

# Performance Comparison of CNN Architectures for Detecting Malaria Diseases

by

Habiba Karim Rinky  
16101252  
Rakeya Rahim Bhuiyan  
16101127  
Humayra Tasnim Rahman  
16101063

Supervisor  
Dr. Amitabha Chakrabarty  
Associate Professor  
Department of CSE

A thesis submitted to the Department of Computer Science and Engineering  
in partial fulfillment of the requirements for the degree of  
B.Sc. in Computer Science

Department of Computer Science and Engineering  
Brac University  
April 2020

© 2020. Brac University  
All rights reserved.

## Declaration

It is hereby declared that this thesis /project report or any part of it has not been submitted elsewhere for the award of any Degree or Diploma.

Student's Full Name & Signature:

*Habiba Karim Rinky*

---

Habiba Karim Rinky  
16101252

*Rakeya*

---

Rakeya Rahim Bhuiyan  
16101127

*Humayra Tasnim Rahman*

---

Humayra Tasnim Rahman  
16101063

# Approval

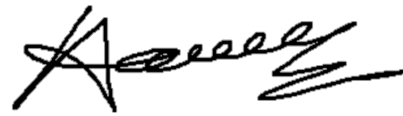
The thesis titled “Performance Comparison of CNN Architectures for Detecting Malaria Diseases” submitted by

1. Habiba Karim Rinky (16101252)
2. Rakeya Rahim Bhuiyan (16101127)
3. Humayra Tasnim Rahman (16101063)

Of Spring, 2020 has been accepted as satisfactory in partial fulfillment of the requirement for the degree of B.Sc. in Computer Science on April 7, 2020.

## Examining Committee:

Supervisor:  
(Member)



---

Dr. Amitabha Chakrabarty  
Associate Professor  
Department of Computer Science and Engineering  
Brac University

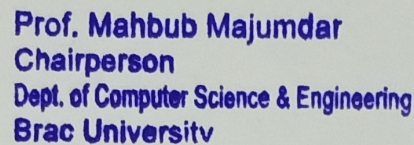
Program Coordinator:  
(Member)



---

Dr. Md. Golam Rabiul Alam  
Associate Professor  
Department of Computer Science and Engineering  
Brac University

Head of Department:  
(Chair)



**Prof. Mahbub Majumdar**  
**Chairperson**  
**Dept. of Computer Science & Engineering**  
**Brac University**

---

DR. Mahbubul Alam Majumdar  
Professor  
Department of Computer Science and Engineering  
Brac University

## **Ethics Statement**

The project is conducted in complete accordance with the principles of research morality, and the codes and hones set by BRAC University. We are collecting the details from primary sources in our proposal. We collect knowledge from esteemed representatives and we use our possess dataset for our proposal. We guarantee that we make correct use of references and quotations in text. We the three co-authors take full responsibility for violation of the thesis code. We perused distinctive blogs, study report, youtube tutorials and various apparatuses for fathoming problems. In addition, we took assistance from individuals at our university faculty. Finally, we announce that we are giving credit to any person from whom we have obtained assistance in the bid. We made no ransom that could mean finishing the thesis. Our job conforms to the standard of morality set by BRAC University.

## Abstract

World is facing an acute health crisis for the disease named malaria caused by the bite of female mosquitoes of parasite named genus plasmodium. From different research of all time it is clear that this disease is not confined within a certain specific region or area rather this infection is common all over the world. Many researchers from all over the globe discovered many processes or techniques to determine malaria infection from host body. Malaria Detection consumes huge time to detect. This study aims to determine the infected malaria cells using deep learning algorithms as it is important part in this advanced technological era to determine objects. This research used deep learning algorithms like VGG-16, VGG-19, VGG-16 binary, VGG-19 binary, Alexnet, MobileNet, ResNet34, ResNet50 and CNN2D to determine malaria infected cells from images. Thereby, also finds the comparative analysis between these algorithms to determine the best accuracy giving algorithm. From the study it is evident that algorithms named AlexNet, VGG-16, VGG-19, VGG-16 binary, VGG-19 binary, MobileNet, CNN2D, ResNet34 and ResNet50 give an accuracy of 94.84%, 92%, 92%, 97.4%, 96.53%, 95.42%, 96.91%, 97.06% and 85% respectively. From the comparative analysis between these nine algorithms, this study concludes to find ResNet34 with model accuracy 97.06% as the best accuracy giving algorithm.

**Keywords:** *Malaria, Plasmodium falciparum, Plasmodium vivax, Plasmodium malaria, Plasmodium ovale*

# Dedication

This thesis work is dedicated to our parents as well as all the faculties who keep us hungry every day to learn something new not only about academics but also about life.

## Acknowledgement

To begin with of all, we would like to specific our appreciation to the Almighty for keeping us secure and sound to start the investigate work and to put our best endeavors and effectively complete it. Secondly, we would like to thank and pay tribute to our honorable supervisor, Dr. Amitabha Chakrabarty, for his tremendous contributions, incomparable guidance and tireless support in the conduct of the research work and in the preparation of this study. His consistent association and supervision guaranteed our slow advance towards the completion of this thesis work. We are deeply grateful and respectful to have him as our supervisor. We would also like to thank our parents and our good friends for the encouragement, moral support and assistance. They helped us a lot with their helpful feedback and direct or indirect involvement that helped us maintain a better workflow and achieve our target. Finally, we would like to thank uncommonly our exceptionally claim BRAC University for giving us the opportunity to conduct this thesis.

# Table of Contents

<b>Declaration</b>	<b>i</b>
<b>Approval</b>	<b>ii</b>
<b>Ethics Statement</b>	<b>iii</b>
<b>Abstract</b>	<b>iv</b>
<b>Dedication</b>	<b>v</b>
<b>Acknowledgment</b>	<b>vi</b>
<b>Table of Contents</b>	<b>vii</b>
<b>List of Figures</b>	<b>ix</b>
<b>List of Tables</b>	<b>xi</b>
<b>Nomenclature</b>	<b>xi</b>
<b>1 Introduction</b>	<b>1</b>
1.1 Background . . . . .	1
1.2 Problem Introduction . . . . .	1
1.3 Aims and Objectives . . . . .	2
<b>2 Related Work</b>	<b>3</b>
2.1 Literature Review . . . . .	3
<b>3 Dataset Description</b>	<b>5</b>
3.1 Dataset Collection . . . . .	5
3.2 Dataset Analysis . . . . .	6
<b>4 Prediction Accuracy of Different CNN Algorithms and Result Analysis</b>	<b>7</b>
4.1 Convolution Neural Network (CNN) . . . . .	7
4.1.1 Predictive accuracy using AlexNet: . . . . .	8
4.1.2 Predictive accuracy using Visual Geometry Group (VGG-16):	11
4.1.3 Predictive accuracy using Visual Geometry Group (VGG-19):	14
4.1.4 Predictive accuracy using MobileNet: . . . . .	16
4.1.5 Predictive accuracy using Visual Geometry Group Binary (VGG-16 Binary): . . . . .	19



4.1.6	Predictive accuracy using Visual Geometry Group Binary (VGG19 Binary): . . . . .	20
4.1.7	Predictive accuracy using Convolutional Neural Network 2D (CNN 2D): . . . . .	23
4.1.8	Predictive accuracy using Residual Network 34 (ResNet34): . .	26
4.1.9	Predictive accuracy using Residual Network 50 (ResNet 50): .	30
4.2	Result Analysis and Comparison: . . . . .	35
<b>5</b>	<b>Conclusion</b>	<b>37</b>
	<b>Bibliography</b>	<b>38</b>

# List of Figures

3.1	Images of infected and healthy malaria cells . . . . .	6
4.1	Working Mechanism of CNN . . . . .	8
4.2	Faster training error rate of AlexNet . . . . .	9
4.3	Loss vs learning Rate Graph of AlexNet . . . . .	10
4.4	Loss vs Learning Rate Graph of AlexNet . . . . .	11
4.5	Loss vs Batch Process Graph of AlexNet . . . . .	12
4.6	Confusion matrix of AlexNet . . . . .	13
4.7	VGG-16 Architecture . . . . .	14
4.8	Convolutional Neural Network with three hidden layers . . . . .	15
4.9	Validation Loss Vs Training Loss of VGG16 . . . . .	16
4.10	Train Loss Vs Valid Loss of VGG19 . . . . .	16
4.11	Input image of MobileNet . . . . .	17
4.12	Layer 1 of MobileNet . . . . .	17
4.13	Layer 2 of MobileNet . . . . .	18
4.14	Layer 3 of MobileNet . . . . .	18
4.15	Layer 4 of MobileNet . . . . .	19
4.16	Precise Zoomed Infected Area Shown in MobileNet . . . . .	20
4.17	Model Accuracy of MobileNet . . . . .	21
4.18	Model Loss of MobileNet . . . . .	22
4.19	Loss vs Learning Rate Graph of VGG-16 Binary . . . . .	23
4.20	Loss vs Learning Rate Graph of VGG-16 Binary . . . . .	24
4.21	Loss vs Batches processed Graph of VGG-16 Binary . . . . .	24
4.22	Loss vs Learning Rate Graph of VGG-19 Binary . . . . .	25
4.23	Loss vs Learning Rate Graph of VGG-19 Binary . . . . .	26
4.24	Loss vs Batches processed Graph of VGG-19 Binary . . . . .	26
4.25	Input image of CNN 2D . . . . .	27
4.26	Layer 1 of CNN 2D . . . . .	27
4.27	Layer 2 of CNN 2D . . . . .	28
4.28	Layer 3 and Layer 4 of CNN 2D . . . . .	28
4.29	Layer 5 of CNN 2D . . . . .	29
4.30	Model Accuracy of CNN 2D . . . . .	29
4.31	Model Loss of CNN 2D . . . . .	30
4.32	ResNet 34 (right) . . . . .	31
4.33	Loss vs Learning Rate Graph of ResNet34 . . . . .	32
4.34	Loss vs Learning Rate Graph of ResNet34 . . . . .	32
4.35	Loss vs Batches Process of ResNet34 . . . . .	34
4.36	Confusion Matrix of ResNet34 . . . . .	34

4.37 Identity Shortcut Link . . . . .	35
4.38 Detection of parasitized and uninfected cells using ResNet50 . . . . .	36
4.39 Chart of Accuracy Vs Algorithm . . . . .	36

# List of Tables

4.1	First Learning Cycle of AlexNet . . . . .	10
4.2	Second Learning Cycle of AlexNet . . . . .	11
4.3	Model Learning of VGG 16 . . . . .	13
4.4	Model Learning of VGG 19 . . . . .	14
4.5	First Learning Cycle of VGG-16 Binary . . . . .	20
4.6	Second Learning Cycle of VGG-16 Binary . . . . .	21
4.7	First Learning Cycle of VGG-19 Binary . . . . .	22
4.8	Second Learning Cycle of VGG-19 Binary . . . . .	23
4.9	Model Learning of CNN 2D . . . . .	25
4.10	First Learning Cycle of ResNet34 . . . . .	30
4.11	Second Learning Cycle of ResNet34 . . . . .	30
4.12	Training Loss and Validation Loss of ResNet 50 . . . . .	33
4.13	Results of different models . . . . .	35

# Chapter 1

## Introduction

### 1.1 Background

Malaria is mosquito born disease and a great threat to the people all around the world. Malaria should be detected promptly as a good way to treat the person infected in period as well as to avoid further development of the people all around the world. Lag time in diagnosis will lead to death in patients with malaria worldwide. [1] . In any case, for an authoritative conclusion to be made, laboratory tests must illustrate the malaria parasites or their components. The wide variety of malaria instances worldwide appears to be growing, because of increasing transmission danger in regions in which malaria manipulate has declined, the increasing prevalence of drugresistant traces of parasites, and in a highly few instances, huge will increase in worldwide journey and migration [2]. According to WHO about 1 million people died every year from 200-300 million malaria ted patients [3]. A report on Sub-Saharan Africa and South Asian region by “Bill and Melinda Gates Foundation” showed that about 219 million people were affected by malaria in 2017 out of which about 435000 people died. More than 90% of deaths were in Africa and over 60% were among children under 5 .This shows children are more likely to be affected by this disease [4]. According to UNICEF in 2016 about 216 million people were affected by malaria out of which 440,000 patients died. Out of these about two third (290000) were children under 5 years. This translate into a daily death rate of children under 5 years is nearly 800 [5]. Malaria can be found in many countries in the world, mainly in heated areas. Demographically Bangladesh lies in malaria prone region specially the south-eastern hilly region of Chittagong, Bandarban, Khagrachari and Rangamati. The prevalence rate in Khagrachari, Bandarban and Rangamati districts was 15.25 percent, 10.97 percent and 7.42 percent respectively [6]. In this paper we will show a comparison study using deep learning algorithms to detect malaria cell and estimate accuracy.

### 1.2 Problem Introduction

Malaria needs to be detected early, so that it will not spread the infection to the other people. Malaria nevertheless represents a chief public health trouble regardless of the essential reductions inside the mortality and morbidity rates of malaria executed worldwide by means of the implementation of numerous anti-malarial strategies. It is expected that each one endemic countries get rid of malaria through adapting

then to be had interventions to their nearby context and mixing them. Therefore the Global Technical Strategy for malaria 2016–2030 is based on five principles, the primary of that's universal get right of entry to malaria prevention, prognosis and treatment. This made difficult to differentiate from infected malaria and not infected people. Again, malaria diagnosis from blood smear requires parasite staining under a microscope and this consumes lot of time and can be unsuccessful in many times.

### **1.3 Aims and Objectives**

As Malaria identification technique is both time consuming and expensive. By the deep learning algorithms this can be identified easily, the prerequisite for using these algorithms is just a image of the blood cell and we can determine in seconds whether the individual is infected or not. The main motive is to find out the deep learning algorithms that can detect infected malaria cells accurately. This research will also show a comparative analysis of accuracy given by different deep learning algorithms.

# Chapter 2

## Related Work

### 2.1 Literature Review

Malaria is a dreadful disease all over the world and the infection of malaria spread through mosquitoes which become epidemic in different part of the world in different times. As, it is an very important issue many work on detection of malaria were already implemented in different part of the globe using different machine learning algorithms like supervised learning, unsupervised learning and deep learning. Kuang, Gu, Cai and Wang [7] explored on PSI-blast search and supervised SVM learning using profile-kernel(PF-SVM) to improve prediction of malaria degradomes. The PF-SVM was proven to be able to identify new proteases that were not detected by PSI-blast because PF-SVM is not misled by widely shared structure motifs and PF-SVM doesn't suffer from "profile-drift" problem. Again, if the number of false positives to be small the PF-SVM also achieves higher sensitivity and accuracy than PSI-blast. Our result indicates malaria parasites possess a code degradome structure consisting of 29 families of proteases. These families falls in 4 classes named cysteine proteases, metallo and serine proteases, aspartic proteases, threonine proteases. Patel and Dobariya [8] detected malaria parasite using K-Mean Clustering. This process has been done through seven steps. Acquire images of malaria samples. Malaria slides are collected from Supratech Micro path pathology and research institute Ahamdabad. Partial Contrast Stretching (PCS) is used to improve the quality of images which uses linear mapping function. Three types of color models are used to detect the malaria parasites which are RGB, HIS and C-Y color models. Image segmentation using K-Mean Clustering is used to extract the meaningful region from the malaria images. Image filtering is done using Median Filter Algorithm to remove some unwanted regions or noises. Modified version of conventional seed based region growing algorithm, Seeded Region Growing Area Extraction (SRGAE) algorithm has been applied on segmented images. Then Canny edge detection is done on the images. This process is done in five steps. Canny edge detection is better than compared to region growing with respect to time comparison. Razzak [9] have used ANN and described an approach for classification of malaria infected cells using BPNN and Rao's method based segmentation. There has been used all geometrical and intensity features along with GLCM based texture features. For classification, back propagation neural network (ANN) has been used. ANN is a simulated structure and function of biological neural network. The accuracy for detecting P.falciparum is around 93 94% for different feature sets. Ahirwar, Pat-

tnaik, and Acharya [10] used Back propagation feed forward neural network (BFF) on images of Giemsa stained blood smears and the database consists of 90 images. SUSAN(Smallest Univalve Segment Assimilating Nucleus) principal was used for pre-processing stage which performs edge and corner detection and structure preserving noise reduction. The final classification was done through back propagation feed forward neural network(BFF) for accuracy and measured sensitivity and positive predictive value(PPV). The features selected for the classifier are those that describe the color and texture of the parasites. The goal of the training is to minimize squared error and to avoid overtraining because it stopped when the error of validation set increased. Park, Rinehart and Walzer et al. [11] used three types of machine learning techniques were examined on dataset. These techniques were Linear Discrimination Classification(LDC),Logistic Regression(LR) and K-nearest neighbor classification(NNC).The dataset of 1237 cells which includes both infected and uninfected cells divided into 10 subsets in even size.9 of the subset are used as training dataset and rest is used for testing. This is repeated until all 10subsets have been used once as a testing set. Within these three methods, NNC gave low performance on distinguishing early trophozoite (ET). While LDC and LR methods gave 93.5% and 90.8% accuracy. Moreover, all these techniques have 99.6% accuracies on schizont stage. The rate of true or specific accuracy is 99.1% for NNC, 98.7% for LR and 99.8% for LDC. Lastly, the classification errors that rarely confused between infected and uninfected are 9.9%( 17cells) for NNC,3.8%( 7cells) for LR and 6.5%( 12cells) for LDC. Hung, Goodman and Lopes et al. [12] used faster reason base convolution neural network (faster R-CNN) which is used for object detection. This model detects and classifies in two stages. In stage one object detection framework faster RCNN identifies bounding boxes around objects and classifies them as RBC or others. In stage two the detection from stage one labeled as other are feed into AlexNet to obtain a 4096 dimensional feature vector used to classify them more fine trained categories.



# Chapter 3

## Dataset Description

### 3.1 Dataset Collection

Gathering a broad dataset is the core focus of study into deep learning, and most significantly, collecting data from a credible source with clear understanding is important. As deep learning algorithms highly depend on data collection so data preparation is the most important procedure in terms of deep learning algorithm. Data preparation involves defining the appropriate method for gathering data.

The identification of infected cells of malaria parasites may create difficulties. In some cases, malaria transmission and the effect can be so dangerous that a large portion of people may be infected but not ill. In some cases, having malaria parasite in one's biological body does not mean that the parasite cause the disease.

On the basis of the symptoms of malaria patient and physical outcomes throughout examination the clinical diagnosis occurred. There are several symptoms i.e. fever, headache, muscle pain etc. which are the common symptoms of malaria but these are also common for other flues. Clinical results that includes respiratory difficulties, neurological focal signs are more alarming. It increase the possibility to be infected by malaria disease.

In microscopic diagnosis, the detection of malaria parasite is a sophisticated process which include observation of a drop of patients' blood under a microscope.

It is a matter of great privilege that researchers from the Lister Hill National Center for Biomedical Communications (LHNCBC), part of the National Library of Medicine (NLM), who carefully gathered and annotated this collection of safe and polluted photographs of blood smear of both malaria infected cells and healthy cells. The Chittagong Medical College Hospital, Bangladesh, obtained and photographed Giemsa-stained thin blood smear slides from 150 *P. falciparum*-infected and 50 healthy patients. An expert slide reader at the Mahidol-Oxford Tropical Medicine Research Unit in Bangkok, Thailand, has manually annotated the images.

The dataset contains a total of 27,558 cell images with equal instances of parasitized and uninfected cells. The dataset contains 13,779 parasitized images and 13,779 uninfected cells images. This also include CSV files containing the patientID to cell mappings for the parasitized and uninfected classes,it contains 151 patient-ID entries for parasitized class [13].

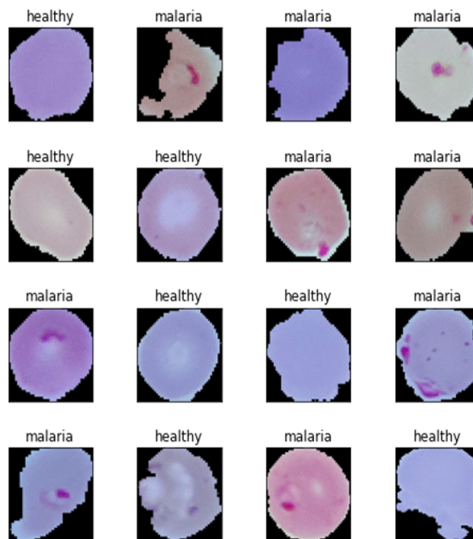


Figure 3.1: Images of infected and healthy malaria cells

## 3.2 Dataset Analysis

There are two folders which contain images of cells which are infected and healthy, which is a balanced dataset of 13,779 malaria and 13,779 non-malaria (uninfected) cell images in jpeg format.

The goal is to detect the cell of infected and healthy successfully. To implement the algorithms first the images, need to be processed. For MobileNet and CNN 2D algorithms, the images have been resized to 50 X 50 pixel and then normalize the images then the algorithms have been implemented.

For VGG-16 and Vgg-19 algorithms resize the 224 X 224 pixel which is the shortest length then normalized the images and implemented further process of the algorithms. For AlexNet, ResNet34, ResNet50, VGG-16 binary and VGG-19 binary the data is taken using ImageDataBunch where the size is 224 for images. The algorithms have been implemented on the images by resizing the images according the algorithms. Lastly, we used scipy framework to split our dataset in 80% and 20% where 80% were used for training and 20% for testing for all the algorithms.

# Chapter 4

## Prediction Accuracy of Different CNN Algorithms and Result Analysis

### 4.1 Convolution Neural Network (CNN)

Convolutional neural network (CNN) is a subsection of Deep Learning which is used for image classification. Other deep learning algorithms are used for images classification but CNN gives better performance for that because of its architecture.

CNN mainly divided into three layers. First layer is input layer, second layer is hidden layer and the final layer is output layer. All the calculation is done in the hidden layer. Basically, in CNN neurons of one layer is connected to some particular neuron (one neuron is not connected with all the neurons of the next layer) of its immediate next layer but in other deep learning algorithms, one neuron is attached with all the other neurons of the next layer which become very costly to calculate.

Convolutional Neural Network (CNN) has few layers which works together to classify images properly. It has convolutional layer, pooling layer, ReLU layer and fully connected layer.

**Convolutional Layer:** Convolutional layer has filters which does convolution operation. To do this operation it requires volume size of input image, filter size, stride, zero padding as parameters. With all the information as parameters, it calculates and gives an output which goes to the next layer of CNN.

**ReLU Layer:** ReLU is an activation function. In convolution or pooling layer, it works as a function. If any negative value is given to the function, then the function converts the value into zero. But if any positive value is given, then it remains the same. This ReLU layers works in parallel with convolution and pooling layer.

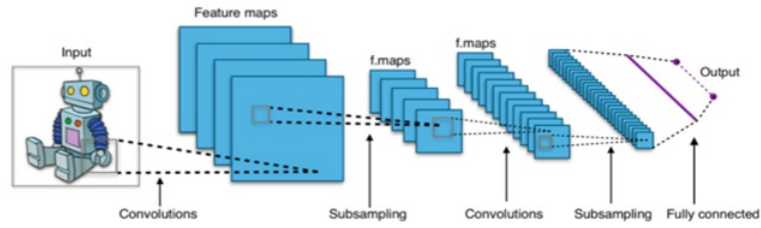


Figure 4.1: Working Mechanism of CNN

**Pooling Layer:** Pooling layer is used to reduce the size of images which helps to classify images easily. In this pooling layer, it takes filter size and stride as parameters. Depending on the filter size and stride the output changes. Whatever image size is given in the convolution layer, it becomes half of that after the pooling layer.

#### 4.1.1 Predictive accuracy using AlexNet:

AlexNet is one of the subsection of deep learning algorithms, which is designed by Alex Krizhevsky, and is published with IlyaSutskever and Krizhevsky's doctoral advisor Geoffrey Hinton which competed within the ImageNet Large Scale Visual Recognition Challenge on September 30, 2012[14].

The input of AlexNet algorithmic program is associate degree RGB image of size 256256. The input image should be reborn to 256256 if it's in several sizes before victimization it to coach the network. To achieve this goal, the smaller dimension is resized to 256 and so the ultimate image is cropped to get a 256256 image. Once obtaining the input image that is in grayscale, it should be reborn to associate degree RGB image by replicating the one channel to realize a 3-channel RGB image. Several crops of size 227227 were gained from within the 256256 pictures which can feed the primary layer of AlexNet.

The network had virtually the same design as LeNet by YannLeCun et al however was deeper, with a lot of filters in every layer, and with stacked convolutional layers. It is consisted of some operation like (11x11), (5x5),(3x3), convolutions, max pooling, dropout, information augmentation, ReLU activations, SGD with momentum. It used ReLU activations once each convolutional and fully-connected layer.

The architecture has eight layers: five convolutional layers and three fully-connected layers. These are some of the features which are also new approaches used in convolutional neural networks:

Multiple Convolutional Kernels (a.k.a filters) extract fascinating options in a picture. In every convolutional layer, there square measure typically several kernels of constant size. For instance, the primary Convolutional Layer of AlexNet contains

ninety-six kernels of size (11x11x3). Note that, the breadth and height of the kernel square measure typically constant and also the depth is that the same because the variety of channels.

From 5 convolutional layer, the first two convolutional layer and the fifth convolutional layer works with a maxpooling layer. But there is no maxpooling layer in the third and fourth layer which are directly connected. The first five layers are then connected with two fully connected layers and then all the layers of this architecture are connected with softmax layer which is the last layer of AlexNet algorithm.

Rectified Linear Unit (ReLU) is used is AlexNet algorithm over any other activation function like tanh activation function because of giving better performance. ReLU has low computational cost than other activation function.

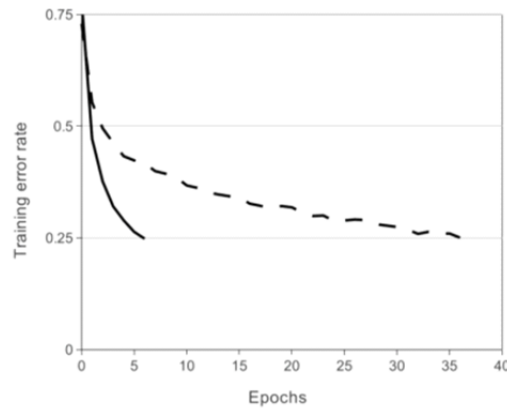


Figure 4.2: Faster training error rate of AlexNet

Overlapping pooling layer is used to reduce the dimensionality of the images by reducing the pixels. It also reduces the size of the filters which helps to make the computation easier. There are two type of pooling operation. One is Max pooling and another is average pooling.

In this model, to train the dataset for the first time will need six iterations to find the training loss, validation loss and accuracy.

To minimize the loss, 4 more epochs implied on training dataset to find training loss, validation loss and accuracy.

A confusion matrix is given below which shows that how many parasite and uninfected cell this model can detect

Iteration	Train Loss	Valid Loss	Accur
0	.258521	.204668	.935402
1	.257038	.165299	.942660
2	.208809	.154592	.947015
3	.194607	.144580	.950281
4	.173225	.138765	.951189
5	.200191	.136228	.952640

Table 4.1: First Learning Cycle of AlexNet

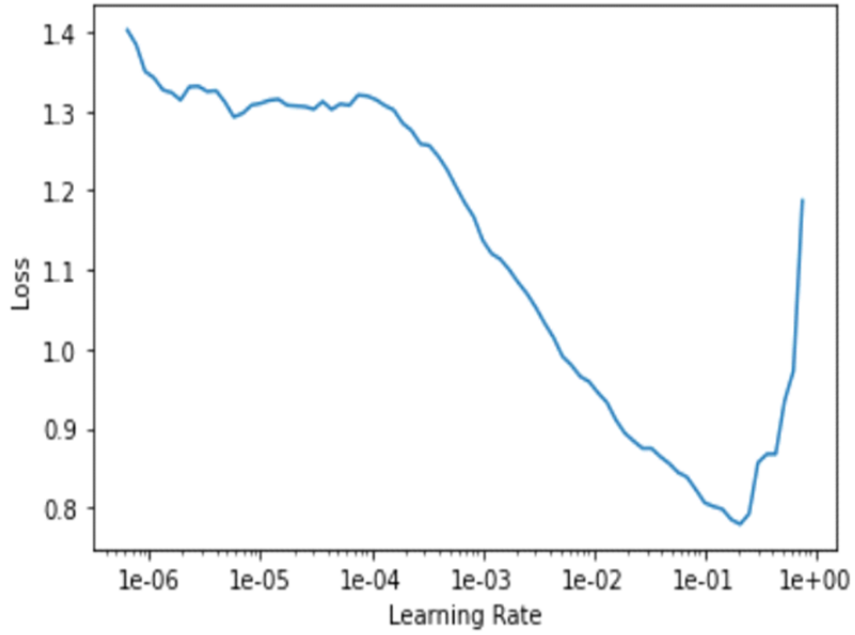


Figure 4.3: Loss vs learning Rate Graph of AlexNet

**Test Analysis:**

Total model accuracy of AlexNet is 95.84% and the loss in 1400 batch is almost 0.12.

Iteration	Train Loss	Valid Loss	Accur
0	.161857	.128799	.953729
1	.157624	.119450	.957539
2	.149487	.115929	.957902
3	.145985	.114725	.958447

Table 4.2: Second Learning Cycle of AlexNet

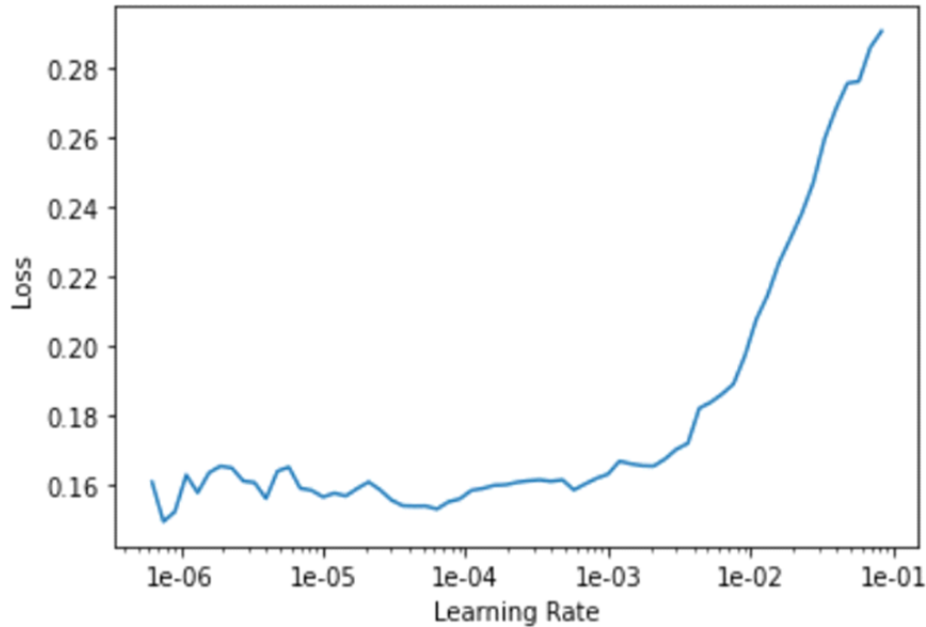


Figure 4.4: Loss vs Learning Rate Graph of AlexNet

### 4.1.2 Predictive accuracy using Visual Geometry Group (VGG-16):

In the paper “Very Deep Convolutional Networks for Large-Scale Image Recognition” by K. Simonyan and A. Zisserman from the University of Oxford proposed a Convolutional Neural Network model named VGG-16. This design was accustomed win ILSVR (Imagenet) competition in 2014[15]. It makes the advance over Alex Net by substitution massive kernel-sized filters (11 and 5 within the 1st and second convolutional layer, respectively) with multiple 33 kernel-sized filters one after another.

In VGG-16 there are convolution layers are of 3X3 filters and stride is 1 and for padding and maxpool layer are of 2X2 filters and stride is 2. It has 2 fully connected layers which lead to the output. VGG-16 has 16 layers which holds the 16 in VGG-16. VGG-16 has a network with 138 parameters. In this 16 layers there are 13 convolution layers, 5 of maxpooling layers and lastly 3 dense layers, this are the total 16 layers of VGG-16 architecture.

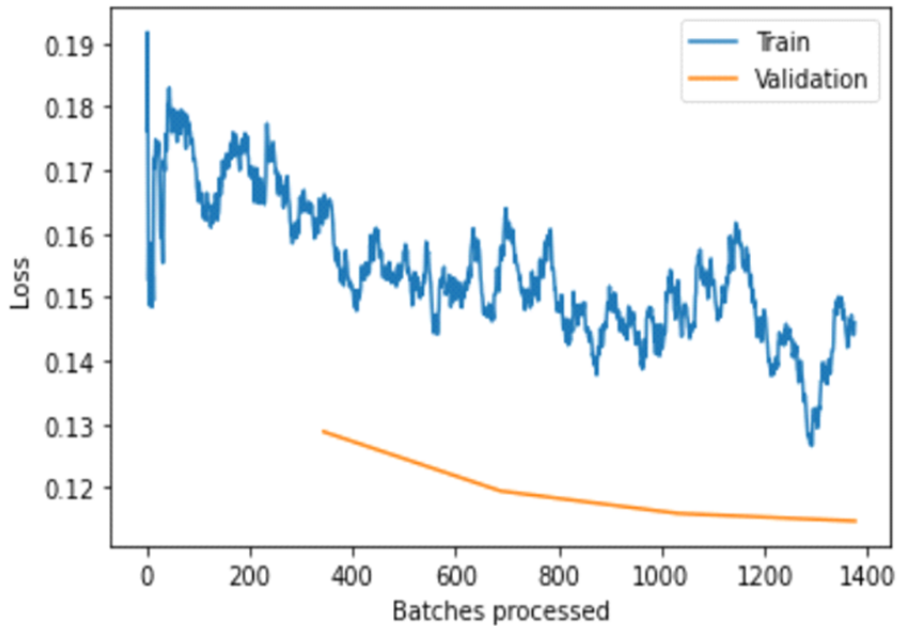


Figure 4.5: Loss vs Batch Process Graph of AlexNet

**VGG Neural Networks** VGG not only focused on smaller window sizes and strides in the first convolutional layer but also addresses another very important aspect of CNNs: depth. The architecture of VGG16 as follows Convolutional Layers: In VGG, the convolutional layers use a very small receptive field (3x3, the smallest scale always catching left / right and up / down). Also, there are 1x1 convolution filters which function as a linear input transformation followed by a ReLU unit. The convolution stage is set at 1 pixel, so that after convolution the spatial resolution is retained. CNNs are obtained by the composition of multiple operators, singly known as layers. The Rectified Linear Unit (ReLU) operator is probably the simplest and most valuable example

$$Y_{ijk} = \max(0, x_{ijk}) \quad (4.1)$$

In a certain sense, ReLU functions as a detector, with the tacit rule that a certain pattern is detected when a corresponding filter response is large enough. Upon convolution the bias is applied, essentially subtracting 0.2 from the filter responses.

**Fully-Connected Layers:** In VGG-16 there are three Fully-Connected layers, in this three layers first two layers have 4096 channels each and third one has 1000 channels. Softmax is the last layers among these three layers.

**Hidden Layers:** Both secret layers of VGG are using ReLU (a major breakthrough from AlexNet that is reducing training time). Local Response Normalization (LRN) is usually not used by VGG, since LRN improves memory usage and training time



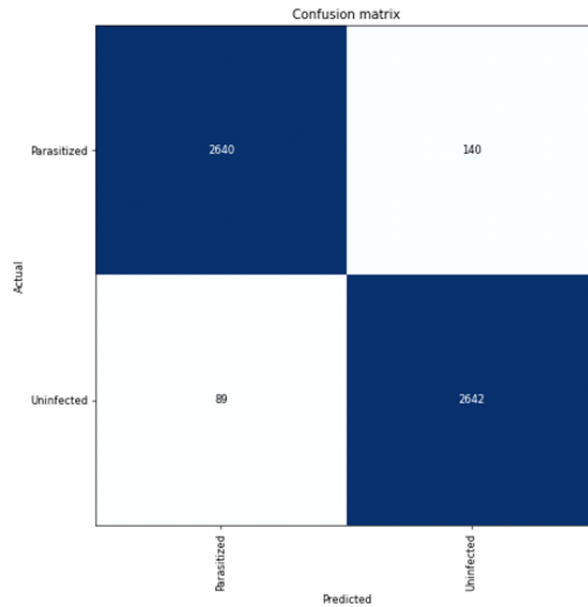


Figure 4.6: Confusion matrix of AlexNet

without any apparent improvement in accuracy.

Convolution neural network has marked an important place in image classification. It gives good accuracy in complex image classification as well. It has also gave an average accuracy in malaria detection.

Iterarion	Train Loss	Valid Loss
0	.519670	.244179
1	.438315	.217107
2	.415432	.196815
3	.407959	.196958
4	.396108	.194092
5	.392155	.186212
6	.389084	.181385
7	.389054	.192596

Table 4.3: Model Learning of VGG 16

**Test Analysis:**

Test Loss: 0.190826

Test Accuracy of Parasitized: 90% (1864/2053)

Test Accuracy of Uninfected: 94% (1964/2075)

Test Accuracy (Overall): 92% (3828/4128)

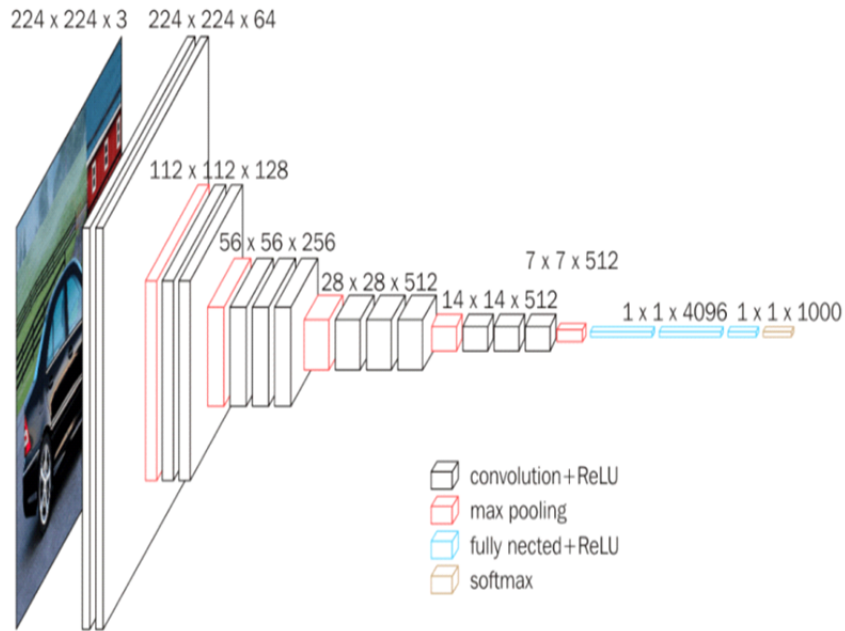


Figure 4.7: VGG-16 Architecture

### 4.1.3 Predictive accuracy using Visual Geometry Group (VGG-19):

VGG-19 is a convolutional neural network that is 19 layers deep. This pre trained network can classify images into 1000 object categories. This model network can show features of huge dataset of images. VGG-19 gives better result in rich dataset.

Iteration	Train Loss	Valid Loss
0	.368390	.202388
1	.375559	.184800
2	.374460	.194257
3	.368414	.193492
4	.370428	.191359
5	.369407	.189218
6	.369920	.190072
7	.368402	.181866
8	.363685	.181866
9	.366421	.190959

Table 4.4: Model Learning of VGG 19

#### Test Analysis:

Test Loss: 0.186976

Test Accuracy of Parasitized: 90% (1860/2053)

Test Accuracy of Uninfected: 95% (1979/2075)

Test Accuracy (Overall): 92% (3839/4128)

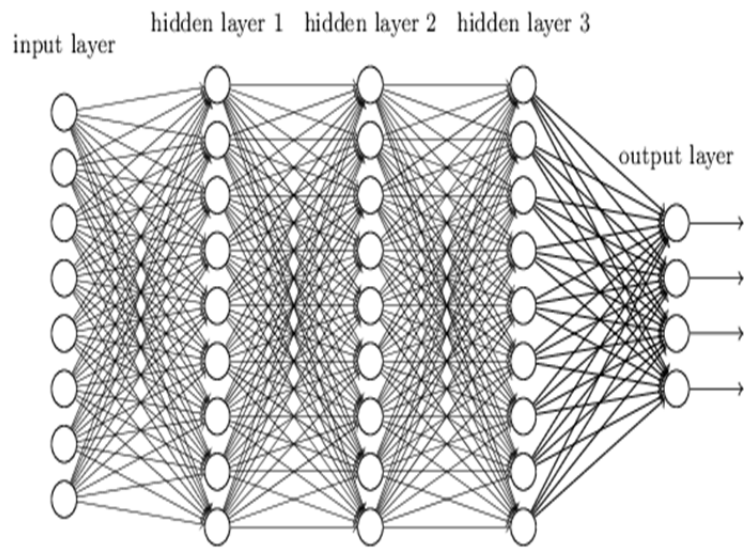


Figure 4.8: Convolutional Neural Network with three hidden layers

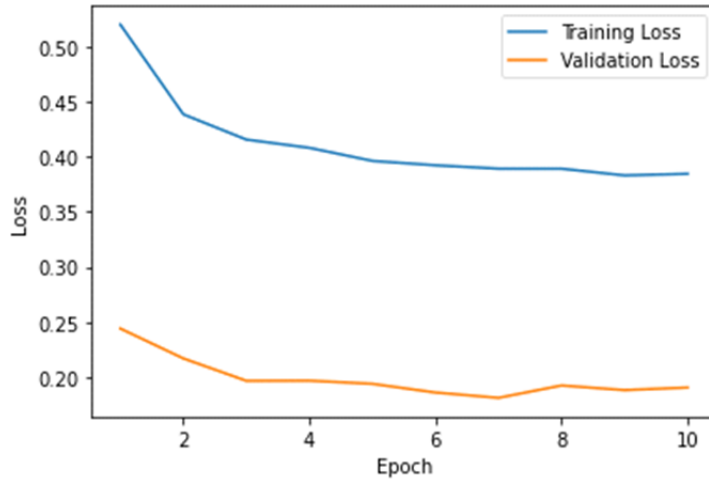


Figure 4.9: Validation Loss Vs Training Loss of VGG16

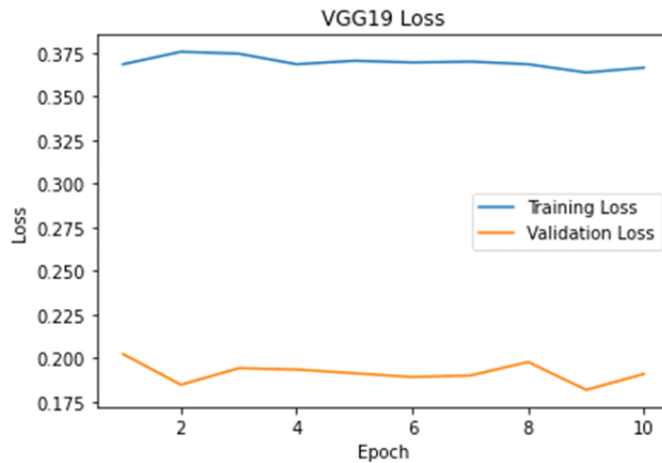


Figure 4.10: Train Loss Vs Valid Loss of VGG19

#### 4.1.4 Predictive accuracy using MobileNet:

Profound learning has fueled huge advance within the field of computer vision in later a long time, with neural systems more than once pushing the wilderness of visual acknowledgment innovation. Because of the portable gadgets with internet, the advance technology empowers and MobileNet can be used in this gadgets which can be easily handled by the people all over the world. Mobilenet is lightweight in its design. It employs depthwise distinguishable convolutions which fundamentally implies it performs a single convolution on each colour channel instead of combining all three and smoothing it. This has the impact of sifting the input channels.

MobileNet can have mobile vision, its architecture has depth-wise convolution and it creates deep learning network with light weight. It presents comprehensive experiments on resource and accuracy tradeoffs, and shows good performance on Im-

ageNet classification compared to other common models. It then illustrate the viability of MobileNets over a wide extend of applications and utilize cases counting protest discovery, finegrain classification, confront qualities and expansive scale geo-localization.

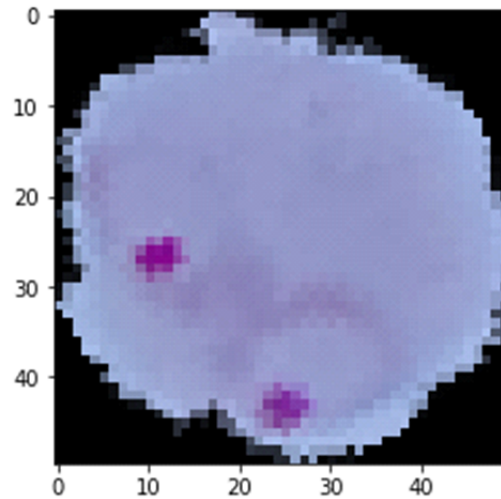


Figure 4.11: Input image of MobileNet

Input image is classified into diverse layers through changing color and contrast to find whether the cell is infected or not.

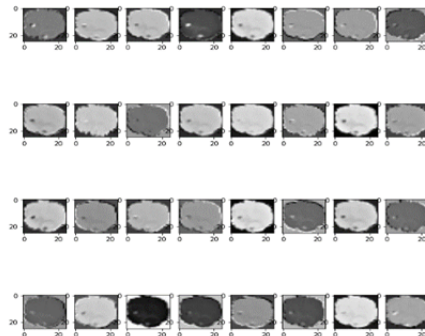


Figure 4.12: Layer 1 of MobileNet

In layer 4 the infected area of the cell is visible. The white dots in the cells are the infected regions.

It resembles the magnified version of the infected area and the black dots represents the infection in the cell.

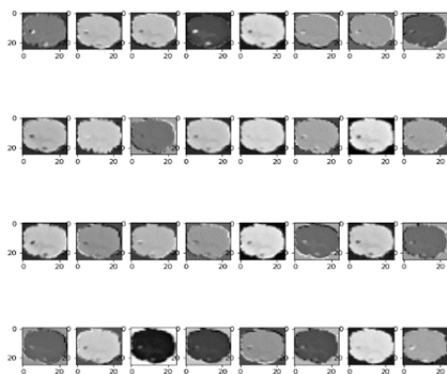


Figure 4.13: Layer 2 of MobileNet

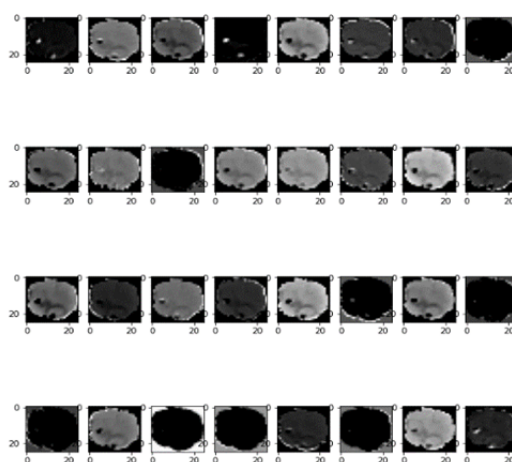


Figure 4.14: Layer 3 of MobileNet

**Test Analysis:**

Uninfected cells showing uninfected: 0.93774532

Infected cells showing infected: 0.97600768

Total Model Accuracy: 0.954279197531634

**Test Analysis:**

Uninfected cells showing infected: 0.08181382

Infected cells showing uninfected: 0.0182565

Total Model Accuracy: 0.1694294586758376

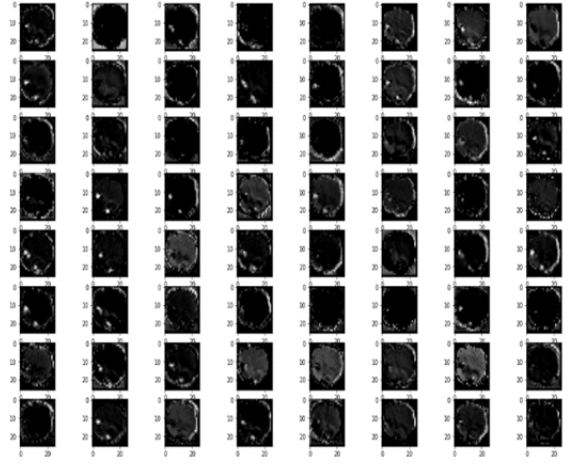


Figure 4.15: Layer 4 of MobileNet

#### 4.1.5 Predictive accuracy using Visual Geometry Group Binary (VGG-16 Binary):

Convolutional neural networks are now able to outperform humans on certain tasks related to computer vision, such as image recognition. VGG-16 Binary work on binary image segmentation of classified image (in which it have 224x224 size RGB images and corresponding grayscale masks) where it want to identify each pixel either as part of a sign (1) true or not (0) , i.e. foreground (1) or background (0). The VGG-16 Binary architecture work on parallel picture division of activity signs (of RGB pictures of estimate 224x224 and going with grayscale covers) where it need to classify each pixel as either portion of a activity sign (1) means the input malaria cell is uninfected or (0) means the input malaria cell is infected. It takes `tf.keras.applications.vgg16.VGG-16` pre-trained on ImageNet and freeze all layers (i.e. do not prepare them) then pop off the last Dense layer of 1000 units (one for each of the original 1000 image classes) followed by installing Dense layer of 50176 units (one for each of the  $224*224=50176$  pixels) and then reshape. Beginning with the stock pre trained weights from ImageNet, at that point solidifying the primary 10 layers. This takes off two trainable Conv2d-Conv2D-Conv2D-MaxPool squares (the two last ones from the first demonstrate). It will train this model on tens of thousands of yes / no binary malaria cell images to ensure that the VGG-16's last (trainable) convolution layers are completely optimized to classify malaria cell images characteristics of healthy and infected cells. This will give the individual pixels a very strong base so they can respond to the right features.

In this model, the first training the dataset contains six epochs to find the training loss, validation loss and accuracy.

To optimize the loss in  $1e-02$ , four more epochs implied on training dataset to find training loss, validation loss and accuracy.

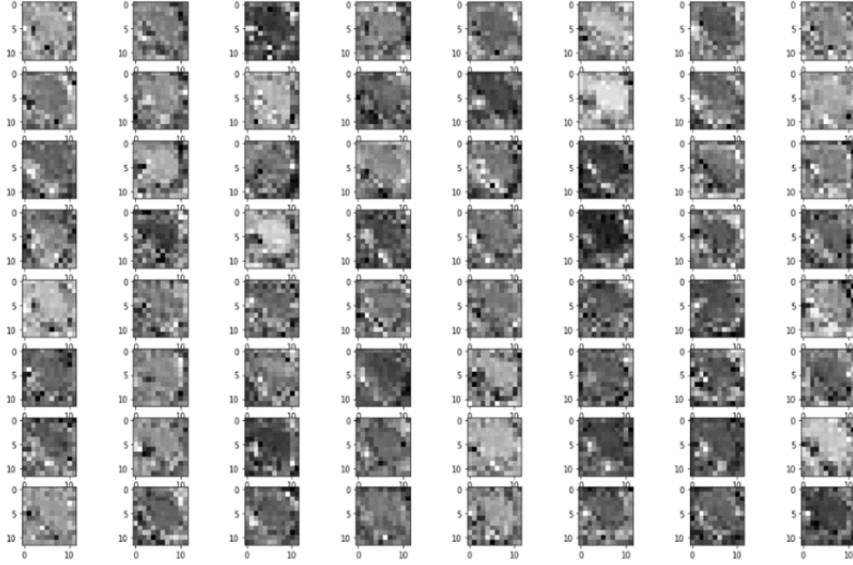


Figure 4.16: Precise Zoomed Infected Area Shown in MobileNet

Iteration	Train Loss	Valid Loss	Accur
0	.189879	.275028	.896571
1	.178610	.125146	.955725
2	.156615	.117337	.959354
3	.138689	.097226	.964253
4	.100415	.090345	.967701
5	.105238	.084673	.968245

Table 4.5: First Learning Cycle of VGG-16 Binary

#### Test Analysis:

Total model accuracy of VGG-16 Binary is 97.04% and the loss in 1400 batch is almost 0.08.

#### 4.1.6 Predictive accuracy using Visual Geometry Group Binary (VGG19 Binary):

The objective of a binary classification problem is to construct a model of deep learning that enables a choice in situations where one in all only two possible values will be taken from the item to predict. Binary classification problems suggest, by evaluating a set of attributes, assigning an individual to one of two categories. Binary image segmentation of a classified image in which each pixel is marked as part of a sign (1) true or not (0). In VGG-19 Binary the binary classification is applied on the image segmentation. The VGG-19 was trained on the ImageNet that challenges 1000-class classification task and the input is a (224, 224, 3) RGB image. The VGG-19 Binary architecture operates on the parallel division of activity signs (from RGB pictures of estimate 224x224 and going for grayscale covers) where each pixel needs to be marked as either portion of an activity sign (1) means the malaria



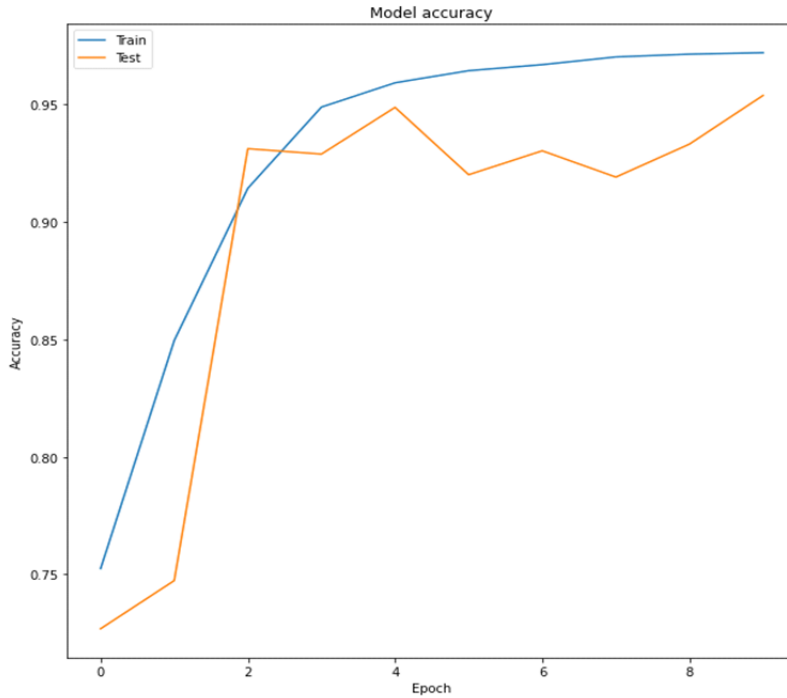


Figure 4.17: Model Accuracy of MobileNet

Iteration	Train Loss	Valid Los	Accur
0	.099307	.081669	.970241
1	.096231	.077268	.970967
2	.091850	.082390	.968427
3	.085006	.078626	.970423

Table 4.6: Second Learning Cycle of VGG-16 Binary

input cell is uninfected or (0) means the malaria input cell is infected. In VGG-19 all the convolution layers use (3 X 3) filters and that the number of filters increases in powers of two (64, 128, 256, 512) and stride length is 1 (pixel) and used a padding of 1 (pixel) on each side. There are total 5 sets of convolution layers, 2 of them have 64 filters then next set has 2 convolution layers with 128 filters then next set has 4 convolution layers with 256 filters, and next 2 sets have 4 convolution layers each with 512 filters. Max pooling layers have (2 X 2) filters with stride length 2 (pixels). A fed to a completely connected layer with 4096 neurons is flattened output of last pooling layer. The output goes to another fully connected layer with 4096 neurons and the output of this layer is again used to feed into another fully connected layer with 1000 neurons[16]. All the layers use ReLU activation function.

In binary classification, VGG-19 pre-trained on ImageNet and freeze all layers then pop off the last Dense layer of 1000 units (One for each of the original 1000 picture classes) followed by installing 50176 Dense layer (one for each of the  $224 \times 224 = 50176$  pixels) and then it reshapes. This will train this model on tens of thousands of yes / no binary malaria cell images to ensure that the last (trainable) convolution layers

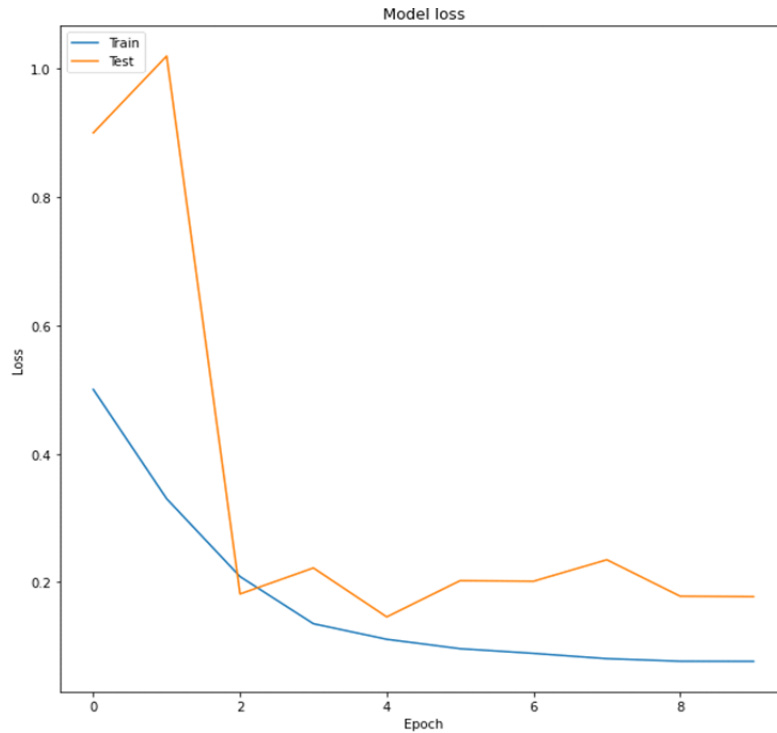


Figure 4.18: Model Loss of MobileNet

of the VGG-19 are completely trained to identify malaria cell images of healthy and infected cells.

In this model, the first training the dataset contains six epochs to find the train loss, valid loss and accuracy.

Iteration	Train Loss	Valid Loss	Accur
0	.257198	.162980	.947598
1	.178984	.126233	.956162
2	.143483	.118257	.963275
3	.134386	.100298	.964146
4	.117349	.091477	.966904
5	.119747	.090081	.967630

Table 4.7: First Learning Cycle of VGG-19 Binary

To optimize the loss in le-01, six more epochs implied on training dataset to find train loss, valid loss and accuracy.

### Test Analysis:

Total model accuracy of VGG-19 Binary is 96.53% and the loss in between 3000 and 3500 batch increased high but after 4000 batch processed, the loss is almost 0.4.

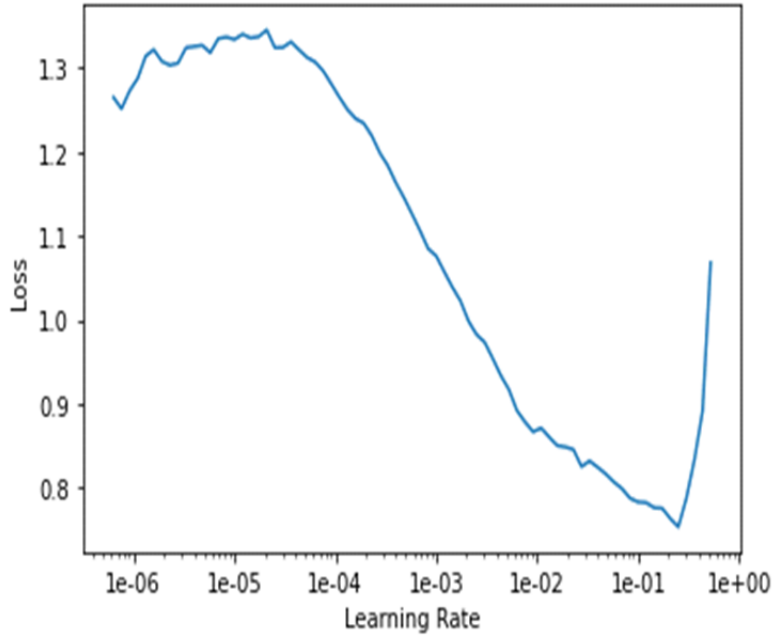


Figure 4.19: Loss vs Learning Rate Graph of VGG-16 Binary

Iteration	Train Loss	Valid Loss	Accuracy
0	.187219	.240482	.942517
1	.204989	.125563	.959501
2	.159911	.183916	.940485
3	.132649	.195313	.955727
4	.112481	1.265499	.961533
5	.111002	.374296	.965307

Table 4.8: Second Learning Cycle of VGG-19 Binary

#### 4.1.7 Predictive accuracy using Convolutional Neural Network 2D (CNN 2D):

CNN 2D is a part of Convolutional neural network. It takes three-dimensional images as inputs. The advantage of this model is, less parameters are used to run the model. The specialty of this model is it focuses more on the features of the same place that is why it also consume less time to give the output. Moreover, CNN 2D can give good accuracy in complex image dataset and CNN 2D has given a good accuracy in malaria detection which is almost 96.91%.

##### Data Pre-Processing:

Through manipulating color and contrast, the input image is categorized into different layers to figure out if the cell is infected or not.

The infected area of the cell is visible in layer 5. White spots in the cells are the

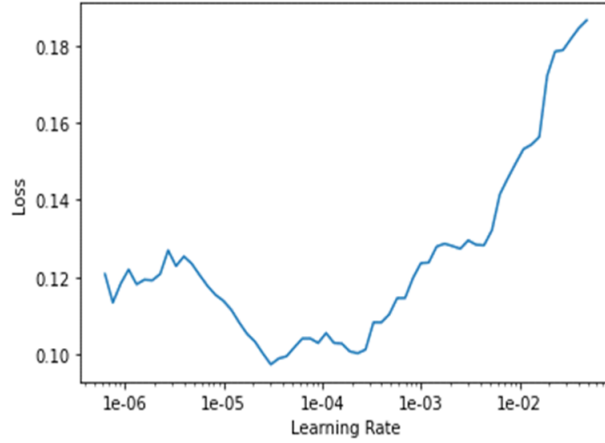


Figure 4.20: Loss vs Learning Rate Graph of VGG-16 Binary

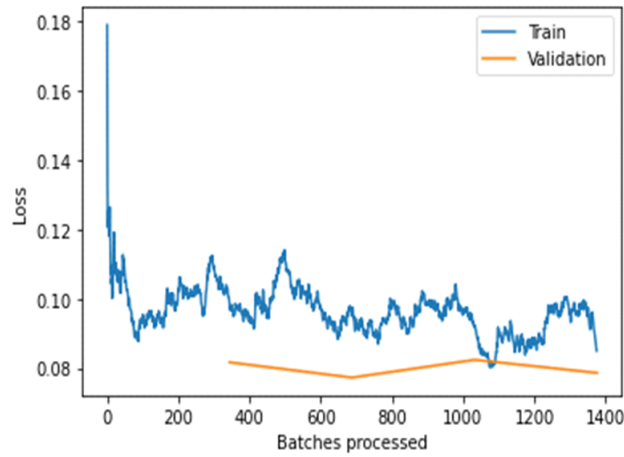


Figure 4.21: Loss vs Batches processed Graph of VGG-16 Binary

areas that have been infected. This represents the magnified version of the area infected, and the black dots reflect the cell infection.

**Model Training and Testing:** In this model, Dense 500 layers have been used and binary cross-entropy equation (4.2) has been used as loss function.

$$H_p(q) = -1/N \sum_{i=1}^N (y_i \cdot \log(p(y_i)) + (1 - y_i) \cdot \log(1 - p(y_i))) \quad (4.2)$$

To train the dataset many epochs have been implied to find the train loss, validation loss, validation accuracy and accuracy.

**Test Analysis:**

Uninfected cells showing uninfected:0.96175262

Uninfected cells showing infected:0.05026392

Infected cells showing infected:0.97684741

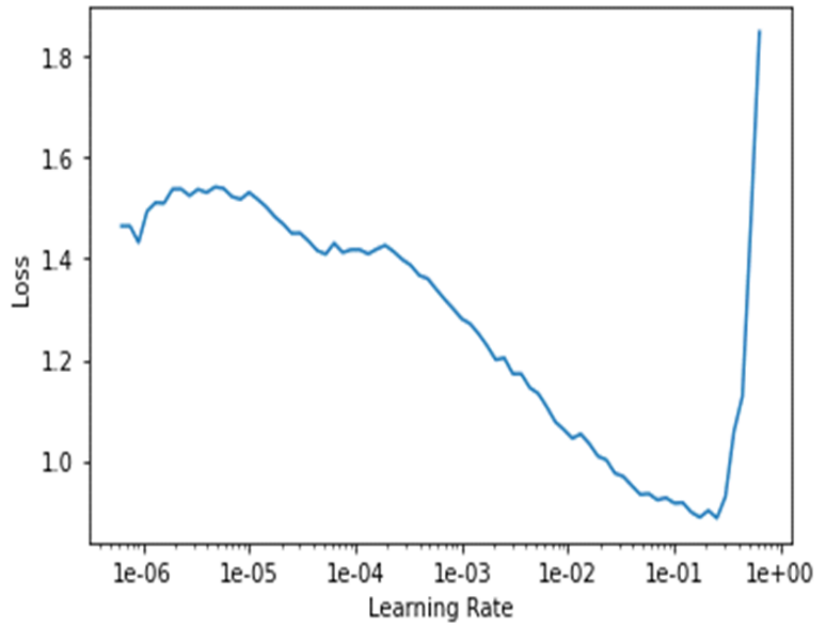


Figure 4.22: Loss vs Learning Rate Graph of VGG-19 Binary

Iteration	Train Loss	Accur	Valid Loss	Valid Accur
0	.2272	.9074	.1240	.9602
1	.1251	.9598	.1181	.9620
2	.1163	.9617	.1098	.9643
3	.1094	.9628	.1070	.9632
4	.1062	.9642	.1046	.9655
5	.1017	.9647	.1065	.9648
6	.0970	.9665	.1033	.9652
7	.0941	.9676	.1002	.9680
8	.0909	.9685	.0992	.9667
9	.0893	.9691	.0992	.9670

Table 4.9: Model Learning of CNN 2D

Infected cells showing uninfected:0.01761753

Total model accuracy: 96.91%

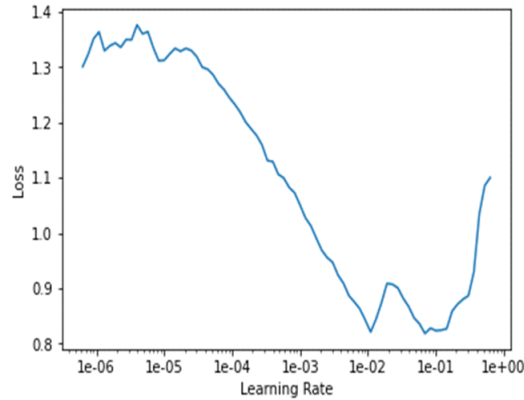


Figure 4.23: Loss vs Learning Rate Graph of VGG-19 Binary

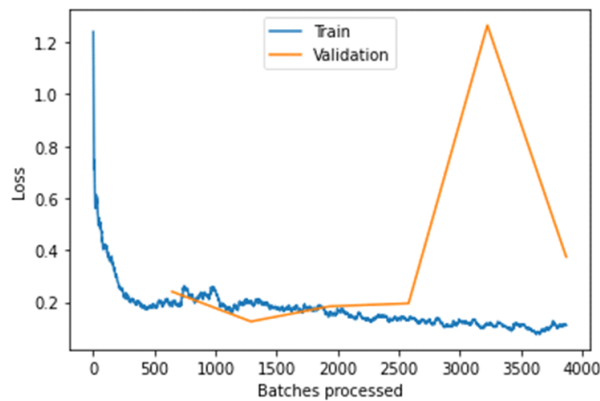


Figure 4.24: Loss vs Batches processed Graph of VGG-19 Binary

#### 4.1.8 Predictive accuracy using Residual Network 34 (ResNet34):

Deep Residual learning system for picture classification assignment which underpins a few structural arrangements, permitting to attain a reasonable proportion between the speed of work and quality.

An outfit of these remaining nets accomplishes 3.57% error on the ImageNet test set. This result won the 1st place on the ILSVRC 2015 classification errand. We moreover show investigation on CIFAR-10 with 100 and 1000 layers.

One of the issues ResNets fathom is the famous known vanishing slope. This is often since when the arrangement is as well profound, the angles from where the misfortune work is calculated effortlessly shrivel to zero after a few applications of the chain run the show. This result on the weights never overhauling its values and thus, no learning is being performed. Each layer of it is composed of a few squares.

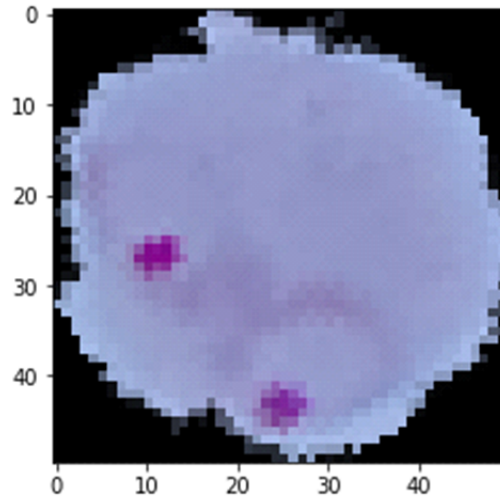


Figure 4.25: Input image of CNN 2D

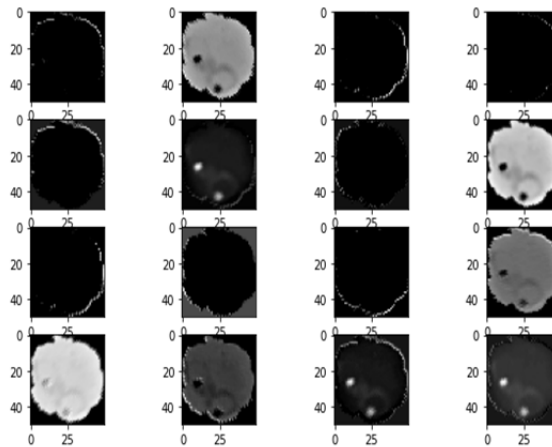


Figure 4.26: Layer 1 of CNN 2D

ResNet34 comprises on one convolution and pooling step (on orange) taken after by 4 layers of comparative behavior. The algorithm performs 3x3 convolution with a settled include outline measurement (F) [64, 128, 256, 512] separately, bypassing the input each 2 convolutions. Moreover, the width (W) and tallness (H) measurements stay consistent amid the complete layer.

The dabled line is there, absolutely since there has been an alter within the measurement of the input volume (of course a lessening since of the convolution). Note that this diminishment between layers is accomplished by an increment on the walk, from 1 to 2, at the primary convolution of each layer; rather than by a pooling operation.

CIFAR10 input pictures are (32x32) rather than (224x224), the structure of the

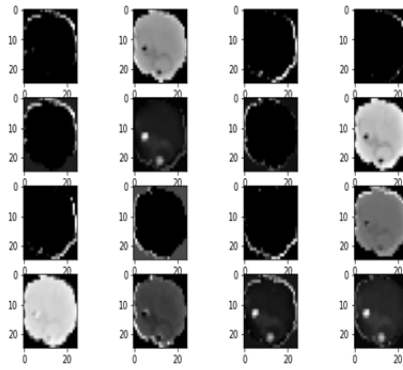


Figure 4.27: Layer 2 of CNN 2D

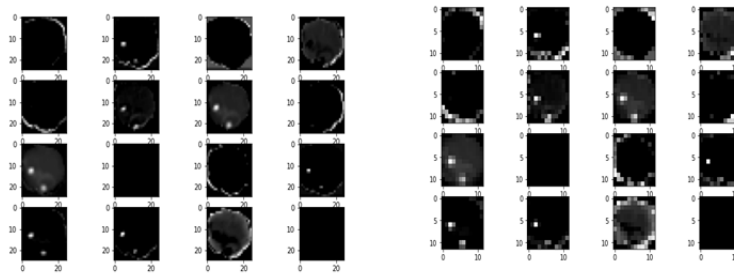


Fig-22.3: Layer 3

Fig-22.4: Layer 4

Figure 4.28: Layer 3 and Layer 4 of CNN 2D

ResNets have to be modify. The first step on the ResNet sometime recently entering the common layer behavior could be a piece — called here Conv1 — comprising on a convolution + batch normalization + max pooling operation.

In the convolutional layer, the filter size will be 64 and the size of the output pictures will be changed. Because of having 64 filters, the total volume will be multiplied by 64.

The next step is max pooling which is also called batch normalization. This Max Pooling operation does not change the original volume. The stride of 2 is needed to complete this operation.

Each layer of a ResNet34 is composed of a few blocks. This can be since when ResNet go more profound, they ordinarily do it by adding more extra layers, but the mechanism of the each layers does not change.

Another step is to heighten from the complete square to the complete layer. Down testing of the volume though the organization is accomplished by expanding the



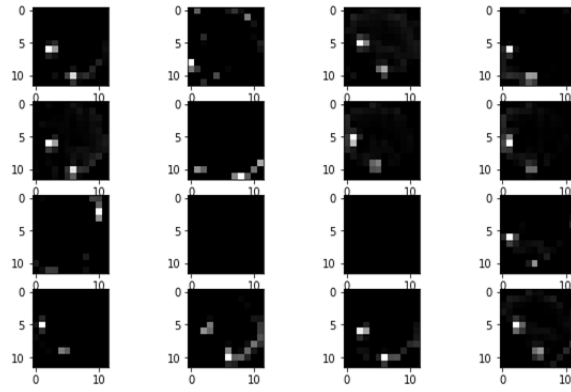


Figure 4.29: Layer 5 of CNN 2D

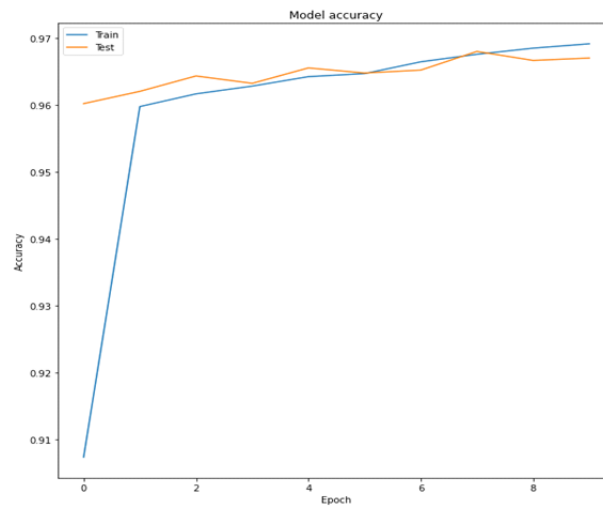


Figure 4.30: Model Accuracy of CNN 2D

walk rather than a pooling operation like ordinarily CNNs do. In truth, as it were one max pooling operation is performed in our Conv1 layer, and one normal pooling layer at the conclusion of the ResNet34, right some time recently the completely associated thick layer.

In this model, the first training the dataset contains six epochs to find the training loss, validation loss and accuracy.

To minimize the loss, 4 more epochs implied on training dataset to find training loss, validation loss and accuracy.

A confusion matrix is given below which shows that how many parasite and uninfected cell this model can detect.

**Test Analysis:** Accuracy of the model ResNet34 is 97.06% and the loss in 1400 batch is almost 0.08.

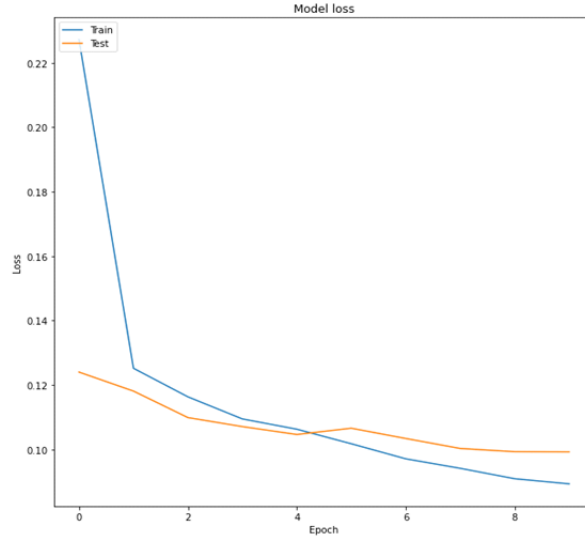


Figure 4.31: Model Loss of CNN 2D

Iteration	Train Loss	Valid Loss	Accur
0	.197310	.164542	.938850
1	.179227	.317878	.837960
2	.143181	.147928	.957177
3	.126815	.110075	.962257
4	.107863	.092104	.965705
5	.099012	.086012	.967338

Table 4.10: First Learning Cycle of ResNet34

#### 4.1.9 Predictive accuracy using Residual Network 50 (ResNet 50):

Deep convolutional neural systems have accomplished the human level picture classification result. Profound systems extricate moo, center and high-level highlights and so on. The stacked layer is crucially essential, looking at the outcome of ImageNet. As the deeper network starts to converge, a question of deterioration arises. This deterioration is not caused by over fitting or by adding more layers to a deep network, resulting in an increased training error. The declining accuracy of the training indicates that not all systems are easy to optimize. The Microsoft implemented a deep residual learning system to solve this problem. More than hoping that a few stacked layers fit a desired underlying mapping directly, they specifically let these

Iteration	Train Loss	Valid Loss	Accur
0	.098187	.089448	.967701
1	.095736	.084179	.967520
2	.087380	.079147	.969153
3	.089504	.078606	.970604

Table 4.11: Second Learning Cycle of ResNet34



Figure 4.32: ResNet 34 (right)

layers match a residual mapping. Feedforward Neural Networks with shortcut connections will realize the formulation of  $F(x) + x$ .

ResNet-50 is a convolutional Network, 50-layer wide, neural network. It can load a pre trained version of the qualified network from the ImageNet database. The pre-trained network is capable of classifying images into 1000 categories of objects, such as infected or healthy malaria cells. As a result, the network has learned rich representations of features for a large variety of images. The Network has a 224-by-224 image input display. The increase in network depth however does not work simply by piling layers together. Due to the infamous vanishing gradient problem, the gradient is back-propagated to earlier layers, repeated multiplication will make the gradient indefinitely small. As a result, as the network deepens, its output becomes saturated, or even quickly starts to degrade. ResNet-50 is a network of deep residuals. The "50" means the amount of layers that it has [17]. It is a subset of convolutional neural networks, with ResNet being most popularly used for classifying images.

ResNet's key breakthrough is the skip-connection. As you know, deep networks also suffer from vanishing gradients without changes, i.e the gradient becomes smaller and smaller as the model propagates back. Lesser gradients can make learning intractable. Until ResNet, there had been many ways to deal with the issue of the vanishing gradient.

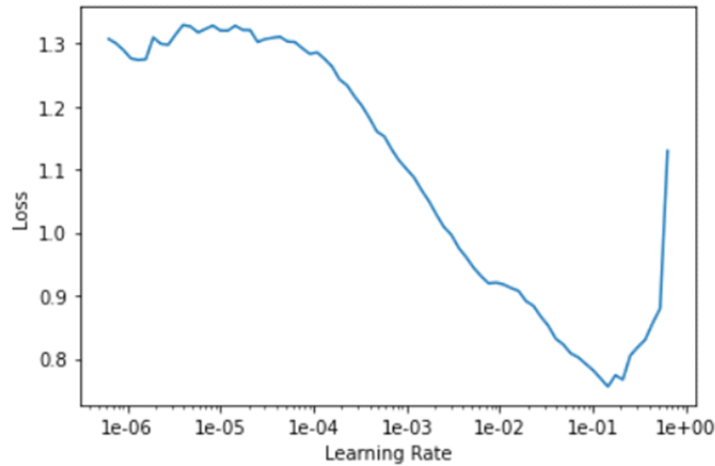


Figure 4.33: Loss vs Learning Rate Graph of ResNet34

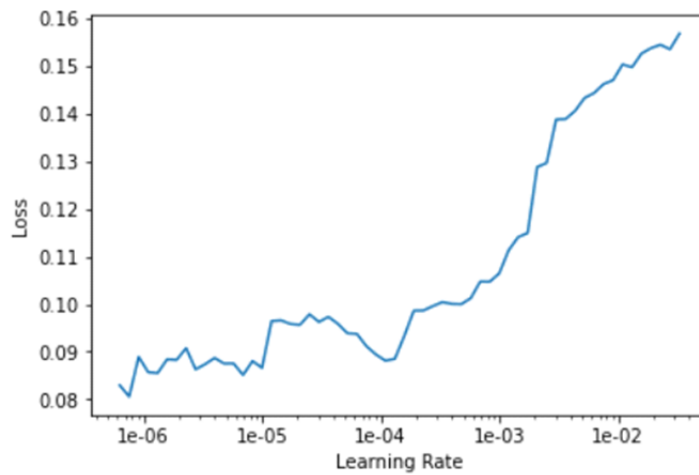


Figure 4.34: Loss vs Learning Rate Graph of ResNet34

ResNet gives better accuracy than others because of the increased depth. ResNet's central concept is to add a so-called "identity link," given in the picture below(fig:12.1).

This allows to stack additional layers and create a deeper network, offsetting the disappearing gradient by allowing your network to skip through layers which feel less important in training.

In this model, the first training the dataset contains twenty-five epochs to find the training loss and validation loss.

This model called ResNet 50 algorithm can detect parasitized and uninfected cell from image dataset.

Iteration	Train Loss	Valid Loss
1	.460365	.379665
2	.386484	.355395
3	.376971	.372811
4	.368806	.351790
5	.368686	.353230
6	.368025	.345160
7	.363806	.338463
8	.355589	.349561
9	.361195	.335808
10	.357549	.341528
11	.362972	.336990
12	.356595	.341415
13	.350642	.346786
14	.351211	.338687
15	.354795	.340201
16	.349408	.323104
17	.353477	.332348
18	.345303	.331600
19	.348563	.320465
20	.349716	.319178
21	.351651	.340456
22	.354326	.318145
23	.344992	.338495
24	.353280	.332735
25	.343593	.324040

Table 4.12: Training Loss and Validation Loss of ResNet 50

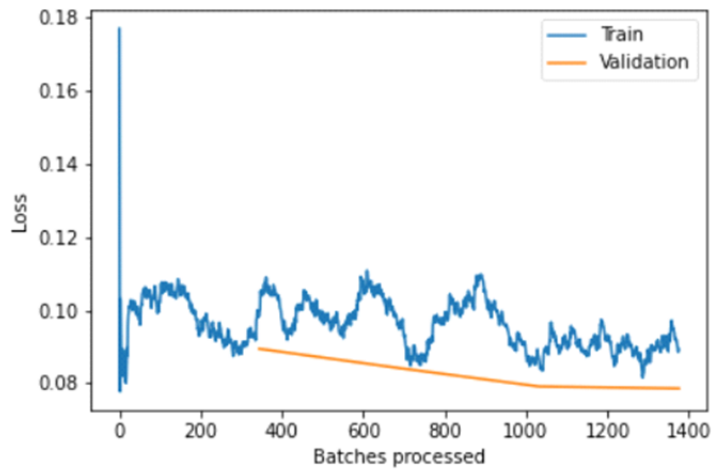


Figure 4.35: Loss vs Batches Process of ResNet34

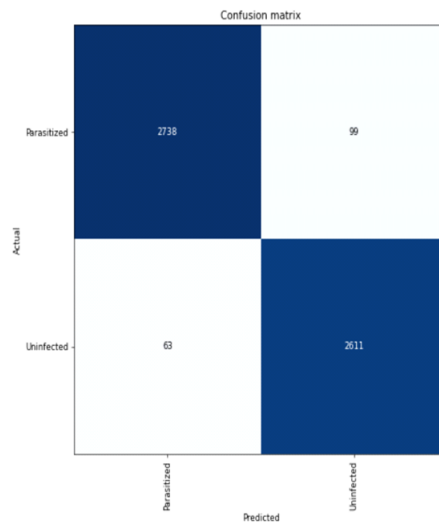


Figure 4.36: Confusion Matrix of ResNet34

**Test Analysis:**

Test Loss: 0.332693

Test Accuracy: 85% (2354/2756)

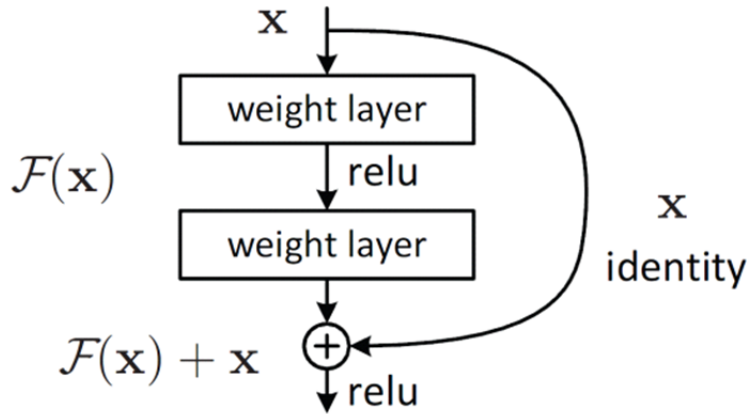


Figure 4.37: Identity Shortcut Link

## 4.2 Result Analysis and Comparison:

There are total nine models that have been applied on the same dataset of malaria infected and uninfected images. Among AlexNet, VGG-16, VGG19, VGG-16 Binary, VGG-19 Binary, MobileNet, CNN 2D, ResNet34 and ResNet50, the best accuracy is given by VGG-16 Binary and ResNet34 (Table-5). VGG-16 Binary has given 97.04% and ResNet34 has given 97.06 % accuracy on malaria dataset.

Algorithm	Training Accuracy	Validation Accuracy	Model Accuracy
AlexNet	85.41%	88.53%	95.84%
VGG-16	61.56%	81%	92%
VGG-19	63.4%	81%	92%
VGG-16 Binary	91.5%	92.2%	97.04%
VGG-19 Binary	89%	63%	96.53%
MobileNet	—	—	95.42%
CNN 2D	91.07%	96.7%	96.91%
ResNet34	91.1%	92.14%	97.06%
ResNet50	65.64%	67.6%	85%

Table 4.13: Results of different models

As AlexNet, VGG-16, VGG-19 has 5, 16 and 19 layers respectively but the rising depth of the network does not work simply by piling layers together. Due to the infamous vanishing gradient problem, deep networks are difficult to train because the gradient is back-propagated back to earlier layers, repeated multiplication will make the gradient endlessly small, and this may degrade the performance. ResNet34 implements “identity shortcut connection” that skips one or more layers which makes it more faster than other models and also give better accuracy as the gradient value does not decrease by the back propagation. Moreover, in VGG-16 and VGG-19 more parameters are used compared to ResNets which may create additional overhead and effect the accuracy. From Table-5 it is visible that VGG-16 and VGG-19 has less accuracy than ResNet34. Both VGG-16 and VGG-19 has 92% accuracy.

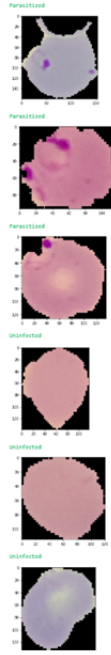


Figure 4.38: Detection of parasitized and uninfected cells using ResNet50

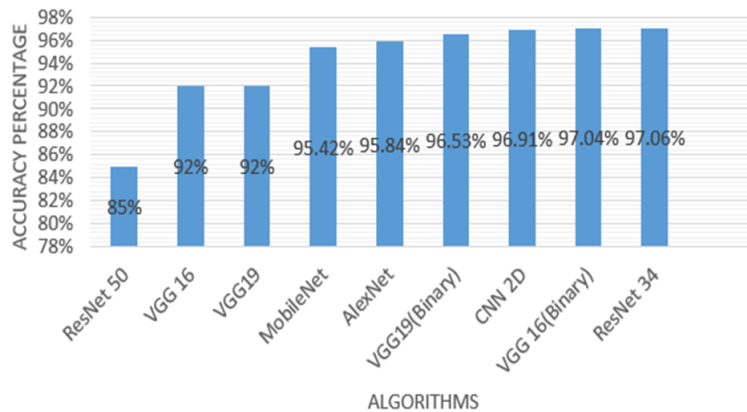


Figure 4.39: Chart of Accuracy Vs Algorithm

AlexNet has shown better accuracy than VGG-16 and VGG-19. One reason is that hyper-parameters tuning is not done for VGG properly while AlexNet is better suited. The accuracy of AlexNet is almost 95.84%. Both VGG-16 Binary and VGG-19 Binary has given better accuracy than AlexNet, VGG-16, VGG-19, MobileNet and ResNet50 because of its binary classification. MobileNet is 30 times smaller and 10 times faster than VGG's but still it gives better accuracy that both of VGG-16 and VGG-19, MobileNet's accuracy is 95.4%. As MobileNet has given 95.42% accuracy, the CNN 2 D has been implied on the same dataset to detect the accuracy and it gives better accuracy than MobileNet which is almost 96.91%. Lastly, on malaria dataset the least accuracy is given by ResNet50. Other eight models have better accuracy than ResNet50, the accuracy of ResNet50 is 85 %.



# Chapter 5

## Conclusion

Malaria is an alarming disease which is taking life of millions of people all over the world. This disease is more prominent among the children and is a contagious disease that spread through mosquitoes. In this paper CNN algorithms are used to detect the infected and uninfected malaria blood cells from images and calculated the accuracy given by different algorithms named VGG-16, VGG-19, VGG-16 Binary, VGG-19 Binary, MobileNet, AlexNet, ResNet34, ResNet50 and CNN 2D. The difficulties of this study is to extract feature from the images and the classification of images using different algorithms to identify infected and healthy blood cells. This research shows a comparative study on a given dataset by different algorithms. From the studies it shows that the algorithm named ResNet34 represent the highest accuracy on the dataset. Algorithms named VGG-16, AlexNet and MobileNet shows an accuracy of 92%, 95.84% and 95.42% respectively.

# Bibliography

CDC - Malaria - Diagnosis Treatment (United States) - Diagnosis (U.S.). (2018, July 23).

Tangpukdee, N., Duangdee, C., Wilairatana, P., Krudsood, S. (2009, June). Malaria diagnosis: a brief review.

Who.int. (2019). Fact sheet about Malaria. [online] Available at: <https://www.who.int/news-room/fact-sheets/detail/malaria> [Accessed 24 Aug. 2019].

Bill Melinda Gates Foundation. (2019). Malaria. [online] Available at: <https://www.gatesfoundation.org/what-we-do/global-health/malaria> [Accessed 24 Aug. 2019].

UNICEF DATA. (2019). Malaria in Africa - UNICEF DATA. [online] Available at: <https://data.unicef.org/topic/child-health/malaria/> [Accessed 24 Aug. 2019].

Haque, U., Ahmed, S., Hossain, S., Huda, M., Hossain, A., Alam, M., Mondal, D., Khan, W., Khalequzzaman, M. and Haque, R. (2019). Malaria Prevalence in Endemic Districts of Bangladesh.

R.Kuang, J.Gu, H.Cai,Y.Wang. (2009). Improved prediction of malaria degradomes by supervised learning with SVM and profile kernel. *Genetica*. 136. 10.1007/s10709-009-9383-x.

A.Patel and Z.Dobariya. (2015). Detection of Malaria Parasite using K-Mean Clustering.

M.I.Razzak(2015).Automatic Detection and Classification of Malaria Parasite.

N.Ahirwar, S.Pattnaik, and B.Acharya,(2012). Advanced image analysis based system for automatic detection and classification malarial parasite in blood images. International Journal of Information Technology and Knowledge Management January. 5. 59-64.

H.park,M.Rinehart,K.Walzer,J.Chi and A.Wax(2016). Automated Detection of P. falciparum Using Machine Learning Algorithms with Quantitative Phase Images of Unstained Cells. PloS one. 11. e0163045. 10.1371/journal.pone.0163045  
C.B.Delahunt,

J.Hung,A.Goodman, S.Lopes,G.Rangel,D.Ravel, F.T.MCosta,M.Duraisingh, M.Marti(2018). Applying Faster R-CNN for Object Detection on Malaria Images.

Malaria Dataset — National Library of Medicine. (n.d). Retrieved from [lh-ncbc.nlm.nih.gov/publication/pub9932](https://ncbc.nlm.nih.gov/publication/pub9932)

Large Scale Visual Recognition Challenge 2012 (ILSVRC2012). (n.d). Retrieved from <http://www.image-net.org/challenges/LSVRC/2012/results.html>

VGG16 - Convolutional Network for Classification and Detection. (2018, November 21). Retrieved from <https://neurohive.io/en/popular-networks/vgg16/>

Petrovska, Biserka Stojanovic, Igor Atanasova-Pacemska, Tatjana. (2018). Classification of Small Sets of Images with Pre-trained Neural Networks. International Journal of Engineering and Manufacturing. 8. 40-55. 10.5815/ijem.2018.04.05.

*DAGNetwork.(n.d).Retrievedfrom  
[https : //ww2.mathworks.cn/help/deeplearning/ref/resnet50.html](https://ww2.mathworks.cn/help/deeplearning/ref/resnet50.html)*