BLOOD TISSUE IMAGE TO IDENTIFY MALARIA DISEASE CLASSIFICATION

T.Keerthika[1], B.Akalya[2], G.Kiritika[3], S.Sineka[4]

[1-4] Student of Department of Information Technology, Meenakshi College of Engineering, Chennai, Tamil Nadu, India

---***---

Abstract - ***Plasmodium falciparum malaria epidemics are common and often lethal, according to reports. Through the use of meteorological characteristics that are determinants of transmission potential, epidemics have been formally attempted to be predicted. Regarding the relative weight and predictive power of these criteria, however, there is little agreement. To identify precise and significant indicators for epidemic prediction we are using ASKalgorithm, it is essential to comprehend the causes of variance. In this study, we extracted several blood cell properties and used convolutional neural network-based models to identify malaria in blood tissue images using structured analysis. Convolutional neural networks (CNNs) were used in deep learning to successfully classify malaria blood tissues. It was described as a new technique that offers effective categorization detection.***

***Key Words*: Malaria detection, Plasmodium parasite, Transfer learning, Convolutional neural networks, Computer aided design (CAD), Alex net, Lenet**

1. INTRODUCTION

Millions of people suffer from malaria, a parasite illness that is most prevalent in underdeveloped nations. Effective malaria treatment and disease management depend on an early and precise diagnosis. Currently, the most used approach for diagnosing malaria is microscopic analysis of blood smears. This strategy of diagnosing malaria is labor and time-intensive, hence automated and effective methods are required.

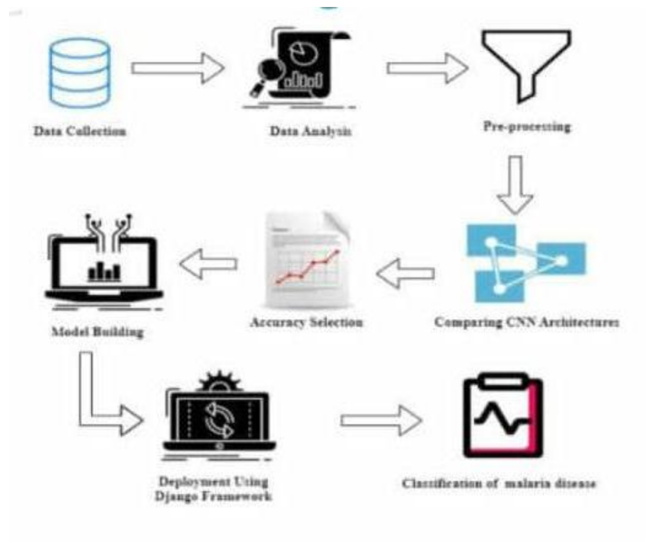
A branch of artificial intelligence called deep learning has demonstrated promise in a number of picture categorization tasks. Deep learning for malaria prediction using blood tissue pictures has attracted more attention in recent years. Researchers have created machine learning models that can accurately predict the presence of malaria using vast datasets of blood tissue pictures that are both malaria-positive and malaria-negative.

In this project, we will explore the use of deep learning for malaria prediction using blood tissue images. We will begin by acquiring a dataset of blood tissue images from malaria-positive and malaria-negative patients, and we will preprocess the data to ensure quality and standardization. We will then develop and train deep learning models, such as convolutional neural networks and deep belief networks, on this dataset to predict the presence of malaria. Finally, we will evaluate the performance of our models using a variety of metrics, such as accuracy, precision, and recall, and compare them to traditional approaches for malaria diagnosis.

The ultimate objective of this research is to create a reliable and effective automated method for diagnosing malaria that may be employed in environments with limited resources. We can enhance malaria early diagnosis and treatment, lowering the total health burden of the illness, by utilizing deep learning to analyze blood tissue pictures.

2. PROPOSED SYSTEM

2.1 ARCHITECTURE DIAGRAM



EXPLANATION

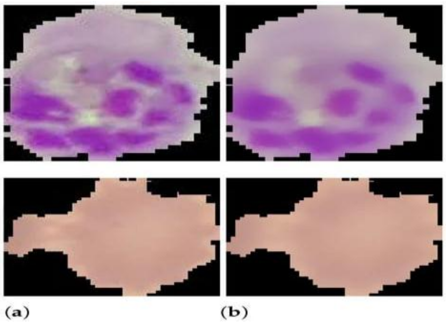
Upload the blood tissue images as dataset. The datasets is preprocessed such as image reshaping, resizing and conversion to the array form. The train dataset is used to train the CNN model.

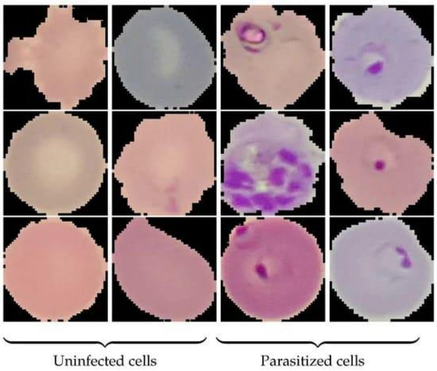
After the model is trained, the blood tissue image dataset undergo the testing model. The model is deployed using Django framework. Atlast the malaria is predicted.

LIST OF MODULES

2.2 Import the Given Image from the Dataset

We have to import our data set using the Keras preprocessing image data generator function. We also create size, rescale, range, zoom range, and horizontal flip. Then we import our image dataset from the folder through the data generator function. Here we set to train, test, and validate; we also set target size, batch size, and class mode. From this function, we have to train using our own created network by adding layers of CNN.





2.3 To Train the Module from the Given Image Dataset

We add training steps for each epoch while utilising the classifier and fit generator algorithms to train our dataset, and we then add up the epochs, validation steps, and validation data. We can train our dataset using this information and this is basis process.

2.4 Convolutional layers:

Convolutional Neural Networks (CNNs) are a type of deep learning algorithm that is commonly used for image classification tasks such as malaria prediction using blood tissue images. Here's a brief explanation of how CNNs work:

Convolutional layers: In this layer, the CNN applies a set of filters to the input image to extract relevant features. Each filter looks for specific patterns in the image, such as edges, curves, or shapes. The output of this layer is a set of feature maps that represent the extracted features.

Pooling layers: The pooling layer down samples the feature maps and reduces the number of parameters needed for the network. It helps to make the CNN more robust to small variations in the input image.

Fully connected layers: These layers take as input the flattened output of the earlier layers and classify the image into malaria-positive or malaria-negative based on the extracted features. These layers are trained using back propagation to adjust the weights of the network and improve its accuracy.

To train the CNN algorithm for malaria prediction using blood tissue images, a large dataset of malaria-positive and malaria-negative blood tissue images is needed. The CNN model then goes through an iterative process of training, validation and testing to optimize the accuracy of malaria prediction.

Overall, CNNs offer an effective and efficient approach for malaria prediction using blood tissue images, providing a potential solution for accurately and quickly diagnosing the disease.

2.5 Alex NET

Convolutional neural network (CNN) architecture called AlexNet is made to identify objects in photos. It was created specifically for the Image Net Large Scale Visual Recognition Challenge (ILSVRC) in 2012. There, it earned a top-5 error rate of 15.3%, which was far better than the prior state of the art. Eight layers make up the architecture, with five convolutional layers at the bottom, two fully linked layers above them, and a soft ax output layer at the top. There are over 60 million parameters in it.

Because of its architecture, AlexNet is able to learn intricate characteristics directly from unprocessed photos. Convolutional layers make up the first five layers of AlexNet, which are each followed by a max-pooling layer. The image's characteristics that are pertinent to the classification job are extracted using convolutions. The picture is down sampled using max-pooling, which also lowers the amount of parameters in the network.

Linear Rectified Units Instead of the sigmoid, AlexNet employs the ReLU activation function. ReLU computes more quickly and aids in preventing the vanishing gradient issue that might happen when using sigmoid.

Normalisation of Local Reaction To normalise each neuron's output based on its nearby neurons, LRN is utilised in the first and second convolutional layers. By enhancing contrast between various areas of the image, this is supposed to aid generalisation.To avoid overfitting, AlexNet uses dropout in the fully linked layers. In order to force the network to learn more robust features, dropout randomly removes part of the neurons during training.

Utilising stochastic gradient descent (SGD) with momentum, the network's weights are modified throughout training. To optimise its parameters for the classification task, the network is trained using a sizable dataset of blood tissue pictures of malaria-positive and malaria-negative individuals. After being trained, the AlexNet algorithm is capable of classifying photos of raw blood tissue.

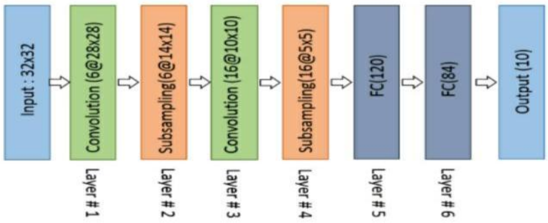
Layer	# filters / neurons	Filter size	Stride	Padding	Size of feature map	Activation function
Input	-	-	-	-	227 x 227 x 3	-
Conv 1	96	11 x 11	4	-	55 x 55 x 96	ReLU
Max Pool 1	-	3 x 3	2	-	27 x 27 x 96	-
Conv 2	256	5 x 5	1	2	27 x 27 x 256	ReLU
Max Pool 2	-	3 x 3	2	-	13 x 13 x 256	-
Conv 3	384	3 x 3	1	1	13 x 13 x 384	ReLU
Conv 4	384	3 x 3	1	1	13 x 13 x 384	ReLU
Conv 5	256	3 x 3	1	1	13 x 13 x 256	ReLU
Max Pool 3	-	3 x 3	2	-	6 x 6 x 256	-
Dropout 1	rate = 0.5	-	-	-	6 x 6 x 256	-

Layer	# filters / neurons	Filter size	Stride	Padding	Size of feature map	Activation function
.	.	.	.	.	.	.
.	.	.	.	.	.	.
.	.	.	.	.	.	.
Dropout 1	rate = 0.5	-	-	-	6 x 6 x 256	-
Fully Connected 1	-	-	-	-	4096	ReLU
Dropout 2	rate = 0.5	-	-	-	4096	-
Fully Connected 2	-	-	-	-	4096	ReLU
Fully Connected 3	-	-	-	-	1000	Softmax

2.5.1 Alexnet Architecture

AlexNet is a popular deep convolutional neural network model that was proposed by Krizhevsky et al. in 2012. It won the ImageNet Large Scale Visual Recognition Challenge (ILSVRC) in 2012, achieving a top-5 error rate of 15.3%. The architecture of AlexNet consists of 5 convolutional layers, 3 max pooling layers, and 3 fully connected layers. Each convolutional layer is followed by a ReLU activation function, and each max pooling layer uses a pool size of 3x3 with a stride of 2 pixels.

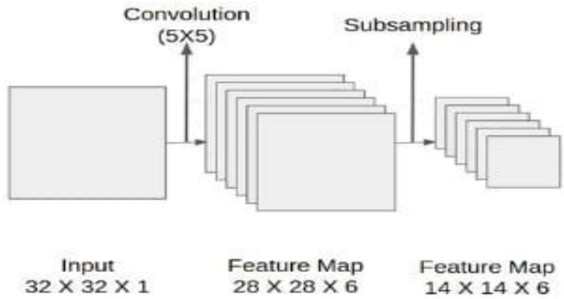
The first convolutional layer in the AlexNet architecture has 96 filters, each with the size of 11x11 pixels and a stride of 4 pixels. This layer is followed by a max pooling layer that reduces the spatial dimensions of the output by half. The second convolutional layer consists of 256 filters with a size of 5x5 pixels and a stride of 1 pixel. Similarly to the first layer, this layer is followed by a max pooling layer. The third, fourth, and fifth convolutional layers each have 384, 384, and 256 filters, respectively, with a size of 3x3 pixels and a stride of 1 pixel.

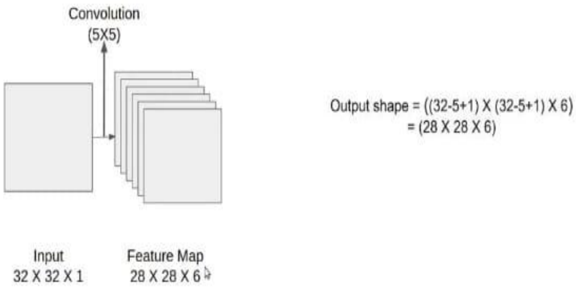


Architecture of AlexNet

2.6 LENET

One of the first pre-trained models was Lenet-5, which Yann LeCun and colleagues developed in the research article Gradient-Based Learning Applied to Document Recognition published in 1998. For reading both machine-printed and handwritten characters, they employed this architecture. This model's simplistic and uncomplicated architecture was largely responsible for its success. It is an image categorization convolution neural network with many layers.





2.6.1 Architecture of Lenet

Published on March 18, 2021, and updated on March 30th, 2021 by Shipra Saxena

Deep Learning and Advanced Computer Vision Videos

Pre-trained models are a quick and inexpensive way to solve deep learning issues with transfer learning. Recognise the Lenet-5 architecture as described by the authors.

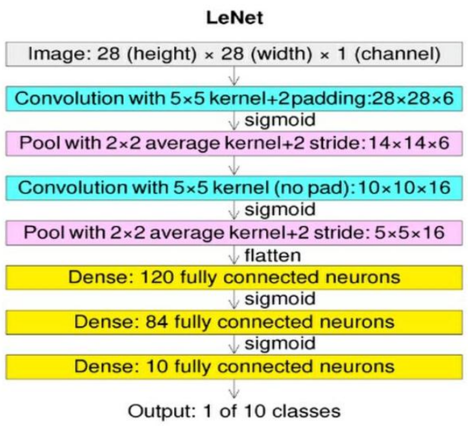
One of the first pre-trained models was Lenet-5, which Yann LeCun and colleagues developed in the research article Gradient-Based Learning Applied to Document Recognition published in 1998. For reading both machine-printed and handwritten characters, they employed this architecture.

This model's simplistic and uncomplicated architecture was largely responsible for its success. It is an image categorization convolution neural network with many layers.

Lenet-5 is among the early pre-trained models that Yann LeCun and colleagues suggested in the research article Gradient-Based Learning Applied to Document Recognition published in 1998. This design was used to identify both machine-printed and handwritten characters.

This model's uncomplicated construction was primarily responsible for its success. A multi-layer convolution neural network is used to classify images.

Let's examine Lenet-5's architecture. The network is known as Lenet-5 since it contains five layers with learnable parameters. It combines average pooling with three sets of convolutional layers. We have two completely linked layers following the convolution and average pooling layers. Finally, a Softmax classifier places the photos in the appropriate class. This model's input is a 32 by 32 grayscale picture, therefore there is just one channel.



Architecture of LeNet

2.7 DEPLOYMENT

Deploying the model in Django Framework and predicting output In this module the trained deep learning model is converted into hierarchical data format file (.h5 file) which is then deployed in our django framework for providing better user interface and predicting the output whether the given material image is Fabric , Glass ,Plastic .

3. ASK ALGORITHM

Step 1: The input image is first processed to remove unwanted noise from the RGB cell image.

Step 2: The preprocessed image is then given as an input to the segmentation stage.

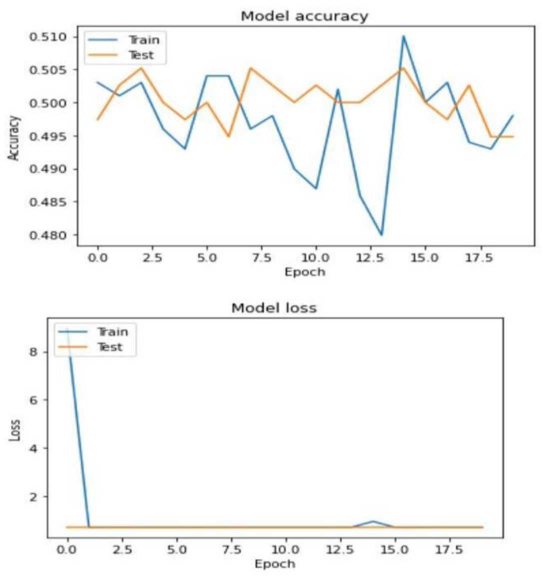
Step 3: The image is segmented to extract the region of interest from the image, and we get the segmentation image.

Step 4: We then feed the images as an input to the feature extraction stage, where the output will be the feature vectors.

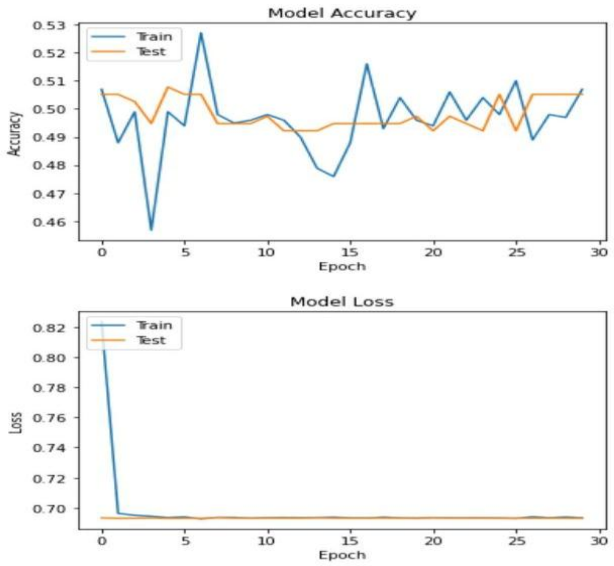
Step 5: The next stage is the classification stage, where the input will be the feature vectors, and output is the classified label as parasitic and non-parasitic.

4. CONCLUSION

It focused how image from given dataset (trained dataset) and past data set used to predict the pattern of malaria diseases using CNN model. This brings some of the following insights about malaria disease prediction. The major benefit of the CNN classification framework is the ability to classify images automatically. Malaria disease is a blood tissue disorder that slowly destroys memory and thinking skills and often can't be remedied because the patients are diagnosed too late with the diseases. In this study, we have discussed the overview of methodologies for detecting the abnormalities in blood tissue images which includes collection of blood tissue image data set, pre-processing techniques, feature extraction techniques and classification schemes.



MODEL ACCURACY OF ALEXNET



MODEL ACCURACY OF LENET

5. FUTURE WORK

Medical department wants to automate the detecting of malaria disease from eligibility process (real time).To optimize the work to implement in Artificial Intelligence environment.

REFERENCES

[1] Wearables Detect Malaria Early in a Controlled Human-Infection Study. Sidhartha Chaudhury, Chenggang Yu, Ruifeng Liu (2022)

[2] Towards an Efficient Prediction Model of Malaria Cases in Senegal.Ousseynou Mbaye, Mouhamadou Lamine Ba1.June, (2019)

[3] Malaria outbreak detection with machine learning methods,july21(2020)

[4] Malaria Epidemic Prediction Model by Using Twitter Data and Precipitation Volume in Nigeria Nduwayezu Maurice,SatyabrataAicha, Han Suk Young, Kim Jung Eon, Kim Hoon,Park Junseok, Hwang Won-Joo,may (2019)

[5] World Health Organization, World Malaria Report, Geneva, Switzerland: WHO, 2018.

[6] M. Spring, M. Polhemus, and C. Ockenhouse, “Controlled human malaria infection,” J. Infect. Dis., vol. 209, no. Suppl 2, pp. S40–S45, 2014.

[7] M. C. Langenberg et al., “Controlled human malaria infection with graded numbers of Plasmodium falciparum NF135.C10- or NF166.C8-infected mosquitoes,” Am. J. Trop. Med. Hyg., vol. 99, no. 3, pp. 709–712, 2018.

[8] M. B. Laurens et al., “A consultation on the optimization of controlled human malaria infection by mosquito bite for evaluation of candidate malaria vaccines,” Vaccine, vol. 30, no. 36, pp. 5302–5304, 2012.

[9] J. E. Epstein et al., “Safety and clinical outcome of experimental challenge of human volunteers with Plasmodium falciparum-infected mosquitoes: An update,” J. Infect. Dis., vol. 196, no. 1, pp. 145–154, Jul. 2007.

[10] United States Food and Drug Administration, “Guidance for industry tox- icity grading scale for healthy adult and adolescent volunteers enrolled in preventive vaccine clinical trials,” 2007. Accessed: Oct. 3, 2021, [Online]. Available: http://www.fda.gov/cber/guidelines.htm

[11] B. Mordmüller et al., “Direct venous inoculation of Plasmodium falci- parum sporozoites for controlled human malaria infection: A dose-finding trial in two centres,” Malar. J., vol. 14, pp. 117, Mar. 2015.

[12] M. Sklar et al., “A three-antigen Plasmodium falciparum DNA prime— Adenovirus boost malaria vaccine regimen is superior to a two-antigen regimen and protects against controlled human malaria infection in healthy malaria-naïve adults,” PLoS One, vol. 16, no. 9, Sep. 2021, Art. no. e0256980.

[13] J. E. Sasaki, D. John, and P. S. Freedson, “Validation and comparison of Actigraph activity monitors,” J. Sci. Med. Sport., vol. 14, no. 5, pp. 411–416, Sep. 2011.

[14] J. Karjalainen and M. Viitasalo, “Fever and cardiac rhythm,” Arch. Intern. Med., vol. 146, no. 6, pp. 1169–1171, Jun. 1986.

[15] J. Radin et al., “Assessment of prolonged physiological and behavioral changes associated with COVID-19 infection,” JAMA Netw. Open, vol. 4, no. 7, Jul. 2021, Art. no. e2115959.