USING DEEP LEARNING, FOLDSCOPE AND MOBILE BASED APPLICATION FOR DETECTING MALARIA PARASITE

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Abstract: Malaria is an infectious disease which is caused by plasmodium parasites. Several image processing and deep learning techniques have been employed to diagnose malaria, using its spatial features extracted from microscopic images. In this work, a model and a technique are introduced for identifying infected falciparum malaria parasites using a transfer learning approach and foldscope *(Origami-Based Paper Microscope)*. transfer learning approach can be achieved by unifying the existing pre-trained model. A malaria digital corpus generated by acquiring blood smear images of infected and non-infected malaria patients and obtaining the result which shows the potential of transfer learning in the field of malaria diagnosis. and further testing on the images taken from mobile using foldscope.

IndexTerms **- cell-phone camera, Deep learning, foldscope, Malaria, Transfer learning, ResNet-50, SoftMax.**

I. INTRODUCTION

Malaria is caused by protozoan parasites of the genus Plasmodium that are transmitted through the bites of infected female Anopheles mosquitoes and that infect the red blood cells. Typical symptoms of malaria include fever, fatigue, headaches, and in severe cases seizures and coma leading to death. Hundreds of millions of blood films are examined every year for malaria, which involves manual counting of parasites and infected red blood cells by a trained microscopist [4]. Malaria is a curable disease with drugs available for treatment, including drugs that can help prevent malaria infections in travellers to malaria-prone regions. However, there exists no effective vaccine against malaria yet, although this is an area of active research and field studies. Accurate parasite counts are essential not only for malaria diagnosis. However, microscopic diagnostics is not standardized and depends heavily on the experience and skill of the microscopist. For false-positive cases, misdiagnosis leads to unnecessary use of antimalarial drugs and suffering from their potential side-effects, such as nausea, abdominal pain, diarrhoea, and sometimes severe complications. The actual microscopic examination of a single blood slide, including quantitative parasite detection and species identification takes a trained microscopist 15-30 minutes, A high optical magnification needed (up to 100x) for malaria diagnosis. Considering that hundreds of thousands of blood slides are manually inspected for malaria every year, this amounts to a huge economic effort required for malaria diagnosis. Although malaria can be diagnosed in many different ways, there is room for improvement for current malaria diagnostic tests including reducing cost, increasing specificity and improving ease of use. Deep learning can be implemented in the classification of cell images which can prevent the wrong diagnostic decisions. Deep learning is an area of machine learning, which performed exceptionally well in many non-medical fields [5] The applications of deep learning have been limited in the medical field due to lack of expert knowledge in that field and privacy concerns. But, in recent years deep learning was used in many medical fields [6].

II. DATA COLLECTION

The dataset contains 27,558 images of infected and uninfected cells. The Dataset is available on the official website of the National Library of Medicine (NLM) [7]. The difference between malaria-infected and uninfected cells from a dataset, chosen randomly, can be seen in **Figure 1**. The work of segmenting the data was done by applying a level set-based algorithm [8].

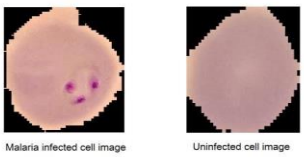

Fig.1: Image of Infected and Uninfected cells

III. DEEP LEARNING

Deep learning is the latest trend in machine learning, which has already boosted performance in many non-medical areas. Deep learning can be seen as an extension of the well-known multi-layer neural network classifiers trained with back-propagation, Deep learning is supervised learning, it requires large training sets. This is the reason why medical applications have been among the last applications to adopt deep learning [9]. First, we need to apply deep learning to malaria diagnosis. Then a convolutional neural network should be used to discriminate between infected and uninfected cells in thin/thick blood smears, after applying a conventional level-set cell segmentation approach. This is an ideal application for deep learning because of images of segmented red blood cells. Deep learning models such as Artificial Neural Networks (ANN) and CNN are feedforward networks

with one input layer, one output layer and many hidden layers. These networks can be trained by backpropagation [3]. Deep learning does not require the design of handcrafted features, which is one of its biggest advantages.

IV. TRANSFER LEARNING

In transfer learning firstly a base network is trained on a base dataset and the features learned from the first task are repurposed or transferred to a second network to train on a second dataset and task. This process will work if the features are suitable for both base and target tasks, instead of only base tasks [10]. Deploying pre-trained models on similar data have shown good results in image classification related tasks. Microsoft ResNet Model which takes weeks to train on modern hardware. These models can be downloaded and integrated with new models which take images as input to bring better results.

V. MICROSOFT RESNET MODEL

ResNet is the short form for Residual Network shows in **Figure 2**. Over the years deep convolutional neural networks have made a series of breakthroughs in the field of image recognition and classification. Going deeper to solve more complex tasks and to improve classification or recognition accuracy has become a trend. But, training deeper neural networks has been difficult due to problems such as vanishing gradient problem [12] and degradation problem. Residual learning tries to solve both these problems [13].

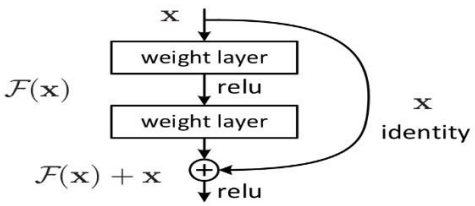

Fig.2: Residual learning: building block

In neural networks, every layer learns low- or high-level features while being trained for the task at hand. In residual learning instead of trying to learn features, the model tries to learn some residual. As we can see in Fig.3 the input 'x' is being added as a residue to the output of the weight layers and the activation is carried out. ReLU activations are being used in the ResNet model. ResNet50 is a 50-layer Residual network and has other variants such as ResNet101 and ResNet152 [11]. Using ResNet as a pre-trained model for medical image classification has brought good results [14].

VI. PROPOSED MODEL

As shown in **Figure 3**. The image will enter the ResNet50 layer with the pre-trained weights and the last layer is a classic fully connected dense layer with SoftMax activation. As shown in **Figure 4** the proposed model consists of 2 layers, Pre-trained ResNet layer, flatten layer, dense layer with 512 units, dropout layer with 30% drop out and final dense layer (output layer with 2 units). Pre-Trained Weights for the ResNet50 model are to be imported. The input data will be trained with the pre-trained weights and the only layer which is learning with backpropagation is the dense layer. Few layers such as Batch Normalization (BN) layers shouldn't be frozen because the mean and variance of the dataset will be hardly matching the mean or variance from pre-trained weights. So, auto-tuning is adapted for the BN layers in ResNet50, i.e. few of the layers which are in the top of ResNet50 shouldn't be frozen. SoftMax is good for multi-class classification. We can also use sigmoid activation which is better than SoftMax for binary classification.

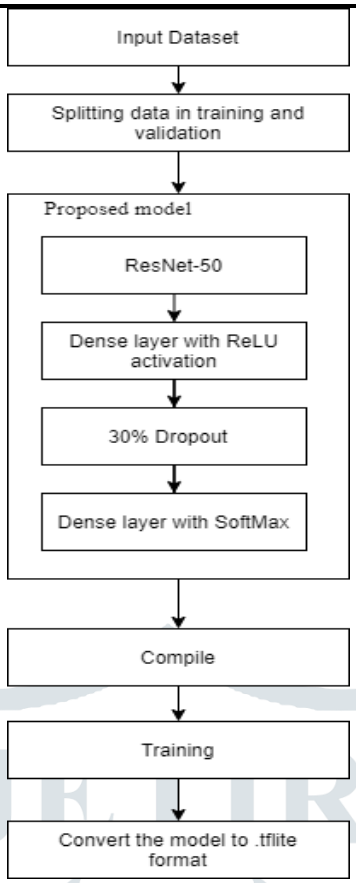

Fig.3: Proposed Architecture

VII. EXPERIMENT

I. Splitting Data

The total number of infected and uninfected cell images in the dataset are 27,558. The split was done with 70, 15,15 per cent for training, validation and testing. Finally, after the split, training data has 19,292 cell images (both infected and uninfected). Whereas, validation data has 4,133 cell images each and testing data has 5512 cell images

II. Data Processing

The input image for the ResNet50 layer should be of size 224*224. So, all the images have to be resized to the target size of 224*224. We've given the batch size to be 20. Which makes 36 steps for each epoch of training. Steps per epoch for training are calculated by dividing the total objects in training with batch size. After Pre-processing and before training of the network the model has to be compiled. Few parameters such as optimizer, loss function and metrics to be calculated during the training have to be declared. The optimizer along with loss function are the key elements that enable the network to work on the data. Optimizer, in simple terms, sets the learning rate (4e-5) of a neural network. The optimizer used for this model is Adam optimizer. Choosing a loss function can also be a difficult task. The loss function used to find the loss for this model is Categorical-Cross Entropy.

III. Training the model

A neural network learns through backpropagation. Top layers in the ResNet50 aren't frozen, i.e. those top layers learn through backpropagation whereas other layers of ResNet50 are frozen. The weights getting updated during back-propagation is called fine-tuning [15]. Fine-tuning of the top layers in the ResNet50 should be done because there is no guarantee that the mean and variance of those layers will be similar to the mean and variance of our dataset

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Model: "sequential_1"
_________________________________________________________________
Layer (type)                 Output Shape              Param #
=================================================================
resnet50 (Model)             (None, 7, 7, 2048)        23587712
_________________________________________________________________
flatten_1 (Flatten)          (None, 100352)            0
_________________________________________________________________
dense_1 (Dense)              (None, 512)               51380736
_________________________________________________________________
dropout_1 (Dropout)          (None, 512)               0
_________________________________________________________________
dense_2 (Dense)              (None, 2)                 1026
=================================================================
Total params: 74,969,474
Trainable params: 74,916,354
Non-trainable params: 53,120
_________________________________________________________________
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Fig.4: shows the Summary of the model

VIII. RESULT

The metrics measured during the training of the dataset were Accuracy and Loss. These metrics were measured for both training and validation data, the model took several hours for training. The accuracy and loss of both training and validation data are tabulated in the table below.

Metrics	value
Training accuracy	96.41%
Validation accuracy	95.2%
Training Loss	0.035
Validation Loss	0.048

Table 1: Training Performance

IX. MAGNIFYING DEVICE

The ideal hardware solution for microscopic malaria diagnosis would be a small portable slide reader into which a blood slide could be inserted and which would then output the parasitaemia. Small camera-equipped computing devices, such as smartphones, which can be attached to a magnifying device and can then compute the parasitaemia automatically, using deep learning. Modern smartphones became powerful computing devices and their cameras provide sufficient resolution for malaria diagnosis. Small magnifying devices that can be attached to a smartphone's camera, allowing true optical magnification compared to mere digital zooming, are commercially available. We are using Foldscope which gives a 140x magnification, and Smartphone zooming can multiply this to give more magnification [16].

X. IMPLEMENTATION

First, take the blood sample from the patient on a slide and place it under the foldscope. then launch the dr.malaria application and place the camera on the eyepiece of the foldscope such that microscopic image is visible on the mobile screen then capture the image and press diagnose button which will predict whether the blood sample is infected or not infected as shown in **Figure 5**.

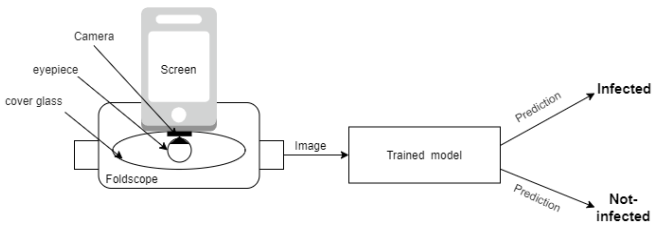

Fig.5: project architecture

XI. CONCLUSION

In summary, a foldscope platform design using a cell-phone to view blood smear for detecting malaria parasite is shown for the first time. The Foldscope is a simple, low-cost, design capable of easily being adapted to multiple mobile device platforms, it gives a magnification of 140x and we can further increase the magnification using the zoom feature in cell-phone camera. Device resolution was determined to be sufficient for observing malaria-infected cells in blood smear, Resolution measurements for the

proposed system were important in determining the number of fields that would be required to determine accurate parasitemia measurements within an infected sample. Detection of malaria presence, parasitemia and strain information for a given sample will be converted into a picture or it can be detected directly through our application using deep learning. We have trained our model on resnet-50 architecture which is proved to be the best choice for training [7] After training the model we have converted the model from .h5 format to. tflite format so that it can run on low powered devices, Using the Android Studio we have developed an application and used the .tflite format to run inference. Finally, it can display whether the image of blood smear taken from mobile using foldscope contains parasites or not.

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