

Malaria Detection in Blood Cell Images using ResNet50

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Abstract—Malaria is a very infectious blood disease that is caused by female anopheles mosquito. This disease harms animals also along with humans. If it is not diagnosed properly in the early stage than it can cause muscular paralysis or even death of the patient in worst case. Early detection of malaria can help in reducing deaths everywhere around the world. Malaria is commonly detected under microscopic examination but the accuracy depends on the blood smear quality and the expertise of the technician in classifying the parasitized and the uninfected cells. In ML techniques meaningful feature representation lies at the core of their success to accomplish desired results. The process demands expertise in analyzing the variability in size, background, angle, and position of the region of interest on the images. To overcome challenges of devising hand-engineered features that capture variations in the underlying data, Deep Learning has emerged as a highly beneficial solution in the diagnosis of the disease, malaria. Convolutional neural networks are the most popular neural networks in image classification and image recognition tasks. This research paper focuses on Transfer learning, a method of deep learning, for malaria cell-image classification.

In this study, the performance of pre-trained CNN namely ResNet50 is evaluated. ResNet50 is used as a feature extractor is used to classify parasite and uninfected cells to aid in advanced disorder screening. This model outperforms the majority of previously produced models over a wide range of accuracy metrics.

Keywords— Deep Learning, Malaria Detection, Image Classification, Convolutional Neural Network, Transfer Learning, ResNet50 model

I. INTRODUCTION

Malaria is a mosquito-borne blood disease caused by the Plasmodium parasites transmitted through the bite of the female Anopheles mosquito. The plasmodium parasites are spread in the human liver, affect the red blood cells and develops into life-threatening symptoms. The typical symptoms of malaria are fever, headache, tiredness, vomiting and it may lead to coma and death in severe cases. This disease not only harms humans but also animals.

According to the estimation of World Health Organization (WHO), in the year 2021, more than two hundred million cases of malaria have been reported and more than 90% of the cases are in the African region. Malaria causes ailment and death in large numbers causing drastic effects on the national economy of a country. It is a genuine cause of worry for the African countries. Early detection of malaria ensures appropriate diagnostic process and increase the chances of the patient being cured.

Blood sample examination is conducted for disease diagnosis and gives a very reliable result. In pathology labs, the blood samples are collected and the diagnosis of malaria

infection is done by identifying the parasites in blood slides through a microscope by the experts. Giemsa staining is a chemical process is used in the detection of malaria parasites. As per the WHO protocol, there are various techniques involving intensive examination that are used in the detection of malaria. In manual testing, the clinician needs to observe 5000 cells at 100X magnification. This process is time-consuming and exhausting. To make the diagnosis faster polymerase chain reaction (PCR) and rapid diagnostic test (RDT) came into consideration. These analyses are fast but less accurate and costly. Detection of parasites from Giemsa blood samples needs trained and experienced technicians. An automatic diagnostic process reduces diagnostic time, improves consistency and can be used as a second opinion for the pathologists.

In the process of applying machine learning (ML) methods to medical data analysis, meaningful feature representation lies at the core of their success to accomplish desired results. A majority of image analysis-based computer-aided diagnosis (CAD) software use ML techniques with hand-engineered features for decision-making. However, the process demands expertise in analyzing the variability in size, background, angle, and position of the region of interest (ROI) on the images. To overcome challenges of devising hand-engineered features that capture variations in the underlying data, Deep Learning (DL), also known as deep hierarchical learning, is used with significant success. DL models use a cascade of layers of non-linear processing units to self-discover hierarchical feature representations in the raw data. Higher-level features are abstracted from lower-level features to aid in learning complex, non-linear decision-making functions, resulting in end-to-end feature extraction and classification. Unlike kernel-based algorithms like Support Vector Machines (SVMs), DL models exhibit improved performance with an increase in data size and computational resources, making them highly scalable.

For images, an important source of information lies in the spatial local correlation among the neighbouring pixels. Convolutional Neural Networks (CNN), a class of DL models, are designed to exploit this information through the mechanisms of local receptive fields, shared weights and pooling. The promising performance of CNNs is possible with the availability of a huge amount of annotated data. With scarcity for annotated medical imagery, Transfer Learning (TL) methods are used where pre-trained DL models are either fine-tuned on the underlying data or used

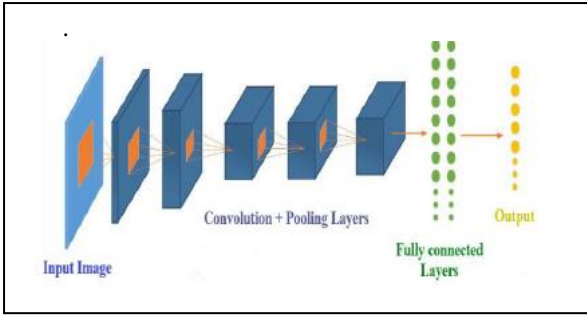


Fig. 1. CNN Architecture

as feature extractors to aid in visual recognition tasks. These models transfer their knowledge gained while learning the generic features from large-scale datasets like ImageNet to the underlying task. The transfer of previously-learned skills to a new situation is generalized, rather than unique to the situation.

A. Related Works

In recent years, a variety of approaches have been proposed for automated detection of malaria parasites.

1) Pattanaik proposed a Computer Aided Diagnosis (CAD) scheme for identifying the presence of malaria parasites in thick blood smears. They performed 10-fold cross validation and achieved an accuracy of 89.10%, sensitivity of 93.90% and specificity of 83.10%. [1]

2) Olugboja presented a comprehensive analysis of different machine learning techniques like Linear Support Vector Machine(SVM), Fine Gaussian SVM, Subspace K-Nearest Neighbors(KNN), Cosine KNN and Boosted KNN for automatic detection of malaria parasite in stained blood smears. Among these, Subspace KNN achieved the best accuracy of 86.3% whereas Fine Gaussian SVM achieved the best True Positive Rate (TPR) of 99.8%. [2]

3) Bibin proposed a novel Deep Belief Network (DBN) approach for malaria detection from blood smear images. The proposed DBN is trained by extracting the features from the images and initializing the visible variables of DBN. This method achieved an F1 score of 89.66%, sensitivity of 97.60% and specificity of 95.92%. [3]

4) Yang developed a deep learning based malaria parasite detection method that can run on smartphones. Their CNN achieved an overall accuracy of 93.46%. [4]

5) Gautham Shekar and his co-authors compared 3 types of CNN models Basic CNN, VGG-19 Frozen CNN, and VGG-19 Fine Tuned CNN. The accuracies were found to be 94, 92 and 96%. [6]

6) Pre-trained convolutional neural networks as feature extractors toward improved malaria parasite detection in thin blood smear images" research article evaluated the performance of pre-trained CNN based DL models as feature extractors toward classifying the parasitized and uninfected cells to aid in improved disease screening and achieved these performance metrics.

Performance metrics.

Models	Accuracy	AUC	Sensitivity	Specificity	F1-score
AlexNet	0.937 ± 0.012	0.981 ± 0.007	0.940 ± 0.017	0.933 ± 0.034	0.937 ± 0.011
VGG-16	0.945 ± 0.015	0.981 ± 0.007	0.939 ± 0.022	0.951 ± 0.019	0.945 ± 0.016
ResNet-50	0.957 ± 0.007	0.990 ± 0.004	0.945 ± 0.020	0.969 ± 0.009	0.957 ± 0.008
Xception	0.890 ± 0.107	0.948 ± 0.062	0.931 ± 0.039	0.835 ± 0.218	0.895 ± 0.100
DenseNet-121	0.931 ± 0.018	0.976 ± 0.023	0.942 ± 0.023	0.926 ± 0.032	0.931 ± 0.017
Customized	0.940 ± 0.010	0.979 ± 0.009	0.931 ± 0.026	0.951 ± 0.030	0.941 ± 0.010

Fig. 2. Performance metrics evaluation for various pretrained CNNs

To summarize, a lot of deep learning methods have been proposed for detecting malaria from cell images. Some of them used large pretrained CNN models for achieving a high classification accuracy, whereas some used custom CNNs for reducing the computational time.

II. PROPOSED WORK

A. Methodology

Convolutional Neural Networks, a type of deep learning architecture have proven to be very useful in image recognition, identification and categorization tasks. CNNs outperform traditional deep learning methods in terms of accuracy and efficiency in disease recognition tasks.

CNNs have multiple layers-convolutional layers, pooling layers, and fully connected layers. The convolutional layer applies filters to the input image to extract features, the pooling layer downsamples the image to reduce computation, and the fully connected layer makes the final prediction. The network learns the optimal filters through backpropagation and gradient descent.

In this report, the overall performance of pre-trained CNN dependent Deep Learning models is examined as an extractor for the classification of parasite and Non-parasite cells. According to many studies it has been found that ResNet outperforms other pretrained networks with respect to accuracy and other performance metrics like specificity, sensitivity, F1 score etc. In this study, for the performance of pre-trained CNN namely ResNet50 is evaluated. ResNet50 is used as a feature extractor is used to classify parasite and uninfected cells to aid in advanced disorder screening.

The input to our model is a RGB (Red Green Blue) image. The image will enter ResNet50 layer with the pretrained weights and the last layer is a classic fully connected dense layer with sigmoid activation. Fig.3 shows the proposed model that consists of 2 layers, Pre-trained ResNet layer and dense layer.

Pre-Trained Weights for the ResNet50 model need to be imported. The input data will be trained with the pre-trained weights and the only layer which is learning with back propagation is the dense layer. Few layers such as Batch Normalization (BN) layers shouldn't be froze 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.

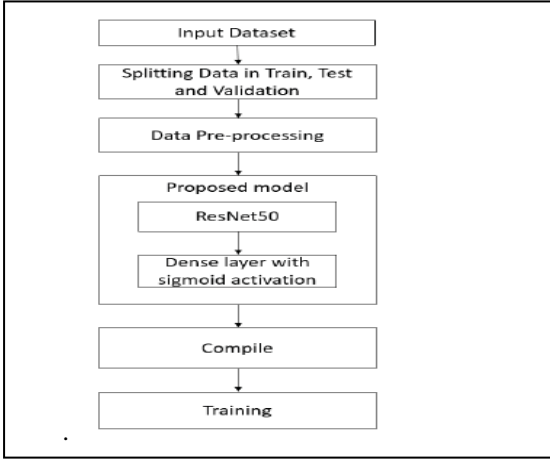


Fig. 3. Proposed Architecture of Model

B. ResNet Architecture

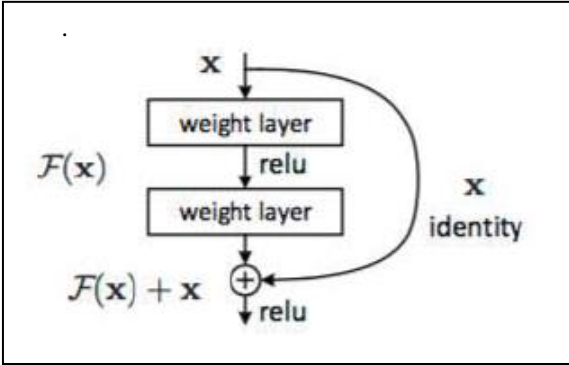
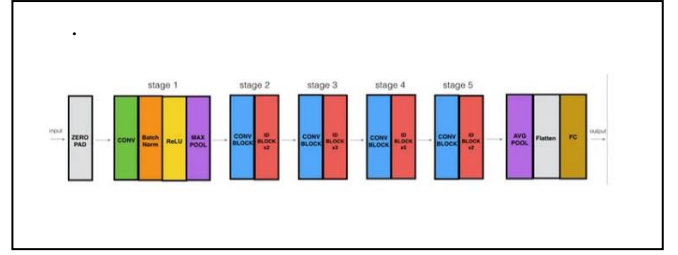


Fig. 4. Residual learning: a building block

ResNet is the short form for Residual Network.

To solve a complex problem, we stack some additional layers in the Deep Neural Networks which results in improved accuracy and performance. The intuition behind adding more layers is that these layers progressively learn more complex features. As we increase the depth of these networks further in order to make the model more robust. Instead of steadily decreasing, after attaining a minimum value, the error rate starts increasing again. This happens due to the exploding and vanishing gradient descent problem which also causes overfitting of the model, hence increasing the error. Fortunately, **Residual Networks** have proved to be quite efficient in solving this problem, as they use a skip connection or a “shortcut” between every two layers along with using direct connections among all the layers. This allows us to take activation from one layer and feed it to another layer, even much deeper in the neural network, hence sustaining the learning parameters of the network in deeper layers.

ResNet-50 is a deep residual that is trained on more than a million images from the ImageNet database. It is a subclass of convolutional neural networks. The 50 refers to the number of



layers that are present. As a result, the network has learned rich feature representations for a variety of images. The details of this ResNet-50 model are:

Zero-padding pads the input with a pad of (3,3)

Stage 1- The 2D Convolution has 64 filters of shape (7,7) and uses a stride of (2,2). Its name is “conv1”. BatchNorm is applied to the channels axis of the input. MaxPooling uses a (3,3) window and a (2,2) stride.

Stage 2- The convolutional block uses three sets of filters of size [64,64,256]. The 2 identity blocks use three sets of filters of size [64,64,256].

Stage 3- The convolutional block uses three sets of filters of size [128,128,512]. The 3 identity blocks use three sets of filters of size [128,128,512].

Stage 4- The convolutional block uses three sets of filters of size [256, 256, 1024]. The 5 identity blocks use three sets of filters of size [256, 256, 1024].

Stage 5- The convolutional block uses three sets of filters of size [512, 512, 2048]. The 2 identity blocks use three sets of filters of size [512, 512, 2048].

Final block- The 2D Average Pooling uses a window of shape (2,2) and its name is “avg_pool”. The flatten layer doesn't have any hyperparameters or names.

The Fully Connected (Dense) layer reduces its input number of classes using the sigmoid function. [6]

C. Experiment

The experiment was carried out on Jupyter Notebook, in an environment of Keras 2.2.4 with Tensorflow 1.13.1. The System in which the experiment was carried out runs on Windows 10 and has a RAM of 8GB and no GPU's were used in this experiment

D. Data Acquisition

The Dataset is available on the official website of National Library of Medicine (NLM). The total number of infected and uninfected cell images in the dataset are 27,558. The examples of the samples obtained are shown in Fig. 6 and Fig. 7.

E. Data Splitting and Pre-processing

The total number of cell images in the dataset are 27,558. The split was done with 70, 15, and 15 percent for train, test and validation. It is a well-known practise to split the data such that training data gets to be more than two-thirds of whole data. Finally after the split, training data has 19,292 cell images whereas, training and validation data has 4,133 cell images each.

The pre-processing done for the classification of images consists of the following steps:

1. Randomization of images is done to get good redistribution of data for when we apply the split.
2. The input image for the ResNet50 layer should be of size 224*224. So, all the images has to be re-sized to the target size of 224*224.

We've given the batch size to be 100. 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 used for this model is Stochastic Gradient Descent (SGD). SGD optimizer has proven to be performing better than many other optimizers. The loss function used to find the loss for this model is Categorical-Cross Entropy.

F. Model Training

Neural network learns through back propagation. The top layers in the ResNet50 aren't frozen, i.e. those top layers learn through back propagation whereas, other layers of ResNet50 are frozen. The weights getting updated during back-propagation is called fine-tuning. 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. To conclude, fine-tuning the top layers will adjust to the mean or variance of the new dataset.

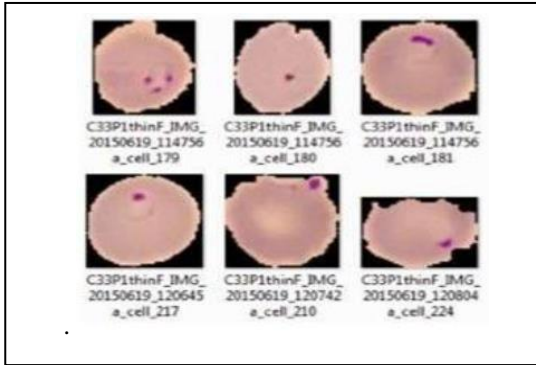


Fig.4. Infected Blood Smear Images

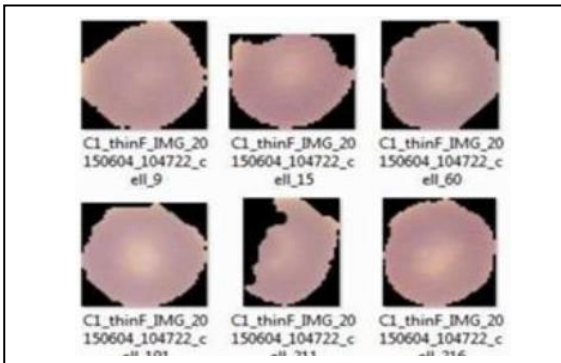


Fig.7. Uninfected Blood Smear Images

G. Results

The metrics measured during the training of the dataset were Accuracy and Loss. These metrics were measured for both training and validation data. As, autotuning was being done and no GPU's were used model took several hours for

training. The accuracy and loss of both training and validation data are shown in figures 6 and 7.

The accuracy for the testing data is 96.25%

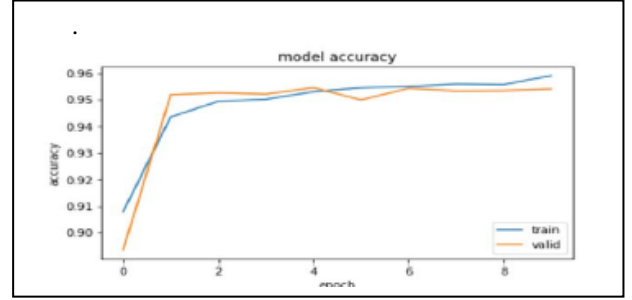


Fig 8. Graph of Accuracy during Training

Metrics	Value
Training Accuracy	95.91%
Validation Accuracy	95.4%
Training Loss	0.1134
Validation Loss	0.1301

Table 1. Training Performance

[6]

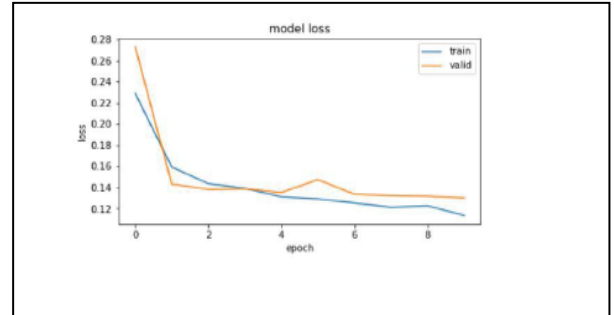


Fig.9. Graph of Loss during Training

III. CONCLUSION

Malaria is a life threatening disease. Its early diagnosis can save a lot of lives. The accuracy of diagnosing malaria from blood smears relies on the efficiency of medical professionals and the quality of instruments used in the diagnostic process. This leads to a heavy strain on medical professionals in rural areas with less medical facilities.

Deep learning methods with high accuracy in diagnosing the disease can reduce this strain on healthcare system. It also make the diagnostic process easier and faster. [7]The proposed method using pretrained ResNet can prove to be an effective medical diagnosis aid as it has high classification accuracy.

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IV. REFERENCES

- [1] M. M. a. M. Z. K. P. A. Pattanaik, "Unsupervised Deep Learning CAD Scheme for the Detection of Malaria in Blood Smear Microscopic Images," *IEEE Access* vol. 8, pp. 94936-94946, 2020, doi: 10.1109/ACCESS.2020.2996022..
- [2] Z. W. Adedeji Olugboja, "Malaria parasite detection using different machine learning classifier," in *2017 International Conference on Machine Learning and Cybernetics (ICMLC)*, 2017.
- [3] M. S. N. P. P. Dhanya Bibin, "Malaria Parasite Detection From Peripheral Blood Smear Images Using Deep Belief Networks," *IEEE Access*, 2017.
- [4] M. P. Y. S. K. A. Feng Yang, "Deep Learning for Smartphone-Based Malaria Parasite Detection in Thick Blood Smears," *IEEE Journal of Biomedical and Health Informatics*, 2019.
- [5] S. R. E. K. G. Gautham Shekar, "Malaria Detection using Deep Learning," in *Fourth International Conference on Trends in Electronics and Informatics (ICOEI 2020)*, 2020.
- [6] P. Chaudhry, "malaria-detection-using-resnet-50-malar-ai," [Online]. Available: <https://medium.com/analytics-vidhya/malaria-detection-using-resnet-50-malar-ai-46345578b461>.
- [7] A. S. B. R. a. D. S. Juliet, "Transfer Learning with ResNet-50 for Malaria," in *International Conference on Communication and Signal Processing*, India, 2020.
- [8] P. A. A. 2. M. I. G. Abdalbasit Mohammed Qadir 1*, "Malaria Parasite Identification from Red Blood Cell Images Using Transfer Learning Models," 2022.
- [9] J. R. A. H. S. B. a. D. C. A. Chowdhury, "Automated Complete Blood Cell Count and Malaria Pathogen Detection Using Convolution Neural Network," *IEEE Robotics and Automation Letters*, January 2020.
- [10] S. S. K. Sivaramakrishnan Rajaraman, "Performance evaluation of deep neural ensembles toward malaria parasite detection in thin-blood smear images," *PeerJ*, May 2019.

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