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Malaria Cell ClassificationUsing Transfer Learning

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Abstract: ***In recent years, machine learning techniques, particularly transfer learning, have shown promise in automating malaria cell classification using digital images of blood smears. Transfer learning involves leveraging pre-trained neural networks to extract relevant features from large datasets and applying them to smaller, specialized datasets for improved performance. This abstract provides an overview of the concept of malaria cell classification using transfer learning. It highlights the advantages of using transfer learning, including reduced training time and improved classification accuracy, while addressing challenges such as dataset bias and model interpretability. Further research and development in this area could potentially contribute to the automation and scalability of malaria diagnosis, particularly in resource-limited settings. This study describes a method for classifying malaria cells using convolutional neural networks. It has been evaluated using a standard dataset obtained from the National Library of Medicine, which consists of 27,000microscopic pictures. The accuracy of the neural network has been improved while the total loss has been reduced using the Adam optimizer. Overfitting has been avoided by using dropout regression***

I. INTRODUCTION

The Plasmodium parasite, which infects mosquitoes and infects humans by their bite, causes the deadly illness known as malaria. For efficient treatment and the avoidance of complications, malaria must be diagnosed quicklyand accurately. The most accurate way to diagnose malaria is by microscopic analysis of blood smears, although this process can take a while and requires specialized people. The automated diagnosis of malaria using digital pictures of blood smears has shown encouraging results in recent years thanks to machine learning techniques, notably deep learning. Using pre-trained neural networks to extract pertinent characteristics from huge datasets and apply them to smaller, more focused datasets for enhanced performance, transfer learning, a sort of machine learning technology, has emerged as a potent strategy for classifying malaria cells.

Transfer learning in malaria cell classification involves using a pre-trained neural network, such as VGG, Res- Net, or Inception, which has been trained on a large dataset from a different domain, such as general image classification tasks. The pre-trained network is then fine-tuned using a smaller dataset of malaria-infected and uninfected blood smear images to learn specific features related to malaria cells. The extracted features are thenused to classify blood smear images as infected or uninfected. The advantages of using transfer learning in malaria cell classification include reduced training time, improved classification accuracy, and the ability to work with limited datasets, which is common in medical image analysis. However, challenges such as dataset bias, domain adaptation, and model interpretability need to be addressed to ensure reliable and clinically relevant results.

In conclusion, transfer learning has emerged as a promising approach for malaria cell classification, leveraging pre-trained neural networks to improve accuracy and efficiency in malaria diagnosis. Further research and development in this area could potentially contribute to the automation and scalability of malaria diagnosis, particularly in resource-limited settings where access to skilled

II. RELATED WORK

Several studies have been conducted on malaria cell classification using transfer learning, showcasing the effectiveness of this approach. Here are some relevant works". Malaria Parasite Detection in Blood Smear Images Using Deep Transfer Learning" by Rajaraman et al. (2018): This study utilized transfer learning with convolutional neural networks (CNNs) to classify blood smear images as infected or uninfected. They fine-tuneda pre-trained CNN model, Inception-V3, on a dataset of blood smear images and achieved high accuracy in malaria parasite detection.

"Malaria Detection Using Deep Learning Techniques: A Comparative Study" by Hussein et al. (2020): This study compared the performance of different transfer learning models, including VGG-16, ResNet-50, and Inception- V3, for malaria cell classification. They found that transfer learning significantly improved the accuracy of malaria detection compared to training from scratch, with Inception-V3 achieving the highest accuracy. "Malaria Cell Image Classification Using Deep Learning" by Acharya et al. (2019): This study employed transfer learning with pre-trained VGG-16 and ResNet-50 models for malaria cell classification.

They also introduced a novel technique called "patch-based augmentation" to increase the training dataset and improve the model'sperformance. The results demonstrated the efficacy of transfer learning in malaria cell classification.

"Malaria Diagnosis using Convolutional Neural Networks with Microscopic Blood Smear Images" by Ghosh et al. (2020): This study compared the performance of various transfer learning models, including VGG-16, VGG-19, Inception-V3, and ResNet-50, for malaria cell classification. They found that transfer learning outperformed training from scratch, with VGG-19 achieving the highest accuracy.

"Automatic Malaria Parasite Detection in Thin Blood Smear Images using Deep Convolutional Neural Networks" by Singh et al. (2019): This study employed transfer learning with pre-trained VGG-16 and VGG-19 models for malaria parasite detection. They also proposed an ensemble model to combine the predictions of multiple models for improved accuracy.

These related works collectively highlight the effectiveness of transfer learning in malaria cell classification, showcasing its potential for accurate and efficient malaria diagnosis using digital blood smear images.

III. PROPOSED WORK

The proposed system uses digital microscopic images that are obtained from stained blood smears as a source image, later it classifies the given source image as either infected or non- infected falciparum malaria. This can be made possible through two functional stages namely image acquisition and recognition of infected malaria using proposed VGG-19 model. Figure 1 shows the functional flow diagram of the proposed work and rest of the section provides detailed discussion about image acquisition and infected malaria recognition.

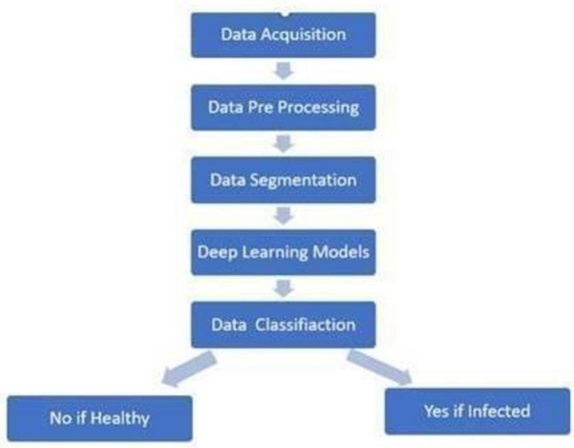

Fig. 1. Proposed model

IV. METHODOLOGY

In this study, an existing VGG is considered as a reuse model because it shows the promising performance in recognizing infected malaria compared to other state-of-the-art convolution neural network viz., LetNet- 5,AlexNet and GoogleLeNet for the dataset in hand.

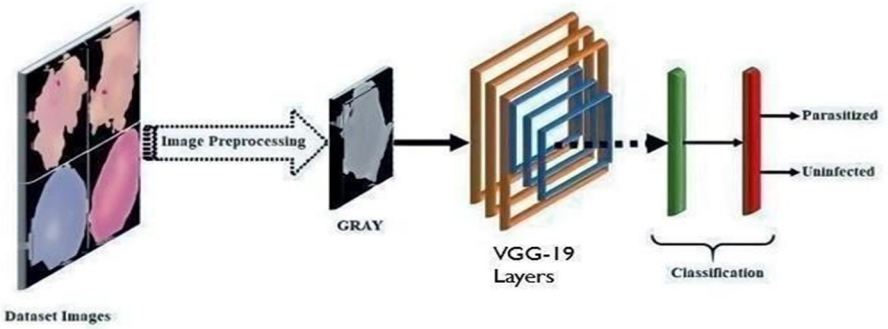

Figure 2. Model Diagram Used in Classification of Malaria Parasite

Figure 3. Dataset of Uninfected Cells

Figure 4. Dataset of Infected Cells.

Perform pre-processing on the images, such as resizing to a consistent size, normalization, and augmentation techniques like rotation, flipping, and zooming, to increase the diversity and variability of the training data. Data augmentation is particularly important when working with limited datasets. All the images were resized to be 244*244 pixels. For the performance evaluation of the CNN model, the labeled images were randomly shuffled and split into a training set consists of a total of 27,000 microscopic images of diseased and healthy human blood samples. The taken data has been divided into 13750 uninfected and 13250 infected cells images. The data is stored in a PNG form.

Choose a pre-trained neural network model, such as VGG19 which has been trained on a large dataset from a different domain, usually general image classification tasks. Remove the fully connected layers of the pre-trained model, which serve as the top layers responsible for the final classification, and retain the convolutional layers as feature extractors

Layer (type)	Output Shape	Param #
input_1 (InputLayer)	[(None, 224, 224, 3)]	0
block1_conv1 (Conv2D)	(None, 224, 224, 64)	1792
block1_conv2 (Conv2D)	(None, 224, 224, 64)	36928
block1_pool (MaxPooling2D)	(None, 112, 112, 64)	0
block2_conv1 (Conv2D)	(None, 112, 112, 128)	73856
block2_conv2 (Conv2D)	(None, 112, 112, 128)	147584
block2_pool (MaxPooling2D)	(None, 56, 56, 128)	0
block3_conv1 (Conv2D)	(None, 56, 56, 256)	295168
block3_conv2 (Conv2D)	(None, 56, 56, 256)	590080
block3_conv3 (Conv2D)	(None, 56, 56, 256)	590080
block3_conv4 (Conv2D)	(None, 56, 56, 256)	590080
block3_pool (MaxPooling2D)	(None, 28, 28, 256)	0
block4_conv1 (Conv2D)	(None, 28, 28, 512)	1180160
block4_conv2 (Conv2D)	(None, 28, 28, 512)	2359808
block4_conv3 (Conv2D)	(None, 28, 28, 512)	2359808
block4_conv4 (Conv2D)	(None, 28, 28, 512)	2359808
block4_pool (MaxPooling2D)	(None, 14, 14, 512)	0
block5_conv1 (Conv2D)	(None, 14, 14, 512)	2359808
block5_conv2 (Conv2D)	(None, 14, 14, 512)	2359808
block5_conv3 (Conv2D)	(None, 14, 14, 512)	2359808
block5_conv4 (Conv2D)	(None, 14, 14, 512)	2359808
block5_pool (MaxPooling2D)	(None, 7, 7, 512)	0
flatten (Flatten)	(None, 25088)	0
dense (Dense)	(None, 2)	50178

Total params: 20,074,562
Trainable params: 50,178
Non-trainable params: 20,024,384

Figure 5. Architecture of the model used

Add new fully connected layers on top of the retained convolutional layers of the pre-trained model to adapt it tothe specific malaria cell classification task. Train the model on the training dataset using transfer learning, where the weights of the convolutional layers are frozen and only the weights of the newly added fully connected layers are updated during backpropagation. Fine-tuning the model helps it to learn relevant features from the malaria cell images.

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Evaluate the trained model on the validation set to determine its performance in terms of accuracy, precision, recall, F1 score, and other relevant metrics. If necessary, adjust the model architecture or hyper-parameters to optimize performance.

Once the model has been fine-tuned and evaluated, use the test set to assess its generalization performance and estimate its real-world performance.

After satisfactory performance, the trained model can be deployed in a clinical or real-world setting for automated malaria cell classification, which could potentially aid in malaria diagnosis and treatment.

V. RESULT AND DISCUSSIONS

The first experiment we conducted to obtain the best accuracy was to establish the number of training epochs forour model. The table below displays the accuracy results for various numbers of epochs.

Number of epochs	Accuracy of the model
10	64.18%
20	82.84%
30	86.57%
40	91.04%
50	91.79%

Table I. Accuracy of the Model

The accuracy rises after 50 training iterations, as seen in the table above. The accuracy measure was used to determine the output's precision. As can be observed, accuracy increases and loss decreases with each epoch.

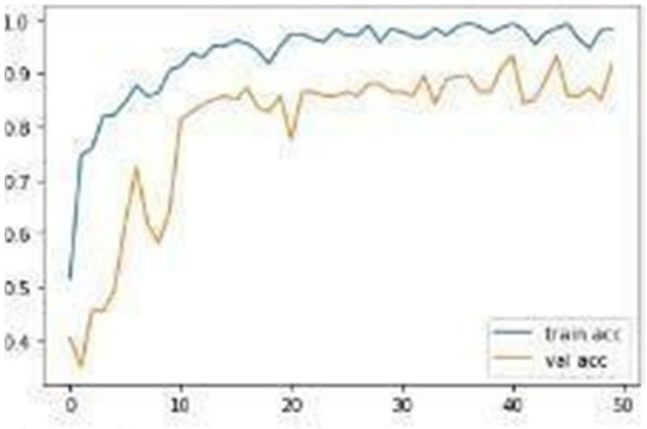

Figure 6(a). Accuracy of model per epoch

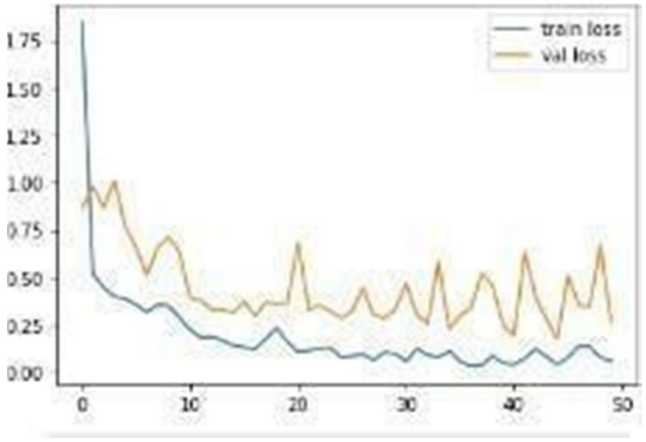

Figure 6(b). Loss of model per epoch

During training the model, we also experimented with using several optimizers. Yet, the maximum accuracy wasobtained when the Adam optimizer was used.

```
Total params: 25,100,046
Trainable params: 25,100,046
Non-trainable params: 0
```

Figure 7. Total Number of parameters in the model

There were 25,100,046 parameters in the model. After adjusting a number of hyper-parameters, it was discoveredthat the model had an optimal accuracy of 91.79% after 50 iterations of training.

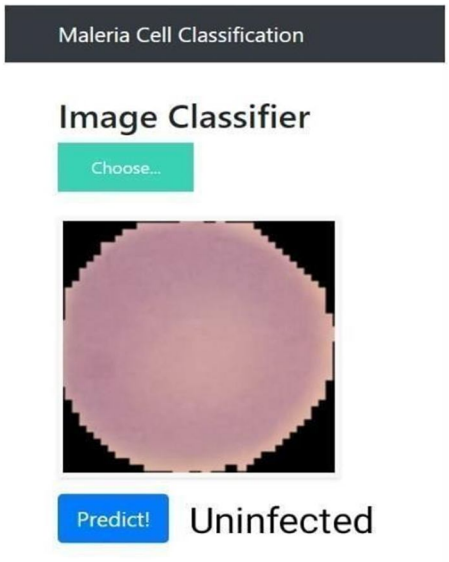

Figure 8. Prediction of Uninfected cell image

Figure 9. Prediction of Infected cell image

VI. CONCLUSION

In conclusion, malaria is a serious disease that affects millions of people around the world. Early detection and accurate diagnosis are critical for effective treatment and management of the disease. In recent years, machine learning techniques such as transfer learning have shown great promise in improving the accuracy of malaria cellclassification from microscopy images.

The proposed transfer learning based VGG19 model is obtained with an accuracy measure of 91.79%. Hence itis implementable with moderate computing infrastructure. Thus, it reduces the dependency of skilled techniciansin rapid diagnosis of malaria. Further, unification of support vector machine on VGG19 indicates better performance when compared to other CNN based models. Though there are four different types of malaria parasites, the proposed system is trained to recognize infected and non-infected falciparum malaria parasites. Infuture, proposed idea couldbe extended to classify other types of malaria parasite also. Overall, the use of transfer learning in malaria cell classification holds great promise for improving the accuracy and speed of diagnosis, andhas the potential to significantly impact global efforts to combat malaria.

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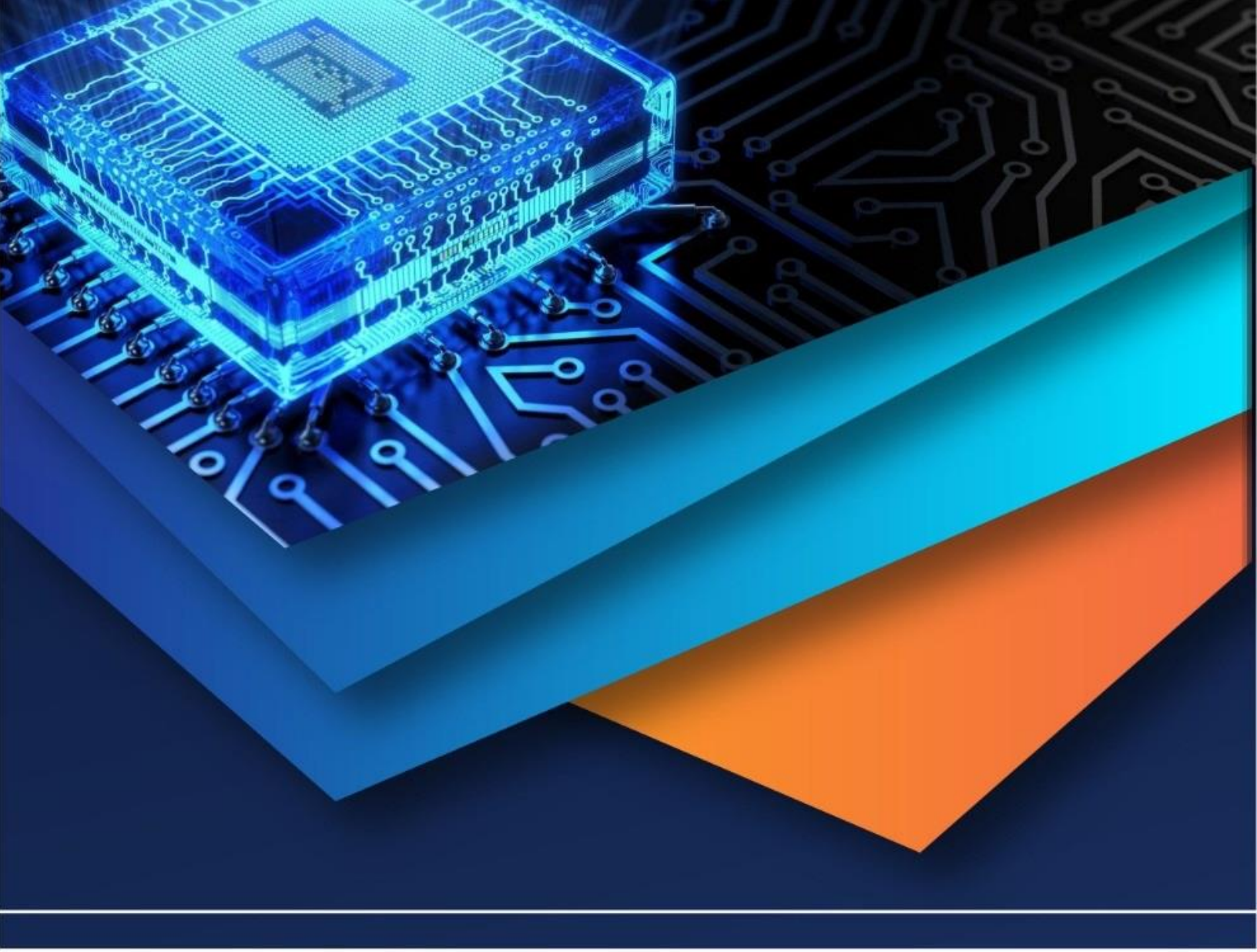

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