Malaria detection in thin blood cells using deep learning

Assigned Project - III (CS 881) report submitted to

Bankura Unnayani Institute of Engineering

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Bachelor of Technology

in

Computer Science & Engineering

by

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(10500119012, 10500119020, 10500119009 & 10500119005)

Under the supervision of

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Computer Science & Engineering

Bankura Unnayani Institute of Engineering

Even Semester, 2023

May 12, 2023

COMPUTER SCIENCE & ENGINEERING

BANKURA UNNAYANI INSTITUTE OF ENGINEERING

DECLARATION

I certify that

(a) The work contained in this report has been done by me under the guidance of my/our supervisor(s).

(b) The work has not been submitted to any other Institute for any degree or diploma.

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Place: Bankura (10500119012, 10500119020, 10500119009 & 10500119005)

COMPUTER SCIENCE & ENGINEERING

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BANKURA - 722146, INDIA

CERTIFICATE

This is to certify that the project report entitled "**Malaria detection in thin blood cells using deep learning** " submitted by **Nayan Mahata, Priyam Dutta, Tamoy Rana & Sougata Dutta** (Roll No. 10500119012, 10500119020, 10500119009 & 10500119005) to Bankura Unnayani Institute of Engineering towards partial fulfilment of requirements for the award of degree of Bachelor of Technology in Computer Science & Engineering is a record of bona fide work carried out by him under my supervision and guidance during Even Semester, 2023.

Prof. Subhashis Misra & Prof. Alok Kumar Roy

Countersigned by:

Coordinator
Date: May 12, 2023
Place: Bankura

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Abstract:-

Malaria is a life-threatening disease that is spread by the Plasmodium parasites. It is detected by trained Microscopist who analyse microscopic blood smear images. Modern deep learning techniques may be used to do this analysis automatically. The need for the trained personnel can be greatly reduced with the development of an automatic accurate and efficient model. In this article, we propose an entirely automated Convolutional Neural Network (CNN) based model for the diagnosis of malaria from the microscopic blood smear images. A variety of techniques including knowledge distillation, data augmentation, Auto encoder, feature extraction by a CNN model and classified by Support Vector Machine (SVM) or K-Nearest Neighbours (KNN) are performed under three training procedures named general training, distillation training and auto encoder training to optimize and improve the model accuracy and inference performance.

Keywords

Plasmodium parasites, microscopic, blood smear, data augmentation, CNN, knowledge distillation, Auto encoder, inference performance, floating point operations, deep learning.

Acknowledgements

We would like to take this opportunity to thank everyone whose co-operation and encouragement throughout the ongoing course of this project remains invaluable to us.

We are sincerely grateful to our guide Prof. Subhashis Misra and Prof. Alok Kumar Roy of the Department of Computer Science Engineering, BUIE, for his wisdom, guidance and inspiration that helped us to go through with this project and take it to where it stands now.

Last but not the least, we would like to extend our warm regards to our families and peers who have kept supporting us and always had faith in our work.

Sougata Dutta

Nayan Mahata

priyam Dutta

Tanmoy Rana

Contents

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"We are what our thoughts have made us; so take care about what you think. Words are secondary. Thoughts live; they travel far."

– Swami Vivekananda

"Take up one idea. Make that one idea your life - think of it, dream of it, live on that idea. Let the brain, muscles, nerves, every part of your body, be full of that idea, and just leave every other idea alone. This is the way to success."

– Swami Vivekananda

"When an idea exclusively occupies the mind, it is transformed into an actual physical or mental state."

– Dr. A. P. J. Abdul Kalam

"Dream is not that which you see while sleeping it is something that does not let you sleep."

– Dr. A. P. J. Abdul Kalam

Chapter 1

Sample

1.1 Introduction

Plasmodium parasites, microscopic, blood smear, data augmentation, CNN, knowledge distillation, Auto encoder, inference performance, floating point operations, deep learning. Here plasmodium parasites is the main virus of malaria. we can detect this disease using blood objection procedure.

Literature Survey The origin of malaria starts from the continent of Africa. The malaria was originated from the virus plasmodium falcipuram virus which is the cause for this disease. The disease has traveled through all around the world by the pathogen of mosquitoes. The virus can survive in hot and mild weather, but itcannot survive in very cold weather. The disease was 40 million years old from a very old age period.Malaria can infect all the animals to humans from infant to adult. Starting from fever to coma and death The disease directly attacks the blood cell of the human body and breaks the white blood cell and stops the functionality of the organs of the human being. Malaria can be detected only by taking the blood samples from the human being and viewed in the microscope.

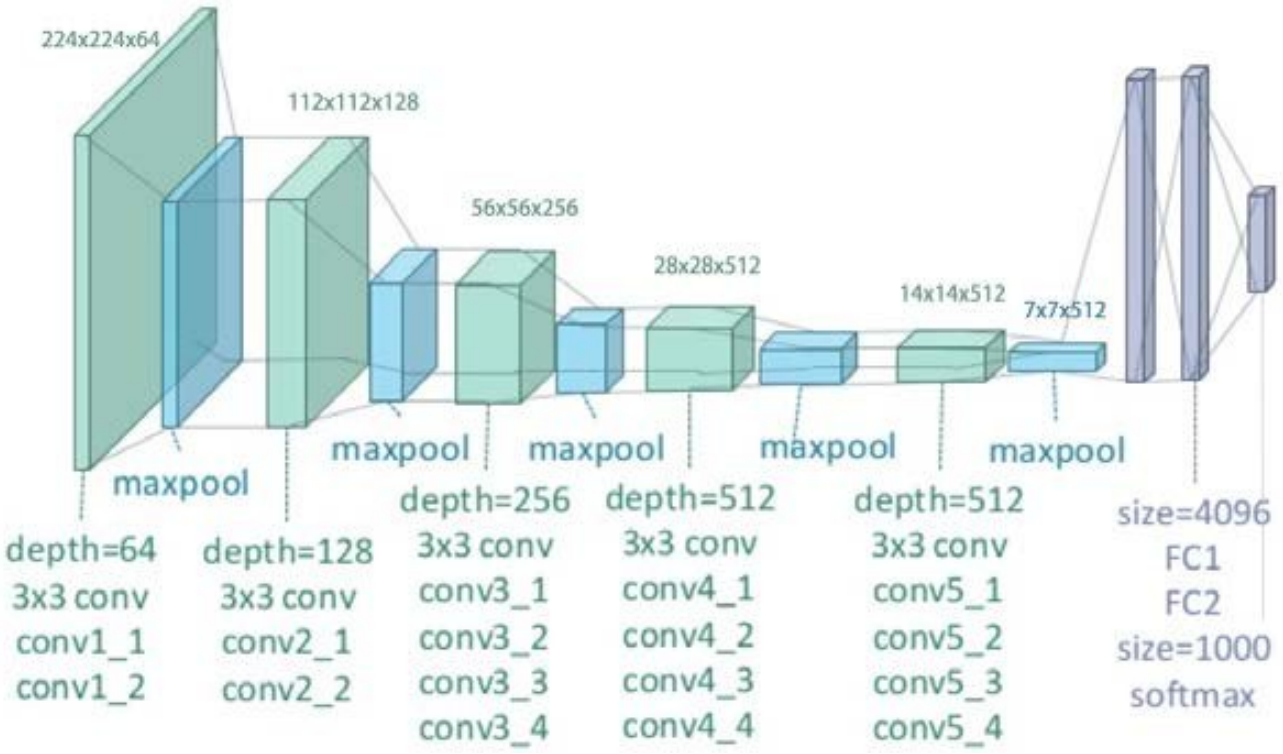

FIGURE 1.1: VGG-19 Model Architecture

Research gaps 1.deficiency of active testing in the public community and no appropriate technique to evaluate elimination. 2.lack of sensitive diagnostic tools for asymptomatic patients.

Objective Provide universal access to malaria diagnostic and treatment services free of charge.

Scope Whenever a malaria patient has been reported, the Regional Malaria Officer (RMO) should take measures to confirm the diagnosis by microscopic examination of blood smears and Rapid Diagnostic Test (RDT).

An algorithm We will see the next portion of this PPT.

1.2 Adding another section

This research focuses on designing an accurate malaria diagnosis model that can be implemented without any dependencies on skilled technicians and testing the model accuracy to get high-quality results. Automated image analysis software could remove the most serious limitation of the worldwide accepted microscopy method in general, dependency on human experts for diagnostic accuracy of the results. Automating the detection process means using the knowledge, the practice of conventional methods, and implementing it to get fast and efficient results.

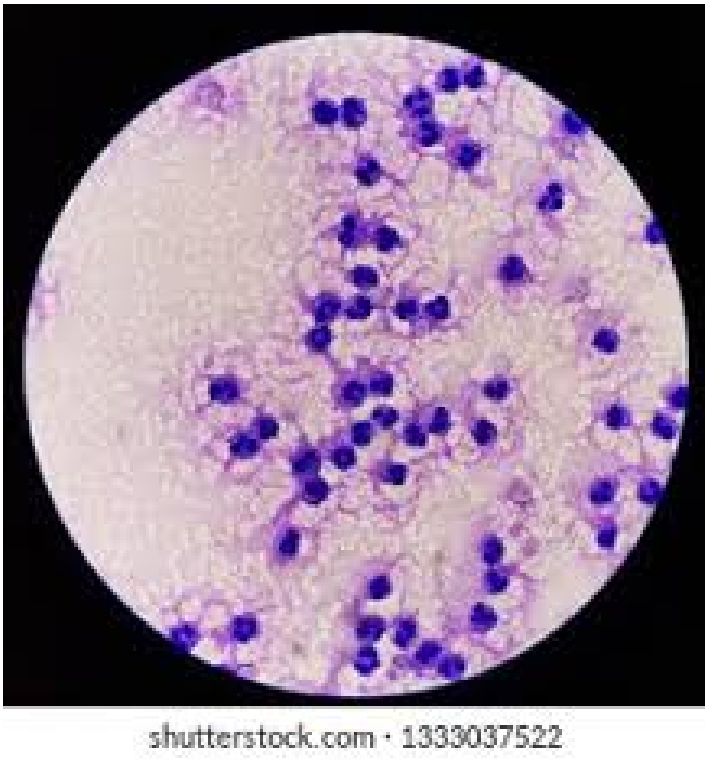

FIGURE 1.2: Sample image taken from the model development dataset

Chapter 2

LITERATURE SURVEY

2.1 Introduction

Malaria being a life threatening disease has caused deep research interests among the scientists all over the world. Earlier, malaria was mostly diagnosed in the laboratory setting requiring a great deal of human expertise. Automatic systems such as those relying on machine learning techniques were initially studied to overcome this problem (Sutskever and Hinton).Techniques reported in this domain of study mostly considered the handcrafted features in decision making.For example, relied on morphological factors for feature extraction and applied SVM and Principal Component Analysis (PCA) for the classification purpose (3). However, the accuracy achieved through these kinds of model is low compared to the more recently studied deep learning based techniques.

Literature Survey For automatic detection of malaria pathogens from the microscopic images, Convolutional Neural Network (CNN) received much attention from the researchers in recent times. Dong et al. for example evaluated the performances of three popular Convolutional Neural Network, namely LeNet-5, AlexNet and GoogLeNet. In addition, they trained an SVM classifier for comparison purposes and concluded that CNN is advantageous over SVM in terms of the capacity of learning image features automatically. To find the optimal layer of a pre-trained

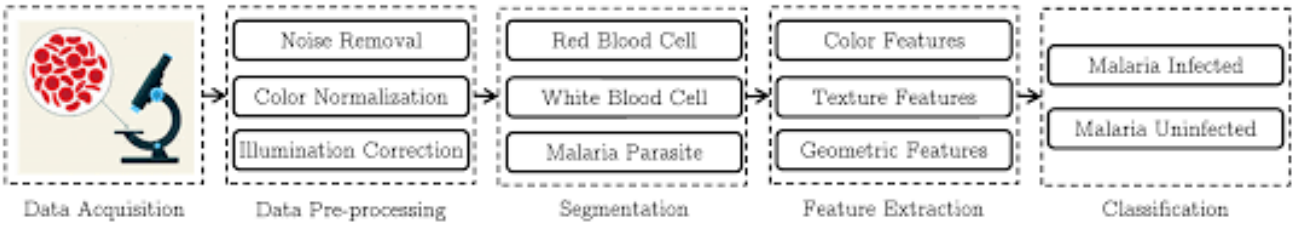

FIGURE 2.1: Traditional automated malaria detection pipeline

model to extract features from underlying malaria parasite data, Rajaraman et al. evaluated the performances of AlexNet, VGG-19, ResNet-50, Xception, DenseNet-121 along with their custom-built model. Liang et al. reported 97.37% accuracy in detection with the help of their 16-layered CNN model and claimed that their model is superior to transfer learning models.

Research gaps 1.deficiency of active testing in the public community and no appropriate technique to evaluate elimination. 2.lack of sensitive diagnostic tools for asymptomatic patients.

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An algorithm

2.2 Adding another section

In contrast, in this work, we propose several deep learning models which achieve classification performance comparable to the previously reported highly accurate deep learning based solutions. In addition, our models are efficient in terms of

required computational resources and have been demonstrated to work efficiently on smart mobile devices, including that are available at very low cost.

Chapter 3

PROBLEM STATEMENT

3.1 DFD

Research on CNNs were not focused on preprocessing techniques, rather they were 14 more relied on getting comparable results using CNNs and transfer learning. Most researches were limited to designing CNN from scratch. We have conducted extensive experiments using the NIH malaria dataset on three different settings, namely, custom network from scratch, fine tuning on pre-trained model and Ensemble model.

Literature Survey The purpose of this study is to compare and contrast the effectiveness of deep learning models, specifically Convolutional Neural Networks, in categorizing human blood smear images as Malaria Parasitized vs.Healthy. This research also focuses on uncovering the effects of preprocessing techniques on model accuracy. Many researches have been conducted on automating the malaria diagnosis using machine learning. Machine learning has shown great results in the health care industry like the google machine learning algorithm to help identify can cerous tumors on mammograms.

Research gaps 1.deficiency of active testing in the public community and no appropriate technique to evaluate elimination. 2.lack of sensitive diagnostic tools for asymptomatic patients.

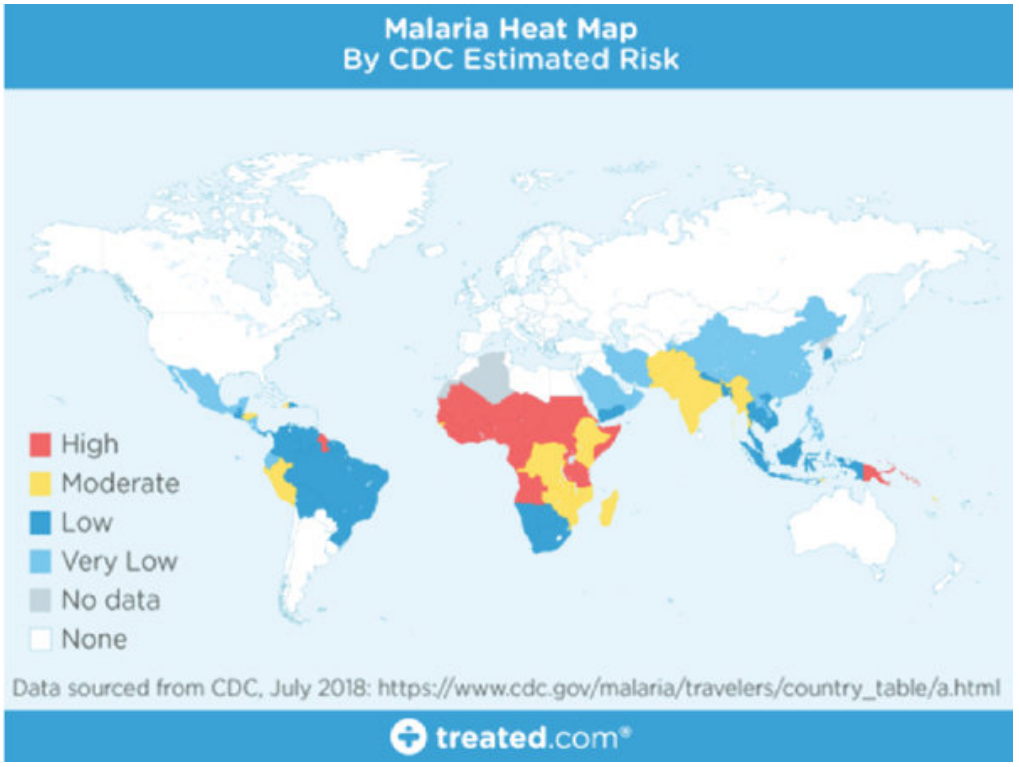

FIGURE 3.1: Malaria Estimated Risk Heath Map (Source: treated.com)

Objective Provide universal access to malaria diagnostic and treatment services free of charges.

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An algorithm

3.2 Adding another section

Research on diagnosing diabetic retinopathy in retinal images is one of the most successful discovery in the IT and Health sector. Many researchers have conducted their study on the malaria diagnosis and have achieved great results, but with the advancement in the technology and availability of much more data, new field of

Artificial Intelligence is gaining popularity that is Deep Learning. Deep learning is a sub field of machine learning that imitates the workings of the human brain in processing data and creating patterns for use in decision making. In this research, we compared the results gained during the research with the preexisting results using machine learning techniques in earlier studies.

Chapter 4

PROPOSED SOLUTION

4.1 Classification:

Build a machine learning algorithm capable of detecting the correct effected cell or normal cell in new unseenimages.

Differences: Traditional algorithms: hand-craft the features.

Deep learning algorithms: done automatically by the algorithm.

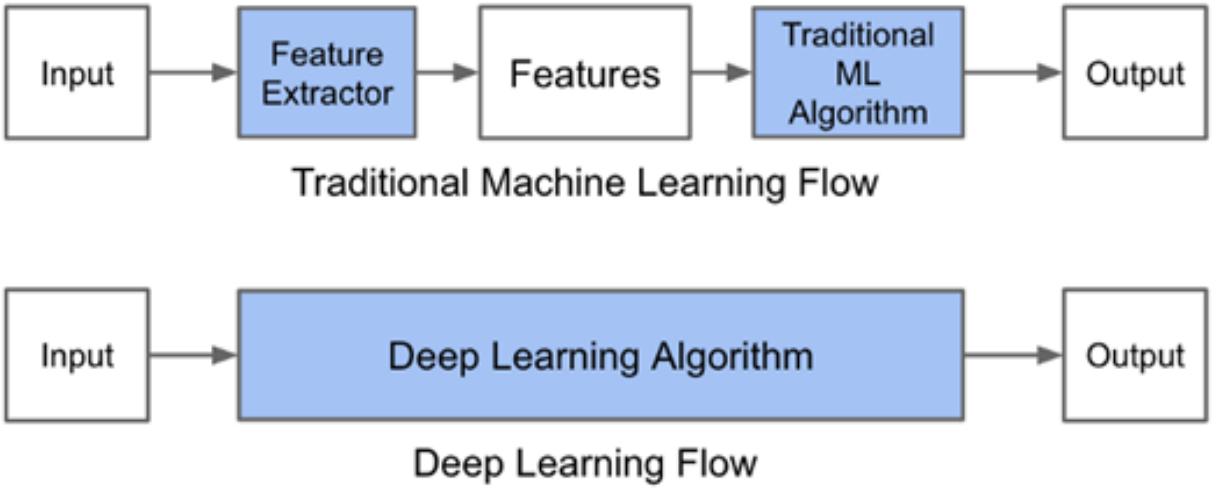


FIGURE 4.1: Deep learning flow

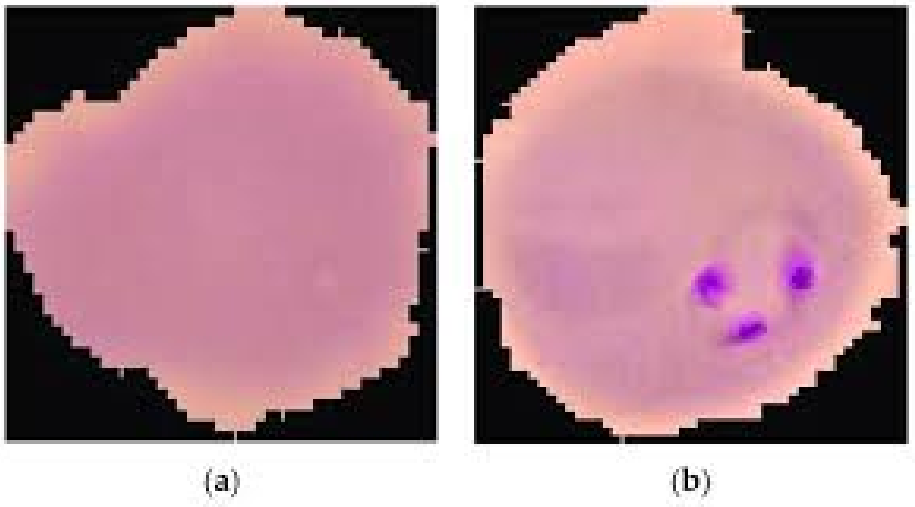


FIGURE 4.2: Deep learning flow

CNN Architecture: Convolutional neural networks are a special type of feed-forward networks. These models are designed toemulate the behaviour of a visual cortex. CNNs perform very well on visual recognition tasks.

Special layers: convolutional layers and pooling layers

The Data: - 27,598 cells images, with 13,780 Parasitized cells images and 13,818 Uninfected cells images.

Tools Used: - Computer Vision Library • OpenCV - Deep Learning Libraries • Tensorflow • Keras with Tensorflow backend - Systems • NVIDIA-SMI 460.32.03 • GPU- Tesla T4 8 vCPU, 32 GB Memory

Tensorflow: The Tensorflow platform helps you implement best practices for data automation, model tracking, performance monitoring, and model retraining. Using production-level tools to automate and track model training over the lifetime of a product, service, or business process is critical to success.

OpenCV: OpenCV (Open Source Computer Vision Library) is an open source computer vision and machine learning software library. OpenCV was built to provide

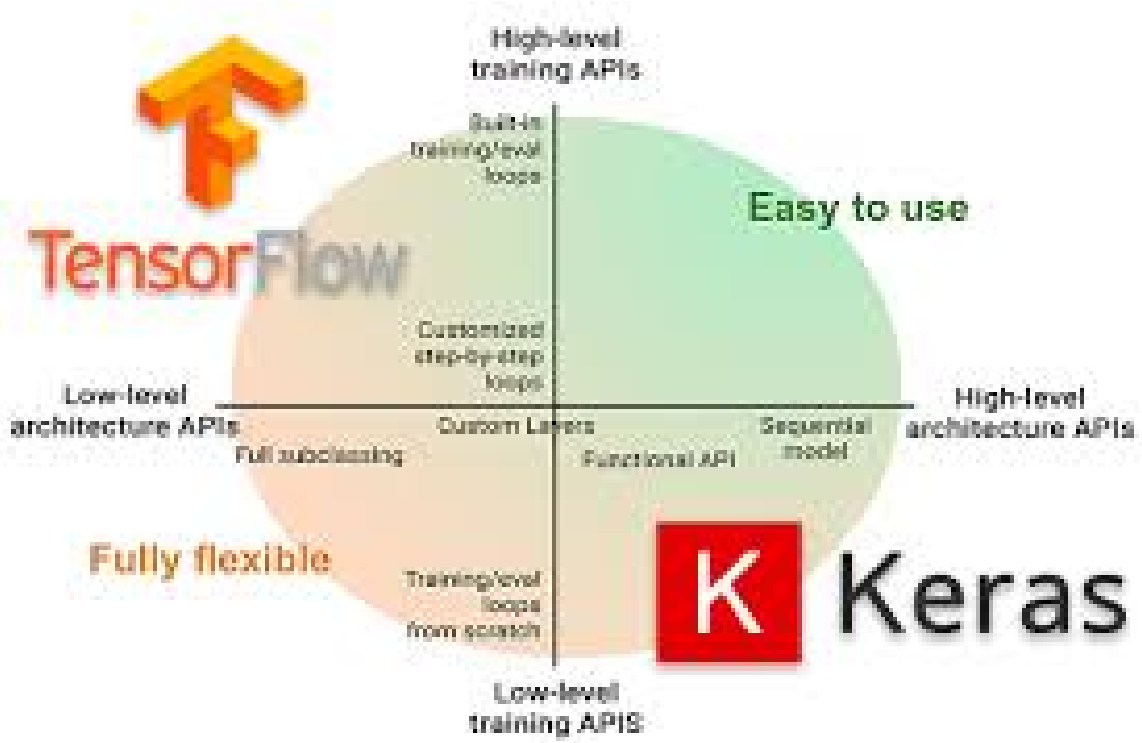


FIGURE 4.3: Deep learning flow

a common infrastructure for computer vision applications and to accelerate the use of machine perception in the commercial products.

4.2 Adding another section

Keras: Keras is a high-level, deep learning API developed by Google for implementing neural networks. It is written in Python and is used to make the implementation of neural easy. It also supports multiple backend neural network computation.

Chapter 5

Dataset

5.1 Introduction

Malaria dataset contains 27,558 cell images classified into two groups called parasitized and uninfected cells, where each cell contains an equal number of instances. Data was taken from 150 P. falciparum and 50 healthy patients and it was photographed at Chittagong Medical College Hospital, Bangladesh using a smartphone by placing it on the conventional light microscope[2]. Manual annotation was performed later by an expert slide reader at the Mahidol-Oxford Tropical Medicine Research Unit. In this data, parasitized samples mean that there is the presence of Plasmodium, whereas the uninfected samples refer to the absence of Plasmodium but there may be presence of other objects like staining artefacts/impurities.

While studying the dataset, some of the labelled data raised suspicion of whether they were correctly labelled. Some of the data seems like uninfected but labelled as parasitized, where some parasitized images are labelled as uninfected. To confirm this rising issue, we consulted with an expert. The expert confirmed that some of the data are genuinely mislabeled which was later manually annotated as per the presence and absence of malarial parasites. While annotating, suspicious, and falsely labelled data was put aside, which resulted in the reduction of data from 27,558 to 26,161. After removing 647 falsely labeled and suspicious parasitized data, the amount of current parasitized data stands 13,132. In this article, correct parasitized

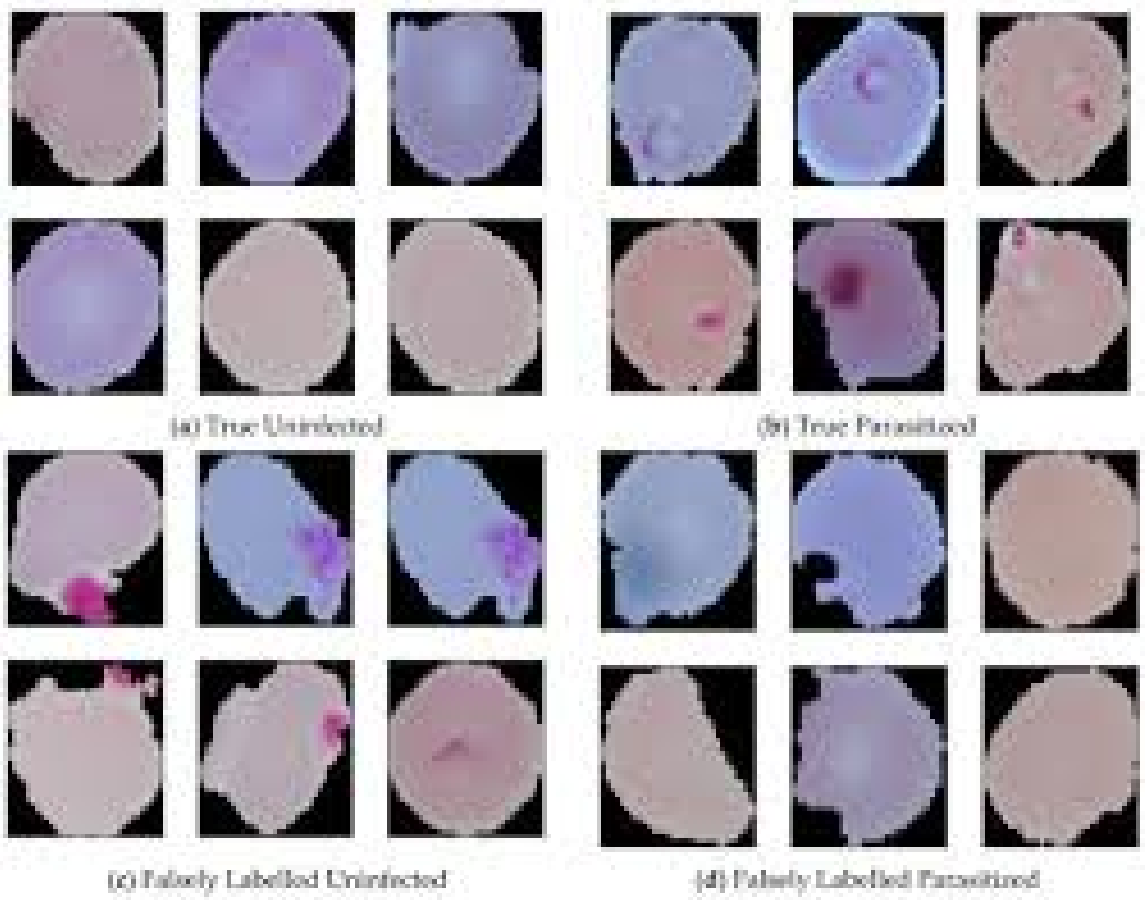


FIGURE 5.1: (a) Correctly labelled uninfected images (b) Correctly labelled parasitized images (c) Falsely labelled uninfected images and (d) Falsely labelled parasitized images

data is considered as true parasitized, and suspicious data is considered as false parasitized. For uninfected malaria data, 750 suspicious images were found, which was named as false uninfected.

Chapter 6

Data Preparation

6.1 Introduction

In supervised learning, the behavior and performances of the model entirely depends on the data that is fed. Therefore, data preprocessing plays a vital role towards conducting experiments. Considering that, in this work manually corrected images were resized as per the model input, and image patches were rescaled to map the features within 0 to 1 range which led to getting faster convergence. The below figure depicts resizing augmented images.

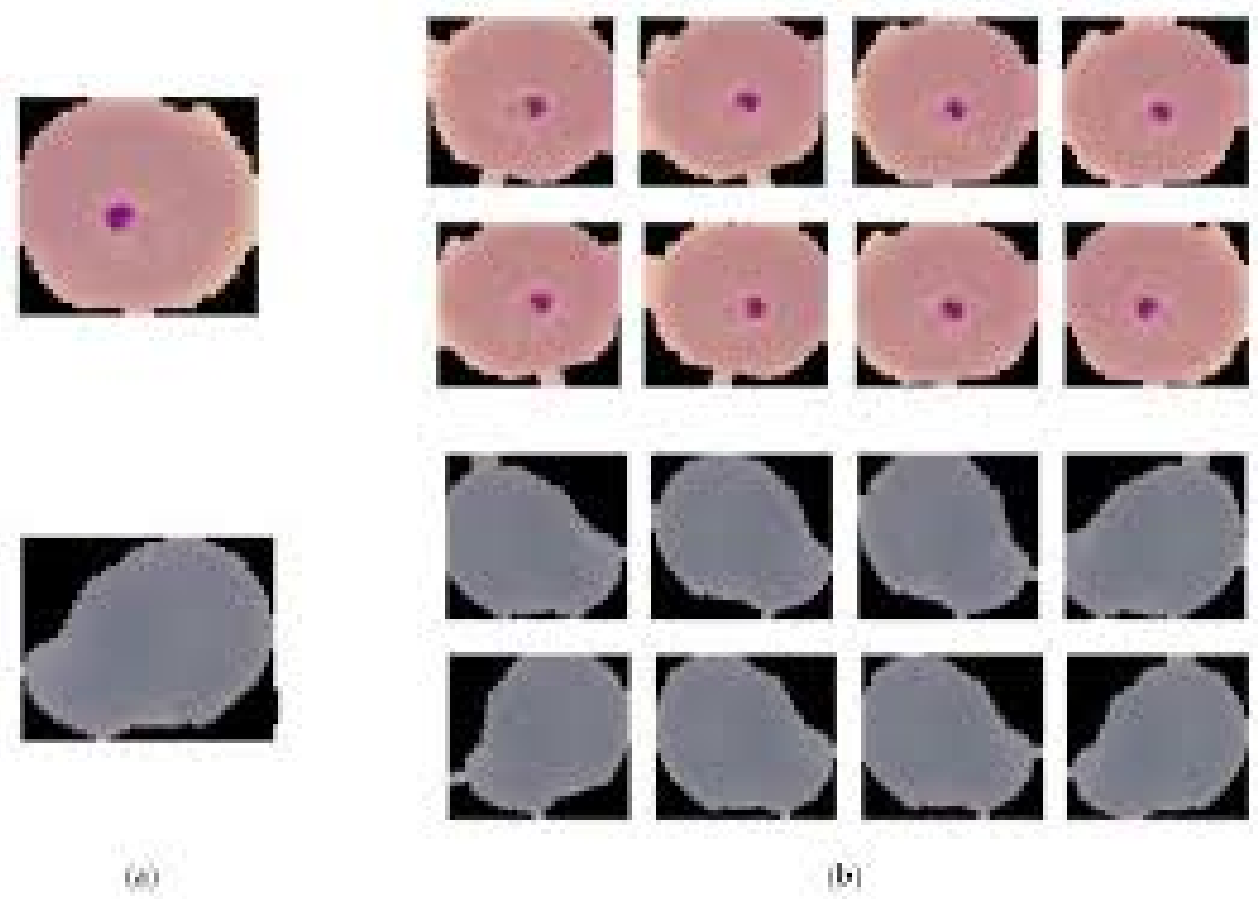


FIGURE 6.1: Image before resizing and performing augmentation is depicted in (a) and image after resizing and applying augmentation is depicted in (b).

Chapter 7

Proposed Model Architecture

7.1 Introduction

To serve the purpose of detecting malaria parasite from blood smear (exactly the similar kind of blood smear collected by (4)), in this article, an autoencoder-based architecture is proposed, which is shown in Figure 3. Autoencoder (5) is a specific type of artificial neural network which compresses input data into lower-dimensional latent space representation and finally reconstruct output from this representation shown in given figure.

Encoder: Encoder compresses the input to latent space representation with the least possible distortion. For Xn = x1, x2, x3, . . . , xn set of input images belongs to training set, encoder compress it to Kn = k1, k2, k3,. . . , kn where Kn is the set of latent representation of Xn (6) The primary purpose of an Autoencoder is dimensional reduction. However, in this task, it is used as a classifier, inspired by (2) (7).

k1,k2,k3. . . . . kn=Encoder(x1, x2, x3. . . . . xn) (1) Kn=Encoder (Xn) (2)

Decoder: The decoder consists of 4 Deconvolutional layers and three Up-sampling layers. The kernel size for all the Deconvolutional layers is 3 × 3 with strides size

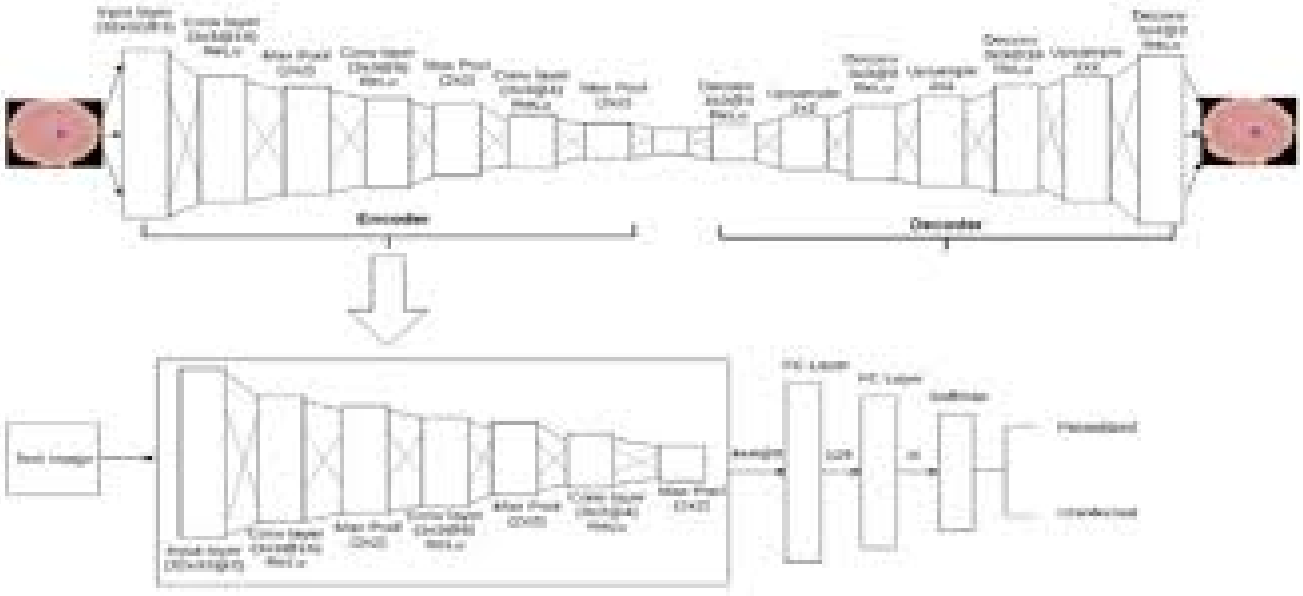


FIGURE 7.1: The outline of autoencoder model.

1 having the same padding and number of kernels were defined as 4, 8, 16 and 3 respectively. Deconvolutional layer is the opposite of convolutional layer and unlike Convolutional layer, instead of mapping 3×3 features into 1 pixel,Deconvolutional layers map 1 pixel to 3×3 features vector. ReLU activation function was applied to the hidden units to introduce non-linearity. Up-sampling with window size 2×2 was applied to get closer input image to reconstruct it from the latent representation (1).

Chapter 8

EXPERIMENTAL SETUP AND RESULT ANALYSIS

8.1 Introduction

Here we use google colab (Colaboratory).

Colab is a free Jupyter notebook environment that runs entirely in the cloud. Most importantly, it does not require a setup and the notebooks that you create can be simultaneously edited by your team members - just the way you edit documents in Google Docs.

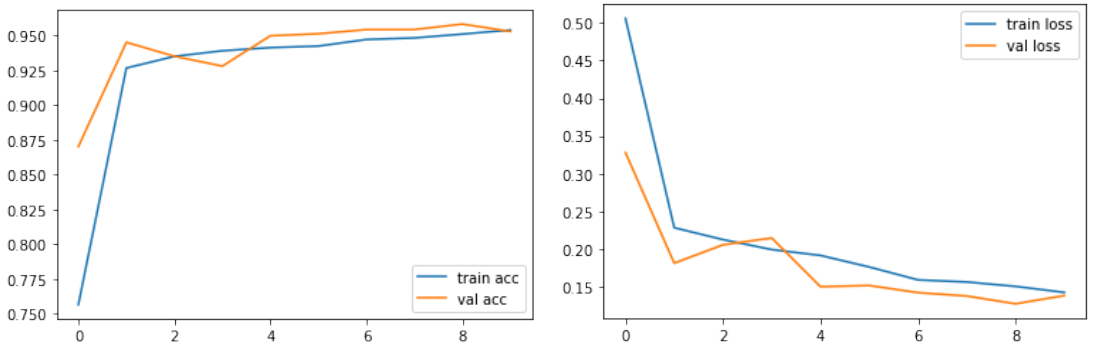
Programming Part:

```
from tensorflow.keras.layers import Input, Lambda, Dense, Flatten,
    Conv2D
from tensorflow.keras.models import Model
from tensorflow.keras.applications.vgg19 import VGG19
from tensorflow.keras.applications.resnet50 import preprocess_input
from tensorflow.keras.preprocessing import image
from tensorflow.keras.preprocessing.image import ImageDataGenerator
    ,load_img
from tensorflow.keras.models import Sequential
import numpy as np
from glob import glob
import matplotlib.pyplot as plt
```

```
11
12 # re-size all the images to this
13 IMAGE_SIZE = [224, 224]
14
15 train_path = '/content/drive/MyDrive/malaria/Dataset/Train'
16 valid_path = '/content/drive/MyDrive/malaria/Dataset/Test'
17
18 # Import the Vgg 19 library as shown below and add preprocessing
      layer to the front of VGG
19 # Here we will be using imagenet weights
20
21 vgg19 = VGG19(input_shape=IMAGE_SIZE + [3], weights='imagenet',
      include_top=False)
22
23
24 # don't train existing weights
25 for layer in vgg19.layers:
26     layer.trainable = False
27
28 # useful for getting number of output classes
29 folders = glob('/content/drive/MyDrive/malaria/Dataset/Train/*')
30
31 # our layers - you can add more if you want
32 x = Flatten()(vgg19.output)
33
34 prediction = Dense(len(folders), activation = 'softmax')(x)
35
36 # create a model objects
37 model = Model(inputs=vgg19.input, outputs=prediction)
38
39 from tensorflow.keras.layers import MaxPooling2D
40
41 ### Create Model from scratch using CNN
42 model=Sequential()
43
44 model.add(Conv2D(filters=16,kernel_size=2,padding="same",activation
      ="relu",input_shape=(224,224,3)))
45 model.add(MaxPooling2D(pool_size=2))
46 model.add(Conv2D(filters=32,kernel_size=2,padding="same",activation
      ="relu"))
47 model.add(MaxPooling2D(pool_size=2))
```

```
model.add(Conv2D(filters=64,kernel_size=2,padding="same",activation="relu"))
model.add(MaxPooling2D(pool_size=2))
model.add(Flatten())

model.add(Dense(500,activation="relu"))
model.add(Dense(2,activation="softmax"))

model.summary()

# tell the model what cost and optimization method to use
model.compile(
  loss='categorical_crossentropy',
  optimizer='adam',
  metrics=['accuracy']
)

# tell the model what cost and optimization method to use
model.compile(
  loss='categorical_crossentropy',
  optimizer='adam',
  metrics=['accuracy']
)

# Make sure you provide the same target size as initialied for the image size
training_set = train_datagen.flow_from_directory('/content/drive/MyDrive/malaria/Dataset/Train',
                                                 target_size = (224, 224),
                                                 batch_size = 32,
                                                 class_mode = 'categorical')

test_set = test_datagen.flow_from_directory('/content/drive/MyDrive/malaria/Dataset/Test',
                                            target_size = (224, 224),
                                            batch_size = 32,
                                            class_mode = 'categorical')
```

```
81
82 # fit the model
83 # Run the cell. It will take some time to execute
84 r = model.fit(
85     training_set,
86     validation_data=test_set,
87     epochs=10,
88     steps_per_epoch=len(training_set),
89     validation_steps=len(test_set),
90 )
91
92
93 # plot the loss
94 plt.plot(r.history['loss'], label='train loss')
95 plt.plot(r.history['val_loss'], label='val loss')
96 plt.legend()
97 plt.show()
98 plt.savefig('LossVal_loss')
99 printf()
100
101 # plot the accuracy
102 plt.plot(r.history['accuracy'], label='train acc')
103 plt.plot(r.history['val_accuracy'], label='val acc')
104 plt.legend()
105 plt.show()
106 plt.savefig('AccVal_acc')
```



(a) Y – Accuracy, X – Num of Epochs

(b) Y – Loss, X – Epochs

FIGURE 8.1: Accuracy and Loss Graph

```
1 # save it as a h5 file
```

```
from tensorflow.keras.models import load_model

model.save('/content/drive/MyDrive/malaria/model_sort/
    model_vgg19_big.h5')

y_pred = model.predict(test_set)
import numpy as np
y_pred = np.argmax(y_pred, axis=1)

from tensorflow.keras.models import load_model
from tensorflow.keras.preprocessing import image

model=load_model('/content/drive/MyDrive/malaria/model_sort/
    model_vgg19_big.h5')
# go to last level

import numpy as np
from tensorflow.keras.preprocessing import image
test_image = image.load_img('/content/drive/MyDrive/malaria/Dataset
    /Test/Parasitized/C101P62ThinF_IMG_20150918_151149_cell_86.png',
     target_size = (224, 224))
test_image = image.img_to_array(test_image)
test_image = np.expand_dims(test_image, axis = 0)
result = model.predict(test_image)
# training_set.class_indices

if result[0][0] == 1:
    prediction = 'Parasitized'
else:
    prediction = 'Uninfected'
print(prediction)

1/1 [==============================] - 0s 17ms/step
Parasitized
```

Result Discussion In this research, we have proposed the use of the current state-of-the-art deep learning model architectures for the task of malaria pathogen detection in thick blood smear images. This introduces an applicable solution for point of care microscopic disease diagnosis which shows both the class and location

of the pathogens and the degree of detection confidence. The experiments carried out also highlight the possible trade-of when extending this work to deployment on smartphones.

Our goal was to investigate if the state-of-art pretrained deep learning models for transfer learning can ably be applied to malaria pathogen detection and if so which is the most suitable architecture for this task. Thus, the experimental results and comparisons between various deep learning architectures have demonstrated how transfer learning-based detection can be translated to successfully detect malaria pathogens in thick blood smear images.

Based on the experiments, it is also evident that there is indeed a speed vs accuracy trade-of. We observe that faster R-CNN models offer the best accuracy when given enough resources resulting in better performance, though it takes a lot longer while training and gives a high inference time in comparison with SSD and Retina Net. It is worth noting that much as SSD models are a bit unstable with lower accuracy, they are much faster in detection and smaller than all the other models which accounts for their ease of deployment on a low-resourced mobile phone.

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