

# Malaria Detection Using Multiple Deep Learning Approaches

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**Abstract-** With about 200 million global instances and over 400,000 fatalities a year, malaria continues an enormous strain on global health. Modern information technology plays a major part in many attempts to combat the disease, along with biomedical research and political efforts. In specific, insufficient malaria diagnosis was one of the obstacles to a promising mortality decrease. The paper offers an outline of these methods and explores present advancement in the field of microscopic malaria detection and we have ventured into utilization of deep learning for detection of Malaria Parasite. Deep Learning over the years has proven to be much faster and much more accurate as it automates feature extraction of the dataset. In this research paper, we investigated various models of Deep Learning and monitored which of these models provided a better accuracy and faster resolution than previously used deep learning models. Our results show that Resnet 50 model gave the highest accuracy of 0.975504.

**Keywords**—Malaria detection, Deep learning, Blood Cell detection, Medical image processing

## I. INTRODUCTION

Malaria is a blood disease that is spread by mosquitoes, triggered by the parasites of Plasmodium borne by woman anopheles. The impacts of *P. falciparum* can however, be fatal, and include *P. ovale*, *P. malariae*, *P. vivax* and *P. falciparum*. In 2016, 212 million cases of the illness worldwide were recorded by the World Health Organization (WHO, 2016).

According to the World Malaria Report 2016, an approximate 3.2 billion individuals are at danger of malaria exposure and emerging disease in 95 nations and regions and 1.2 billion are at high danger. In 2016, there were approximately 214 million instances of malaria worldwide and 438,000 fatalities from malaria. The burden was highest in Africa, with an estimated 92% of all malaria fatalities and over 2/3 of all fatalities for infants > 5 years of age (see also the previous WHO report in Fig. 1 for the malaria death rates). Typical malaria symptoms include fever, exhaustion, headaches, and seizures and coma that lead to death in serious instances.

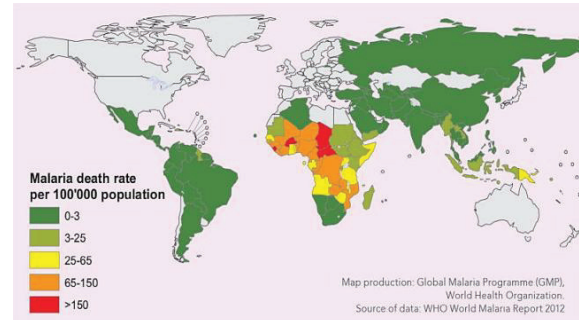


Fig. 1. Worldwide malaria death rates (Source: WHO World Malaria Report 2012).

Precise counts of parasites are not only crucial for the diagnosis of malaria but also they are essential for medication resistance testing, drug efficacy measurement and severe disease classification. Microscopic diagnostics are however not standardized and are highly dependent on the microscopist's knowledge and ability. In low-resource settings microscopist are often isolated, without a strict scheme that can guarantee their abilities remain intact and therefore diagnostic quality. This leads to unnecessary use of antibiotics for false-negative instances, a second consultation, missed working days, and sometimes development into serious malaria [1]. A misdiagnosis involves unnecessary use of anti-malaria drugs for false-positive instances.

Automatic recording of parasites has a range of advantages over conventional counting.

- (1) A more precise uniform understanding of blood films is possible.
- (2) More people can be saved by reducing workloads on the ground of malaria, and
- (3) Therapeutic costs can be reduced.

Typically, several main processing steps are needed to automatically quantify parasitaemia. First, it is necessary to acquire digital blood slide pictures, which often needs pre-processing to normalize for differences in lighting or staining. Blood cells or parasites must be identified in a second phase. This typically involves the segmentation of the proteins in blood cells to recognize individual cells in cell clusters to achieve precise cell counts. In a third phase, characteristics are calculated to define the typical visual appearance of infected and uninfected blood cells after cell identification and segmentation. A classifier that has been educated in an autonomous and traditionally manually

annotated course then discriminates in an ultimate stage of classification between infected and non-infected cells. When the amount of infected and uninfected species is recognized, a simple mathematical test is used for calculation of parasitaemia.

Our paper will provide an outline of the published papers, using the above-mentioned handling measures as a structure and guide we will be able sketch a pathway for improvement in deep learning algorithms for malaria parasite detection. This is not the subject's first study paper. Indeed, several study papers have been released before, bearing witness to automated malaria diagnosis. Early detection of malaria is crucial to ensure correct diagnosis and increase the likelihood of cure.[2] Considering the seriousness and amount of deaths caused by this illness, accepting prospective tiny execution mistakes brought by an automated scheme is reasonable. An automated system comprises of streamlined image processing methods for original filtering and segmentation and shape identification and/or machine training algorithms for robust identification of infected cells in a microscopic light or wholeslide film. A computer-assisted scheme can therefore be essential to quicker and safe treatment as a decision support scheme. It can assist to provide a benchmark and standardized measurement of the degree of disease infection.

## II. RELATED WORK

The most accurate and widely used technique for diagnosing disease is microscopic thick and thin blood smear examinations. Thick blood smears help detect parasites while thin blood smears help identify the parasite species that cause the disease (Centers for Disease Control and Prevention, 2012). Diagnostic precision relies strongly on human knowledge and it can be adversely affected by the inter-observer variation and accountability enforced in pathogen-endemic / resource-constrained areas by high-scale diagnosis and treatment (Mitiku, Mengistu & Gelaw,[3] 2003). Alternative methods such as answer to the polymerase chain reaction (PCR) and fast diagnostic tests RDT) are used; however, PCR assessment Hommelsheim et al. 2015) is however restricted, and in disease-endemic areas RDTs are less economical (Hawkes, Katsuva & Masumbuko, 2009).

Most computer-aided diagnostics (CADx) based on image analysis software use ML methods with hand-crafted feature-making characteristics (Ross et al., 2006; Das et al., 2013; [4] Poostchi et al., 2018). The method, though, requires knowledge in evaluating the variation in the region of interest in magnitude, background, orientation and location, on the images. Deep Learning (DL), also recognized as profound hierarchical training, is used with substantial achievement for solving problems of designing hand-engineered characteristics to detect changes in the fundamental information (LeCun, Bengio & Hinton, 2015).

Alex Krizhevsky suggested AlexNet, a CNN-based DL model which earned the ImageNets ILSVRC [4] and significantly increased CNN efficiency in classifying natural imagery (Krizhevsky, Sutskever & Hinton, 2012). Several CNN representatives such as VGGNet (Simonyan & Zisserman, 2015), GoogLeNet (Szegedy et al., 2014)[5] and ResNet (He et al., 2016) showed important changes in the succession of consecutive ILSVRC problems. It was suggested that a system called Xception use depth-wise

separable convolutions (Chollet, 2016) to outperform the information evaluation function of the Inception-V3 system (Szegedy et al., 2016) (Deng et al., 2009).

A version of CNN called Densely Connected Convolutional Networks (DenseNet) has been suggested (Huang et al., 2016) using a network architecture in which each layer is immediately linked to each previous layer. Transfer Learning (TL) techniques are used with scarcity for annotated medical imaging where pre-trained DL models are either fine-tuned on the fundamental records or used as attribute extractors to assist in image recognition activities (Razavian et al., 2014).

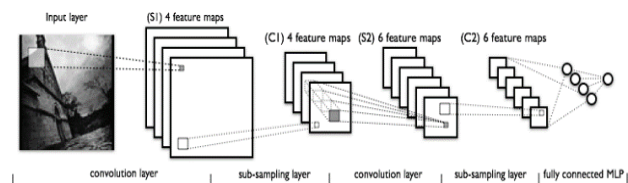


Fig. 2. A typical CNN architecture (Source: deeplearning.net)

The Razavian et al results. (2014) provide CNNs with a large-scale database education with the option of offering various computer vision features, rather than state-of - the-art improved efficiency methods (Busetouane and Morris, 2015). Researchers around the globe are currently using DL instruments and achieving successful outcomes for a range of analyzes and understanding assignments for medical images (Rajaraman et al., 2017; Suzuki, 2017).

The important contributions of this paper are:

- (a) Present a comparative efficacité evaluation as extractors for the classification of parasite and non-parasite cells of custom and Pre-trained DL models;
- (b) Assessment and selection in the pre-trained models for optimum layer feature extraction from the existing data, and
- (c) Test to establish the presence / absence of an important statistical change in CNN models in the findings of the study.

## III. MODELS AND RESULTS:

TABLE. 1. TABLE SHOWING HIGHEST ACCURACY OF MODELS

Model	Highest Accuracy
<b>Densenet121</b>	<b>0.972782</b>
<b>VGG16</b>	<b>0.954455</b>
<b>Alexnet</b>	<b>0.956269</b>
<b>Resnet50</b>	<b>0.975504</b>
<b>FastAI</b>	<b>0.973870</b>
<b>Resnet101</b>	<b>0.970060</b>

### A. DENSENET 121

Dense Convolutional Network (DenseNet), which provides a feed-forward connection between each layer and each other. Whereas conventional L-layer networks have L links— one between each class and the later layer— our network has immediate  $L(L+1)/2$  links.[6] DenseNets have an amount of convincing benefits: alleviating the issue of vanishing gradients, enhancing propagation features, encouraging attribute reuse and significantly reducing the number of parameters. For each phase, the feature maps of

all previous layers are used as inputs and their own feature maps are used as inputs in all stages. Densenet is new and a logical resnet extension. The loss v/s learning rate processed graph obtained is as below:

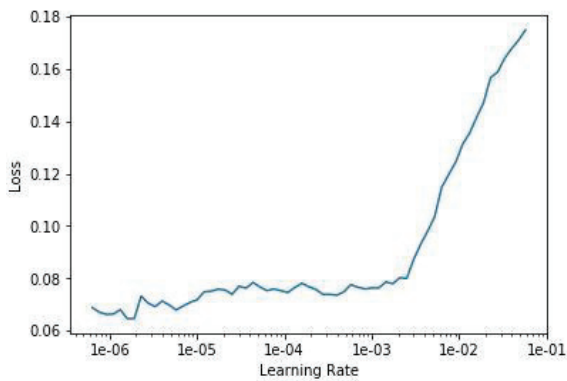


Fig. 3. Graph showing loss versus learning rate for Densenet 121

The loss v/s batches processed graph obtained was as below:

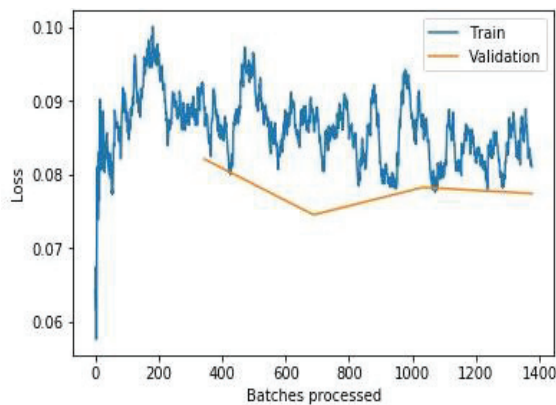


Fig. 4. Graph showing loss versus batches processed for Densenet 121

After running the model, the confusion matrix was as below:

		Confusion Matrix	
Actual	Parasitized	2663	66
	Uninfected	87	2695
		Parasitized	Uninfected
		Predicted	

Fig. 5. Confusion Matrix for Densenet 121

### B. VGG-16

VGG16 is K Simonyan and A. Oxford University's Zisserman's proposed convolutional neural network model. It improves over AlexNet by replacing big kernel-sized filters one after the other with various 3x3 kernel-sized filters. 1x1 Conv helps in fact to increase the non-linearity of the decision function. A deep-learning network improves by adding number of layers [7]. VGG-16 gets an 8.8% error level. The projection mapping is performed in the same high

dimensionality without altering the dimension of input and output. This is called "Network in Network".

The loss v/s learning rate processed graph obtained is as below:

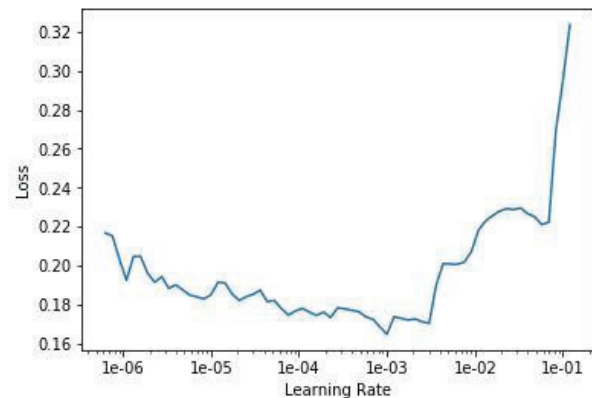


Fig. 6. Graph showing loss versus learning rate for VGG-16

The loss v/s batches processed graph obtained was as below:

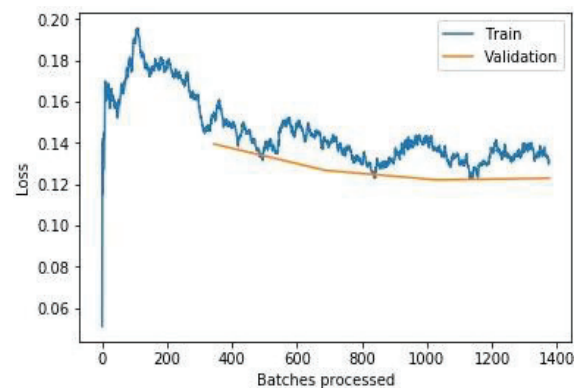


Fig. 7. Graph showing loss versus batches processed for VGG-16

After running the model, the confusion matrix was as below:

		Confusion Matrix	
Actual	Parasitized	2580	136
	Uninfected	119	2676
		Parasitized	Uninfected
		Predicted	

Fig. 8. Confusion matrix for VGG-16

### C. ALEXNET

There are eight layers in AlexNet, with the first five convolutional levels and some of them with maximum pooling layers, and the last three fully interconnected levels. It used the non-saturating ReLU [8] activation function, whereby the tanh and sigmoid were enhanced. ALEXnet is a CNN-setting GPU.

The loss v/s batches processed graph obtained was as below:

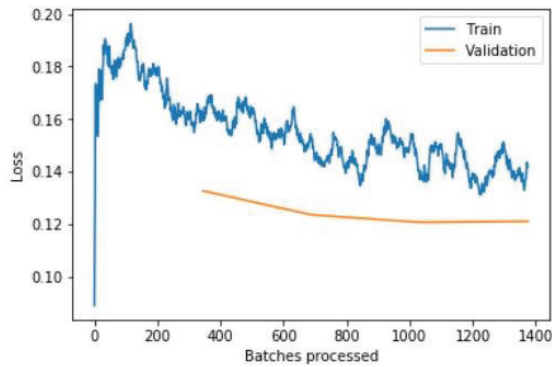


Fig. 9. Graph showing loss batches processed rate for Alexnet

After running the alexnet model, the confusion matrix was as below:

Confusion Matrix		
Actual	Parasitized	Uninfected
	2622	131
Uninfected	110	2648
	Predicted	Predicted

Fig. 10. Confusion matrix for Alexnet

#### D. RESNET 50

ResNet-50 is a convolutionary neural network trained in over a million ImageNet pictures. The network's depth of 50 levels enables the classification of pictures into 1000 classifications of objects such as keyboards, mouse, pencils and many species. The network has therefore gained a broad variety of pictures in a wealth of features [9]. The network has a 224-by-224 picture entry.

The loss v/s learning rate graph obtained was as below:

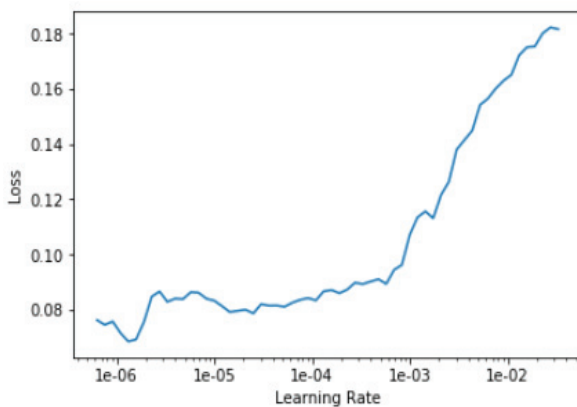


Fig. 11. Graph showing loss versus learning rate for Resnet 50

The loss v/s batches processed graph obtained was as below:

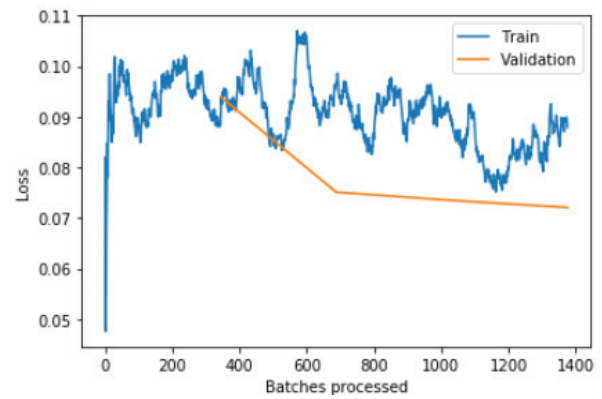


Fig. 12. Graph showing loss versus batches processed for Resnet 50

After running the model, the confusion matrix was as below:

Confusion Matrix		
Actual	Parasitized	Uninfected
	2712	77
Uninfected	58	2664
	Predicted	Predicted

Fig. 13. Confusion Matrix for Resnet 50

#### E. FASTAI V1

Fast.ai releases V1 of FastAi, the latest Free Open Source Library. The library is on bottom of the PyTorch v1 (published in practice today) and offers the most significant deep learning apps and data types with a single coherent API. Recent study advances in Fast.ai are integrated in the software, which considerably improves their precision, speed, and dramatically less code is needed compared to other deep learning libraries.

The loss v/s learning rate processed graph obtained is as below:

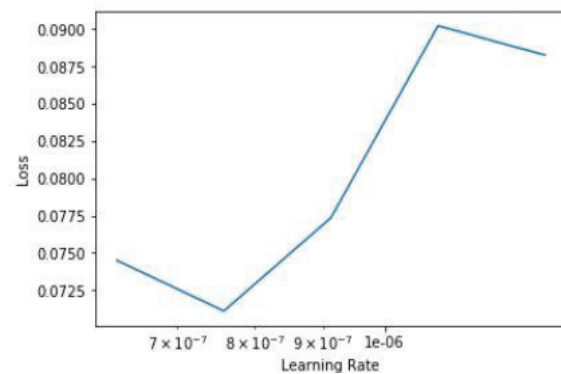


Fig. 14. Graph showing loss versus learning rate for FastAI V1



After running the model, the confusion matrix was as below:

		Confusion Matrix	
Actual	Parasitized	2646	74
	Uninfected	70	2721
		Parasitized	Uninfected
		Predicted	

Fig. 15. Confusion Matrix for FastAI V1

#### F. RESNET 101

ResNet denotes residual learning. ResNet-101 is a convolutional network that is educated in the ImageNet library on more than a million pictures. The network has a 224-by-224 image size.

Instead of learning unreferenced features, it clearly reproduces levels as remaining features with regard to layer inputs. It provide extensive empirical evidence that remaining networks are simpler to optimize,[10] and that they can achieve precision from significantly enhanced depth.

The loss v/s batches processed graph obtained was as below:

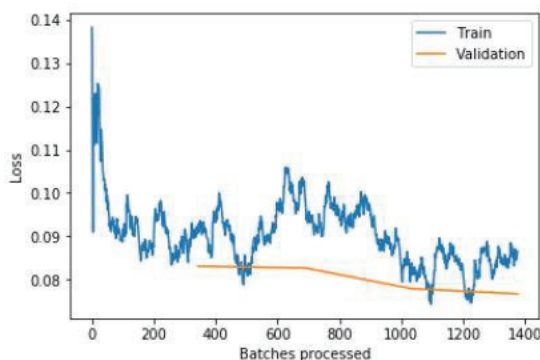


Fig. 16. Graph showing loss versus batches processed for Resnet 101

After running the model, the confusion matrix was as below:

		Confusion Matrix	
Actual	Parasitized	2674	105
	Uninfected	61	2671
		Parasitized	Uninfected
		Predicted	

Fig. 17. Confusion Matrix for Resnet 101

#### IV. CONCLUSION:

Due to the optimization of the hyper-parameter, implicit regularization enforced through decrease convolutionary filter dimensions and aggressive dropouts within the completely related layers, the tailor-made version transformed to an excellent answer. Regularization of l2 decreased the impact of model overfitting and converging right into a higher solution (simonyan & zisserman, 2015). For the required picture, every cnn layer generates an activation. Earlier layers seize primitive traits which include blobs, edges, and hues that the deeper layers summary to create higher-degree traits to present a greater rich illustration of the photo (zeiler & fergus, 2014). [11]

But, we've witnessed resnet-50 display very excessive matthews correlation coefficient, with incredibly more potent overall performance than the other fashions under consideration. Those findings suggest that it is not usually ideal to obtain the residences of fundamental records at the final layer of pre-trained cnns. In our study, functions from shallow layers have achieved advanced than deep capabilities to decorate cell identification parasitised and non-parasited.

Consolidated findings showed that the ResNet-50 pre-trained comparatively outperformed the other models being studied to classify the parasitized and uninfected cells by giving us an accuracy of **0.975504**. By looking at each model's confusion matrix, we can discover the precision, awareness, specificity by using the corresponding formulas.

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