. B. Tek, A. G. Dempster and I. Kale, "Parasite detection and identification for automated thin blood film malaria diagnosis", Comput. Vis. Image Understand., vol. 114, no. 1, pp. 21-32, 2010.
[5] G. Diaz, F. A. Gonzalez and E. Romero, "A semi-automatic method for quantification and classification of erythrocytes infected with malaria parasites in microscopic images", J. Biomed. Informat., vol. 42, no. 2, pp. 296-307, 2007.
[6] S. Raviraja, S. S. S. S. Osman and Kardman, "A novel technique for malaria diagnosis using invariant moments and by image compression", Proc. 4th Int. Conf. Biomed. Eng. (IFMBE), vol. 21, pp. 730-733, Apr. 2008.
[7] D. K. Das, M. Ghosh, M. Pal, A. K. Maiti and C. Chakraborthy, "Machine learning approach for automated screening of malaria parasite using light microscopic images", Micron, vol. 45, pp. 97-106, Sep. 2013.
[8] S. S. Devi, S. A. Sheikh, A. Talukdar and R. H. Laskar, "Malaria infected erythrocyte classification based on the histogram features using microscopic images of thin blood smear", Indian J. Sci. Technol., vol. 9, no. 45, pp. 1-10, 2016.
[9] G. E. Hinton, "Training products of experts by minimizing contrastive divergence", Neural Comput., vol. 14, no. 8, pp. 1771-1800, 2002.
[10] V. Nair and G. E. Hinton, "3-D object recognition with deep belief nets", Neural Inf. Process. Syst., vol. 22, pp. 1339-1347, Jan. 2009.
[11] R. Salakhutdinov and G. Hinton, "Semantic hashing", Int. J. Approx. Reasoning, vol. 50, no. 7, pp. 969-978, Jul. 2009.

[12] Rajaraman S, Antani SK, Poostchi M, Silamut K, Hossain MA, Maude, RJ, Jaeger S, Thoma GR. (2018) Pre-trained convolutional neural networks as feature extractors toward improved Malaria parasite detection in thin blood smear images. PeerJ6:e4568 https://doi.org/10.7717/peerj.4568
[13] Lister Hill National Center for Biomedical Communications, National Library of Medicine, Bethesda, MD, United States of America https://lhncbc.nlm.nih.gov/publication/pub9932
[14] Kunihiko Fukushima (2007) Neocognitron. Scholarpedia, 2(1):1717.
[15] Hubel, D. H.; Wiesel, T. N. (1968-03-01). "Receptive fields and functional architecture of monkey striate cortex". The Journal of Physiology. 195 (1): 215–243. doi:10.1113/jphysiol.1968.sp008455
[16] Fukushima, Kunihiko (1980). "Neocognitron: A Self-organizing Neural Network Model for a Mechanism of Pattern Recognition Unaffected by Shift in Position" . Biological Cybernetics. 36 (4): 193–202. doi:10.1007/BF00344251.
[17] Hahnloser, R.; Sarpeshkar, R.; Mahowald, M. A.; Douglas, R. J.; Seung, H. S. "Digital selection and analogue amplification coexist in a cortex-inspired silicon circuit", 2000.
[18] Xavier Glorot, Antoine Bordes and Yoshua Bengio "Deep sparse rectifier neural networks", 2011.



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