Malaria Cell Image Classification using Deep Learning

Jaspreet Singh Chima, Abhishek Shah, Karan Shah, Rekha Ramesh

ABSTRACT: ***Malaria caused by the Plasmodium parasites, is a blood disorder, which is transmitted through the bite of a woman Anopheles mosquito. With almost 240 million cases mentioned each year, the sickness puts nearly forty percentage of the global populace at danger. Macroscopic usually take a look at thick and thin blood smears to identify a disease or a cause and figure it out what weakens them. However, the accuracy depends upon smear quality and awareness in classifying and counting parasite and non-parasite cells. Manual evaluation, which is the gold standard for diagnosis requires various steps to be performed. Moreover, this process leads to overdue and misguided analysis, even when it comes to the hands of expertise. In our project, we aim at building a robust, minimized reliance of humans, sensitive model for automated analysis of Malaria. A category of deep learning models, namely Convolutional Neural Networks, guarantee especially versatile and advanced outcome with end-to-cease attribute extraction and categorization. The precision, unwavering quality, velocity and cost of the methods utilized for malaria examination are key to the diseases' cure and ultimate eradication. In this study, we compare the overall performance of pre- trained CNN primarily based DL model as characteristic extractors closer to classifying parasite and non-parasite cells to aid in progressed sickness screening. The highest quality model layers for attribute extraction from the underlying records, is determined experimentally. The dataset has a variety of Parasite and Non-Parasite pictures of blood samples. To achieve accurate outcome, we have selected certain dominating features such as size, color, shape and cell count from the images which will help in the categorization process. Pre-trained CNNs are used as a promising tool for attribute extraction; this can be determined by the outcome of its statistical validation. Given these developments, automated microscopy could be a very good deal in the chase towards a low-priced, effortless, and dependable method for diagnosing malaria.***

Keywords: Image Classification, Malaria Cell, ResNet, Deep learning, Convolution Neural Network.

I. INTRODUCTION

Malaria is an infectious disorder caused by Plasmodium group individual Protozoan Parasite. The sickness is spread in particularly via the bite of Anopheles Mosquito, an infected female. With almost 240 million cases reported each year, the disease puts nearly forty percent of the world population at threat. Typical symptoms of malaria comprise fever, nausea, headaches and, in severe instances, yellow skin, seizures, coma that leads to death. The spread of this disorder in the present-day technology is shown in Fig. 1.

Fig. 1. A World Map of Areas presently Tormented By Malaria (July 2018, www.cdc.gov)

Every year trained professionals examine several million blood films to detect malaria infection. Malaria detection involves manually numbering the parasites and infected red blood cells. However, this relies totally upon the microscopist's experience and expertise [13].

Operating in a limited resource set-up with no supportive program for capacity maintenance can affect the quality of the diagnosis. That leads to erroneous diagnostic decisions. Henceforth we have built up this method to give a precise diagnosis [14].

Convolutional Neural Networks (CNN), a category obtained from deep learning (DL) models is used to obtain superior end results with feature extraction and categorization. CNN based DL models are a characteristic extractors towards classifying the blood cells. CNN is a promising device for feature extraction. Automated malaria screening using DL techniques, consequently, function an effective diagnostic aid.

It has been proven in several area studies that manual microscopy isn't always a reliable screening approach when accomplished through non-experts due to lack of training particularly in the rural regions where malaria is endemic. An automated system targets at performing this task without human intervention and to offer a goal, reliable, and efficient tool to accomplish that. The target user segment of the project will be Hospitals, Clinics and other practitioners practicing medicine. This system can also be used in Medical colleges for learning the concepts of Malaria and help the students understand Malaria detection process In this study, for estimating the performance of pre- trained CNN namely ResNet50 as a feature extractor is used to classify parasite and uninfected cells to aid in advanced disorder screening. All this makes deep learning models incredibly a precise option for performing computer vision tasks. CNN on its own learn the feature identification by means of its hidden layers. Each and every layer expands the unpredictability of the educated learned highlighted features [12].

II. RELATED WORK

The correctness, dependability, velocity and fee of the techniques used for malaria prognosis are fundamental keys to the illnesses' treatment.

Revised Manuscript Received on March 30, 2020.

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However, improvement in any one of the factors may lead to the stagnation of the rest, owing to their interdependency [10].

Numerous pictures preparing strategies have been proposed as of now for the character of MPs (Malaria Parasite) in thin blood cells.

The authors [1], found one the most basic principal approach all the way through the use of a better circle Hough changes to make a distinction in RBCs. By breaking down the RGB (red, green, and blue) shading space, the author watched that nucleated parts present particularly high-power esteems in the B channel and at the same time little power in the G channel. Thence, a proposal to broaden the complexity of nucleated objects was proposed hooked into watched differentiations between the 2 color channels.

The foremost application for detecting malaria parasite in human peripheral blood smear images using DBN was given by Bipin, Nair and Punita. For the proposed model, the Accuracy is 0.963, Sensitivity is 0.97, Specificity is 0.959. AUC is nil, F1-score 0.89 and MCC is nil which are less than the ResNet-50[16]. On the other hand, in ResNet-
50 one can find the highest average ranks for accuracy, specificity, F1-score, and MCC [17]. The Literature study analysis reveals that MCC is one of the most useful single score to evaluate the common execution of a dual-fold classifier within a confusion matrix setting that permits you to procure an increasingly detailed examination of contaminated RBCs. We elude the authors for proposing a procedure fixated on distinguishing 3 areas in the interior of these structures: MP core, MP cytoplasm and RBC cytoplasm. For each and every locale, picture highlights dependent on territory proportions and scope of powers were removed. The acknowledgment of contaminated RBCs utilizing a Bayes preference principle classifier introduced about a Sensitivity (SE) and a Specificity (SP) of 92.59% and 99.65% respectively, so far with just 60 and 20 pictures utilized for preparing and testing, independently. A distinct method for RBCs partitioning was proposed [3]. This merges Otsu's partition with edge recognition through Canny's strategy. Subsequent to passing a gap filling strategy, picture highlights were removed for each fragmented structure. Five elite classifiers were tried and tested and the most outstanding outcome was given by KNN (k-closest neighbors) with SE and SP of 80% and 95.5% respectively. J. Somasekar proposed graphical method approach the components of a linear program dependent on the given information and taking care of the given issues, for recognizing parasite [8]. The team implemented some image processing techniques particularly image segmentation and morphological operations. Within the primary application, they had to create a mathematical model from the data accumulated while in the second, they designed a model using Graphical methodology. To select a model depending on both precision and sensitivity working in harmony, as proven with the aid of the F1-score, the pre-prepared ResNet-50 outperformed the alternative models under study. A standard methodology of computer supported system contains four particular picture processing and task scrutiny, which are namely, Preprocessing, Segmentation, attribute extraction and categorization K-means algorithm is used for Segmentation of MPs in another work [5]. The authors aimed to detect the parasites with reported SE of 81.7% and SP of 90.8, using histogram-based texture features.

A sum of 300 pictures with 386 clarified MPs were utilized for the categorization them into 13 classes. K-means clustering, accompanied by diverse textural and shape features, carried out on RGB, HSI and L*a*b color spaces for MPs' segmentation, [6]. The authors utilized a versatile thresholding strategy for division and a SVM with a direct piece for grouping, with detailed high specificity, sensitivity and immaterial bogus positives (~0.0025%). two classifiers had been used, KNN and SVM (support vector machines), with the outstanding performance for KNN with accuracy (AC) and SE of 90.2% and 90.2% respectively.

More recently, for scoring and categorizing MPs' stages used a low-value picture-based cytometer, with the imaginative component of testing the gained parasitemia results with flow cytometry [7]. A versatile thresholding strategy was used by the authors for division and a SVM with a linear kernel for categorization, with announced elevated specificity, sensitivity and irrelevant bogus positives (~0.0025%).

An optical strategy that offers quick recognition of malaria-infected red platelets (RBCs) at a lower value exists as per the paper, [10] by Marcel Akpa Agnero. The strategy depends on the mix of deconvolution, geology and 3D refractive file reproduction of the malaria contaminated RBCs by utilization of the transport of intensity equation. Results for the malaria contaminated RBCs were significantly not quite the same as those of the solid RBCs. This work presents a huge procedure of examining malaria contaminated RBCs at a lower cost and without the utilization of fluorescent marks for the parasites.

It has been shown in numerous fields researches that manual microscopy is not a dependable screening approach when carried out by non-professionals due to lack of training particularly within the rural regions where malaria is endemic.

Regardless of these promising results during the point of reference in few previous years, the greater part of the proposed approaches completely depends upon the two most important necessities inappropriate for most malaria-endemic areas :

(i) Images should be obtained properly under controlled conditions; and
(ii) The necessity for suitable microscopic equipment.

As another option, here we present an alternate procedure for automated investigation of malaria sickness tainted thin blood spreads by utilizing pictures exclusively gained with ease and effectively convenient instrument, for example, a Smartphone.

As far as the chosen systems for image processing and AI, we move past the best in class and accomplish a vastly improved and solidified technique that handles the issue of distinguishing various MPs' species-arrange blends on the comparative picture.

III. IMPLEMENTATION

A. Dataset Collection

The dataset will comprise of large number of Parasitized and Uninfected images of blood samples. Our dataset is specific to the Asian country of Bangladesh. Red blood cells (RBCs) from Giemsa are stained thin blood slides of image, obtained from the U.S. National Library of Medicine are used in this study for training as well as testing. They were acquired from P. falciparum parasite infected and normal patients, in Chittagong Medical College hospital, Bangladesh [15]. The examples of the samples obtained are shown in Fig. 2 and Fig. 3.

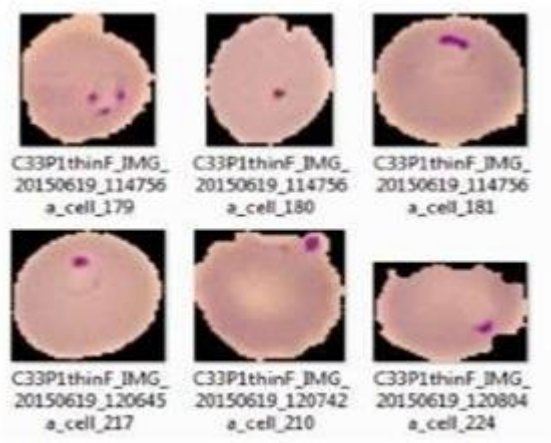

Fig. 2. Infected Blood Smear Image

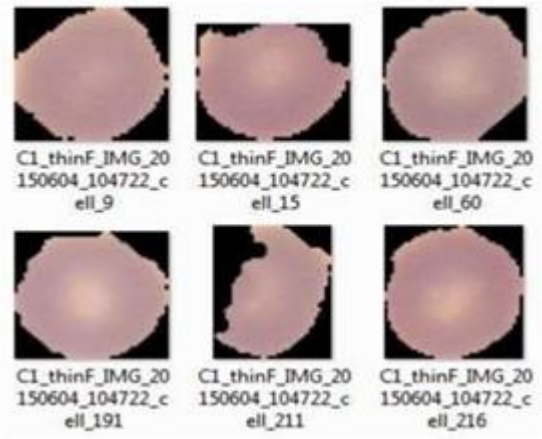

Fig. 3. Uninfected Blood Smear Image

B. Data Preprocessing

The pre-processing done to "Prepare data" for the classification of images consists of the following steps:

1. Randomization of images is done to get good redistribution of data for when we apply the split.
2. The images are divided into a training set and a validation set (10% of original train set) to avoid overfitting
3. Resizing of images into a 3D tensor with shape of width = 64, height = 64, channels = 3 shaped arrays, so that every image will have the same dimensions as each other.
4. All images are then normalized through dividing with 255.
5. All labels are changed into 2 classes utilizing keras.utils bundle to categorical: in order to acquire categorical classification.

To obtain more accurate results we have chosen certain dominating features from the images which help in the classification process. The proposed model learns to detect features like colors and edges in its first convolution layer and more complex (and abstract) concepts inside the deeper layers.

Invasion by the malaria sickness parasite, P. falciparum makes broad changes in the host red cells. These incorporate loss of the:

- regular cylindrical shape.
- Increased inflexibility of the membrane.
- Improved porousness to a large variety of ionic and different species.
- Rupture of the RBC.
- Destruction of both contaminated and uninfected red cells since to membrane alterations.
- Cell Counting- By comparing the overlay of authentic image and masked image and primarily based on the intensity profile, differentiation between the regular and inflamed cells are carried out.

C. CNN

Underneath the class of Deep Learning models, Convolutional Neural Networks (CNN), delivers great scalable characteristic extraction and categorization. In this report, we examine the overall performance of pre-trained CNN dependent Deep Learning models as a characteristic extractor for the classification of parasite and Non-parasite cells for improved screening. In this we experimentally evaluate the optimal model layers for the feature extraction from the underlying data. As a result, we put this into effect as shown in the following Fig. 4.

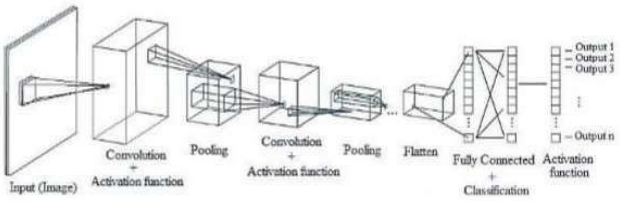

Fig. 4. CNN Model

D. ResNet-50

ResNet-50 is a deep residual that is trained on more than a million images from the ImageNet

database. It is a subclass of convolutional neural networks. The 50 refers to the number of layers that are present. As a result, the network has learned rich feature representations for a variety of images. Before ResNet, teaching very deep neural networks got troublesome due to the setback of vanishing gradients i.e. as soon as the model starts to back propagate, the gradient starts getting smaller and smaller. Moreover, ResNet50 has Skip Connections which is a remarkable advantage. Fig. 5 shows the steps involved in ResNet50.

➢ Convolution: The convolution step is performed to extract features from the specified input image. It is the first step in a CNN model. Consider an input image, which acts like a feature indicator as well as a feature map. After that take the filter and apply it pixel block by block to the input image under consideration. This is done by matrix multiplication.

➢ Filter: The depth of the filter and the depth of the input image are same, the depth for our input image is three; In each and every position, the multiplication of the values inside the filter with that of the original pixel values takes place. This is nothing but element wise multiplication. The resultant array is called a feature map or an activation map.

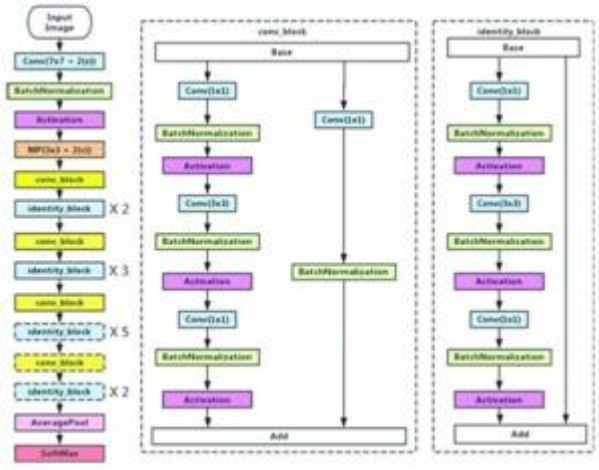

Fig. 5. ResNet50 Layers

- Strides: Stride is the number of pixels shifts over the input matrix. When the stride is 1 then we shift the filters to 1 pixel at an instance. It functions similarly if the stride is 2.

- ReLU layer: Another progression to the convolution layer is the Rectified Linear Unit, which is also called as ReLU layer. In this to increase the non-linearity within the network, one needs to apply activation function onto their feature maps. This is due to the fact images themselves are extremely non-linear. By setting them to zero it eliminates negative values from an activation map.

- Pooling: Progressive reduction in the size of the input representation is done by Pooling. Identification of objects in an image no matter where they're located is possible with the help of Pooling. Pooling also helps in reducing the amount

  of parameters and computation required. It is also capable of managing over-fitting. In max pooling, partitioning the input image into a set of areas that don't overlap takes place. This results in the output of each and every region as the maximum value in each of them. Thus, we get smaller size image with fewer parameters. The main aim of Max pooling is to grab the maximum value at each and every spot in the input image. As a result, 75% of the information that is not the feature gets rid off. By simply dividing the input into rectangular pooling regions and computing the average values of each region, an average pooling layer performs down- sampling.

- The fully connected layer: The fully connected layer is one of the best examples of a traditional Multi- Layer Perceptron. Classifier inside the output layer is used. Often used classifier in the fully connected layer is the softmax activation function. Each neuron in the former layer interacts with each and every neuron in the following layer. This layer aims to use the capabilities from the previous layer output to classify the input image based on the training data.

E. Proposed System

Fig. 6 gives the flowchart for the proposed system which has been implemented.

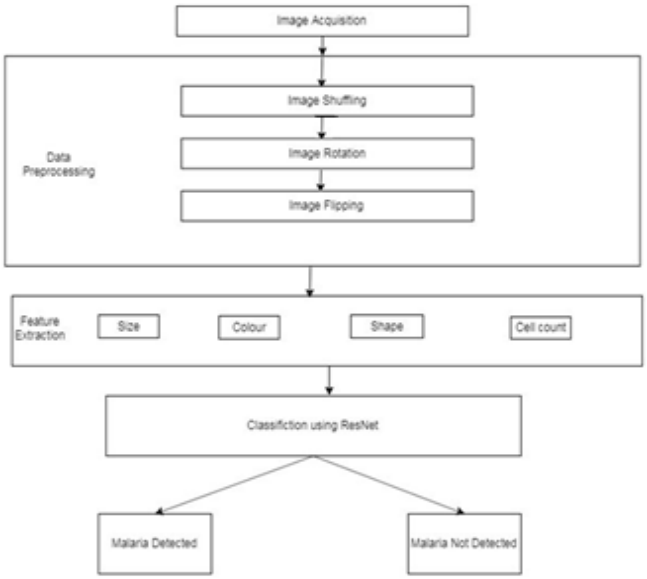

Fig. 6. Proposed System

IV. RESULTS AND ANALYSIS

The dataset we would be using for analysis (training, validation and testing) is taken from The Lister Hill National Center for Biomedical Communications, who have cautiously accumulated and annotated this dataset of fit- healthy and infected blood smear pictures [15]. The dataset consists of 27,558 segmented cellular images, with the same instances of 13,779 parasite and 13,779 Non-parasite segmented RBC images. In Positive samples plasmodium is present and in negative samples plasmodium is absent. After applying data augmentation, a pre-processing technique our count of 27,558 input dataset images would increase and become 163314. Thus, our training dataset increase by 6 folds helping us achieve a good accuracy for the testing dataset. To further check the cross validation and the accuracy of our system, we tested our system with a new dataset other than the previous dataset acquired from the NLM. This new Malaria Parasite Image Database for testing the accuracy of our system has been taken from an article inside the book "Processing and Analysis of Biomedical Information" [11]. MP-IDB which is the open image dataset comprises of 3 species of Malaria parasites: Ovale, Vivax, Falciparum. For all the classes, 4 distinctive stages of life, depicted in the filenames as follows:

- R: implies the occurrence of Ring stage parasites
- T: implies the occurrence of Trophozoite stage parasites
- S: implies the occurrence Schizont stage parasites
- G: implies the occurrence Gametocyte stage parasites

The proportion of execution and exactness of the strategy was assessed by two measurements: sensitivity and specificity. We use binary confusion matrix, to keep a track on the True Positives, True Negatives, False Positives and False Negatives. We printed the classification report to get an idea of accuracy, precision, f1-score and recall for individual class labels.

Sensitivity is characterized as the likelihood (rate) that patients with the contamination will have a positive outcome utilizing the test under assessment. Specificity is characterized as the likelihood (rate) that patients without the disease will have a negative outcome utilizing the test under assessment. The values for sensitivity and specificity are expressed in terms of true positives (TP), false positive (FP), false negative (FN) and true negative (TN) a defined below in expressions 1 and 2:

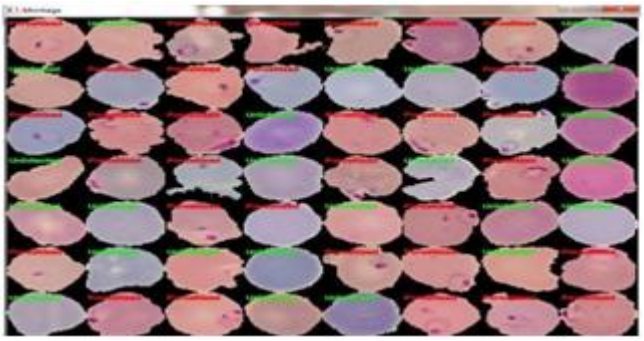

Fig. 7. Single Blood Cell Output

Fig. 8 shows the output for a single blood cell (focusing on the region of interest) as well as multiple blood cell (considering the entire region of the blood smear)

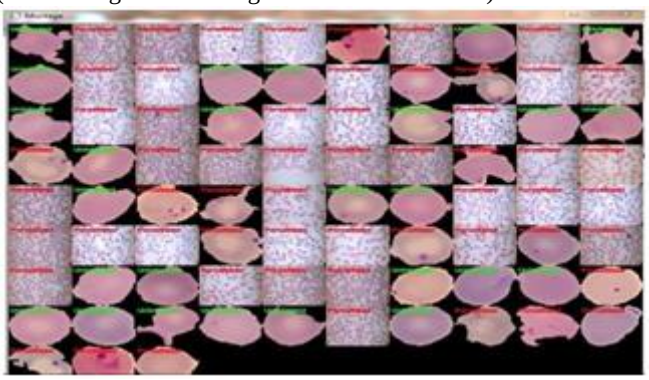

Fig. 8. Multiple Blood Cell Output

Shown below is the model evaluation on unseen data.

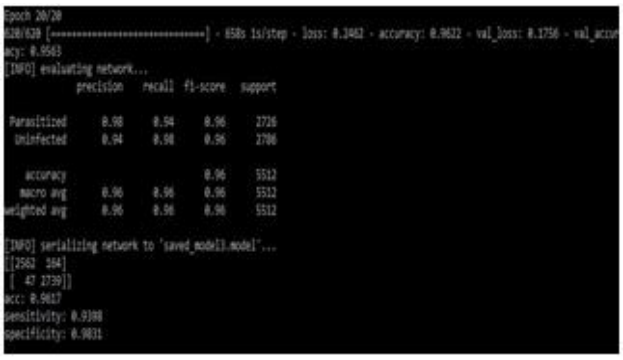

Fig. 9. Result analysis of testing data

$$Sensitivity = TP/TP+FN \quad (1)$$

$$Specificity = TN/TN+FP \quad (2)$$

By using a function, we plot something known as a binary confusion matrix. A confusion matrix will give us information about the true positives, true negatives, false positives and false negatives. It gives us knowledge not just into the blunders being made by a classifier however more significantly the sort of mistakes that are being made. An example of the confusion matrix can be shown in the figure below.

The accuracy for the testing data [15] is 96.17% and the validation accuracy is 95.63%.

164 out of 2726 (6 %) infected cells were classified as clean — False Negative.

47 outof 2786(1.6 %) clean cells were classified as infected —False Positive.

Given below is the description of the sample outputs and the impact it has had on this survey.

The figure 7 shows the output for a single blood cell (focusing on the region of interest).

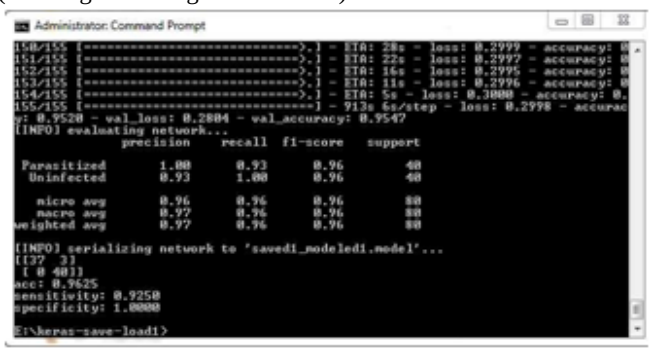

Fig. 10. Result analysis of testing data

This means in Fig. 10,

The accuracy for the testing data [11 & 15] is 96.25% and the validation accuracy is 95.47%.

3 out of 40 (7.5 %) infected cells were classified as clean— False Negative.

0 out of 40 clean cells were classified as infected—False Positive.

augmentation has enormously diminished the odds of over- fitting the model just as the quantity of bogus negatives. Utilizing decaying learning rate demonstrated shockingly powerful as the model could arrive at the actual optimal solution. The latency for a solitary image forecast is quite low, which is acceptable considering the fact that this is an image classification difficulty.

The results obtained state that the blood smear images have been classified into parasite and non-parasitic. After conducting multiple iterations to make the result as accurate as possible we have achieved an average accuracy rate of 95%. This would go to say that there has been some error in detecting a few samples correctly. The reason of the incorrect classification is not established and therefore can only be hypothesized. Certain traits of the image will prompt false impression of parasites and augment the calculation mismatch among manual and digital counting. It could be that the input images may have some missing features which would result in its misclassification or they could be blurry which would make the interpretation difficult. It could also be that the classifier is overfitting the training set. Having an increased n-fold cross validation set could result in better accuracy. This means in the Fig. 9, but it is still not proven and cannot be seen practically.

V. CONCLUSION

Fig. 11. Result analysis of testing data This means in Fig. 11,

- The accuracy for the testing data [15] is 93.87% and the validation accuracy is 95.31%.
- 20 out of 160 (12.5 %) infected cells were classified as clean—False Negative.
- 2 out of 199 (1 %) clean cells were classified as infected—
  False Positive.

Yes, there are different models such as AlexNet, VGG- 16 and DenseNet-121 which can also be used to carry out this project. However, they do have certain limitations which can be solved by using ResNet-50. ResNet-50 is a convolutional neural network that is trained on more than a million images from the ImageNet database. The network is 50 layers profound and can categorize images into 1000 object classification, such as keyboard, mouse, pencil, and numerous animals. Subsequently, the system has learned rich feature representations for a wide collection of images. Previous to ResNet, the problem of vanishing gradients was present in training deep neural networks. in addition, ResNet50 has Skip Connections. The center thought of ResNet is presenting an alleged "identity shortcut connection" that skips at least one layer. The proposed method is working well because the use of large amount of thick blood smear image data which suitable for neural network-based method. Using different techniques such as Dropouts and Batch Normalization have helped in solving the problem of over- fitting the model. Utilizing data

Pathologists use Microscopes to manually detect Malaria parasites and therefore the result can lead into fatal condition due to human error involved in analysis. This error can be limited by using image processing and automation. We achieve the goal of detecting Giemsa stained malaria parasites blood samples by means of the ResNet model. The use of ResNet model helped us in achieving reliable performance in classifying the Malaria Parasite cells as Parasite or Non-Parasite.

For a well-execution system, it would require several factors to communicate with each other. Which basically incorporate the traits of the microscope, the type of staining used, the slide preparation mechanism, along with the image exploration and machine learning software.

There is certainly the capacity that some of those methods gain significance out of doors malaria prognosis, specifically for detecting and separating the RBCs in different applications and for preprocessing.

The use of images with different characteristics in each research has an impact on the difficulty of determining which method is best to use. This suggests that the method proposed in this field of research is highly dependent on the characteristics of the image used.

Given the wide acknowledgment of deep learning, a gigantic support has been lead for data acquisition endeavors. Along with that annotated data image repositories for preparing is currently broadly comprehended These will probably prompt to bigger check suites on patient degree, taking into account more standardized critiques and widespread discipline field testing. Knowing these developments, automated microscopy may be very an awful lot inside the race in the direction of a cheap, simple, and reliable technique for diagnosing malaria.

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I am currently in my final year, pursuing my graduation degree in Computer's from Shah & Anchor Kutchhi Engineering College, Mumbai. He has completed his schooling from D.P.Y.A High School and an under graduate from G.N Khalsa College in the field of Science. His area of interest is Machine Learning and Artificial Intelligence. He has done multiple projects in his areas of interest. This would be his first publication and contribution towards the real world projects involving the use of Deep Learning Models. He is a member of the CSI Organization. He has also been awarded for various curricular and extracurricular activities.

Abhishek Shah.
I am currently a student in my final year of Computer Engineering at Shah & Anchor Kutchhi Engineering College, Mumbai.He graduated Junior College from KC College, Mumbai and studied in St. Mary's ICSE School, Mumbai. This paper will be his first publication. Tremendous amount of effort and research has gone into this project. He is part of the CSI community and has been a part of various events that have been held. He has also taken part in various curricular and extracurricular events and has been rewarded for the same.

Karan Shah
I've been a student of Shah and Anchor Kutchhi Engineering College, studying Computer Engineering for the past 3 years. But he enjoyed working with computer languages since he was a child. He graduated his 10^{th} from ICSE board and 12th from ISC board exams through Hiranandani Foundation School. Apart from certain extracurricular activities, he has completed number of online courses in languages like Java, C and Python. He is currently in his final year, utilizing this opportunity to work towards completing and publishing my first research paper. He is grateful to his teachers and college for giving him and his team this opportunity.

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