Malaria Cell Detection

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1 Motivation

Malaria is a mosquito-borne disease that causes fever, tiredness, vomiting and headaches. In some cases, it can lead to yellow skin, seizures and coma. Sometimes it can also lead to death. Malaria is widespread in the tropical region around the equator. This includes most of sub-Saharan Africa, Latin America and Asia. While malaria is a disease that is commonly associated with poverty, evidence suggests that it also causes poverty and prevents economic development. This is evident in some sub Saharan African countries such as Tanzania, Uganda, etc. These regions have access to limited healthcare facilities and limited medical staff to diagnose malaria patients. Hence, it is important to automate the process, while simultaneously making sure that the implementation is lightweight enough so that it can be run using affordable hardware.

2 Problem statement

Blood smears are the most common and accurate test for the diagnosis of malaria. The attending physician will take a sample of the blood and the sample is sent to a lab where it is stained and observed (manually / by a human) under a microscope.
While the above method has proven to be effective, it can be seen that there is a lot of room for error. There is always the risk that the test will return a false positive or a false negative, both of which engender their own negative consequences. Automating this process will have greater precision and would definitely help reduce the number

of false positives or negatives. Malaria can be fatal within 24 hours after symptoms appear. A false negative result that is not quickly identified can cost a life. Moreover, during these hard times, doctors already have their hands full with COVID running rampant. Taking any load off of technicians or physicians would go a long way. Also, most malaria stricken regions are severely under developed and do not have access to proper healthcare facilities. Hence, using lightweight CNNs to detect malaria would increase the rate of diagnosis and help curb the disease. The current smear tests have an accuracy of 85% detecting infected cells. We hope to achieve a larger number using CNNs.

2.1 Malaria

Malaria is a serious and sometimes fatal disease. The Plasmodium parasite initially infects a certain species of mosquito, the Anopheles mosquito, which then can transmit the parasite to a human by biting them. The parasite is released into the bloodstream and travels to the liver, where the parasite matures. Upon maturing, they re-enter the bloodstream and infect Red Blood Cells. The infected human can transmit the parasite to another anopheles mosquito and hence the cycle continues.
There are four kinds of Malaria parasites known to man: Plasmodium falciparum, P. vivax, P. ovale, and P. malariae. Plasmodium falciparum is the most common cause of malaria accounting for up to 50% of all malaria cases.
Symptoms of malaria include, but are not limited to, chills, headaches, muscle aches, tiredness, fevers, nausea, vomiting. Malaria may also cause anemia and jaundice. In more serious cases, it is also known to cause renal failure, seizures, coma, and death.
There are multiple antimalarial drugs that should be taken as early as possible after the initial infection. It is of paramount importance to catch the disease as early as possible, to visit the doctor immediately upon noticing any of the aforementioned symptoms or upon receiving knowledge of an outbreak of malaria in any place you have recently visited.
In 2019 there were 299 million cases of malaria, a number that increased by 1 million from that of one year ago. Malaria has been responsible for 410,000 deaths in 2019 alone. Its effects are more prominent in Africa. The region was home to 94% of all malaria cases and deaths. India also has been a key site for the Anopheles vector to transmit the parasite to humans according to the CDC.

3 Literature survey

Applying faster R-CNN for object detection on malaria images (Hung, J., Carpenter, A. [1]) for the first time applies an object detection model previously used on natural images to identify cells and recognize their stages in brightfield microscopy images of malaria-infected blood. Many micro-organisms like malaria parasites are still studied by expert manual inspection and hand counting. This type of object detection task is challenging due to factors like variations in cell shape, density, and color, and uncertainty of some cell classes. In addition, annotated data useful for training is scarce, and the class distribution is inherently highly imbalanced due to the dominance of uninfected red blood cells. Faster Region-based Convolutional Neural Network (Faster R-CNN) is used, one of the top performing object detection models in recent years, pre-trained on ImageNet but fine tuned with the data, and compare it to a baseline, which is based on a traditional approach consisting of cell segmentation, extraction of several single-cell features, and classification using random forests.The Faster R-CNN outperforms the baseline and put the results in context of human performance.
Clustering-based dual deep learning architecture for detecting red blood cells in malaria diagnostic smears (Kassim, Y. M., Palaniappan, K., Yang, F., Poostchi, M., Palaniappan, N., Maude, R. J., ... Jaeger, S. [2]) The proposal is a novel pipeline for red blood cell detection and counting in thin blood smear microscopy images, named RBCNet, using a dual deep learning architecture. RBCNet consists of a U-Net first stage for cell-cluster or superpixel segmentation, followed by a second refinement stage Faster R-CNN for detecting small cell objects within the connected component clusters. RBCNet uses cell clustering instead of region proposals, which is robust to cell fragmentation, is highly scalable for detecting small objects or fine scale morphological structures in very large images, can be trained using non-overlapping tiles, and during inference is adaptive to the scale of cell-clusters with a low memory footprint. It was tested on an archived collection of human malaria smears with nearly 200,000 labeled cells across 965 images from 193 patients. Cell detection accuracy using RBCNet was higher than 97%. The novel dual cascade RBCNet architecture provides more accurate cell detections because the foreground cell-cluster masks from U-Net adaptively guide the detection stage, resulting in a notably higher true positive and lower false alarm rates, compared to traditional and other deep learning methods. The RBCNet pipeline implements a crucial step towards automated malaria diagnosis.
A Malaria Diagnostic Tool Based on Computer Vision Screening and Visualization of Plasmodium falciparum Candidate Areas in Digitized Blood Smears (Linder, N., Turkki, R., Walliander, M., Mårtensson, A., Diwan, V., Rahtu, E., ... Lundin, J. [3])

manual evaluation of blood films is highly dependent on skilled personnel in a time-consuming, error-prone and repetitive process. In this study the proposed method is using computer vision detection and visualization of only the diagnostically most relevant sample regions in digitized blood smears.Giemsa-stained thin blood films with P. falciparum ring-stage trophozoites (n=27) and uninfected controls (n=20) were digitally scanned with an oil immersion objective (0.1 µm/pixel) to capture approximately 50,000 erythrocytes per sample. Parasite candidate regions were identified based on color and object size, followed by extraction of image features (local binary patterns, local contrast and Scale-invariant feature transform descriptors) used as input to a support vector machine classifier. The classifier was trained on digital slides from ten patients and validated on six samples.

A semi-automatic method for quantification and classification of erythrocytes infected with malaria parasites in microscopic images (Gloria Díaz, Fabio A González, Eduardo Romero [4]). In this study, a three phase approach is employed. The first phase involves image processing. The images are corrected for luminance differences produced by the acquisition process by means of a local adaptive low-pass filter. The second phase is that of the erythrocyte recognition phase. This phase is further split up into three steps. In the first step, a color pixel classification process uses a machine-learning strategy for classifying a particular color space, which is then used as a look-up table for labeling each pixel as either foreground or background. Secondly, pixels labeled as foreground are grouped into one simplified Inclusion-Tree. The resulting tree is simplified to satisfy the restrictions imposed by the erythrocyte morphological structure and their spatial relationships. Finally, clumped shapes, a possible result of the binarization process, are split using an efficient template matching strategy. This approach searches for the better matching between a chain code representation of the clumped shape contour and an ideal erythrocyte, estimated from the original image by an Expectation-Maximization algorithm.The last phase is the classification of erythrocytes among any of the four possible classes. This classification is achieved upon 25 features which correspond to the statistics of the distributions of color, texture, illumination and edges, extracted from the erythrocytes detected in the previous step. The whole process consists of two steps: firstly, a binary classifier decides whether the erythrocyte is healthy or not. Then a multiclass classifier strategy assigns each erythrocyte to one of the three infection life stages: ring stage, trophozoite or schizont.

Parasite detection and identification for automated thin blood film malaria diagnosis (F. BorayTeka, Andrew G.Dempster, İzzet Kale [5]). The proposal is that of a

novel binary parasite detection scheme that is based on a modified K nearest neighbour (KNN) classifier which provides an adjustable sensitivity–specificity parasite detection. This study affirms the applicability of the method to malaria diagnosis by comparing its results to an expert microscopist's ideal detection performance from a Bayesian perspective. Three different classification schemes for identification are compared. The conclusion states that detection, and species and lifecycle-stage identification tasks can be performed successfully by a single multi-class classification. It also states that the necessity of seeking a high-level generalization in two assumed categories can be removed. The study implements a total of 8 stages for the detection and classification: Stages 1-5: Preprocessing; Stage 6: Object Extraction; Stage 7: Feature Extraction; Stage 8 : Classification using K nearest neighbor clustering algorithm.

Malaria Cell Detection Using Evolutionary Convolutional Deep Networks (Qin, B., Wu, Y., Wang, Z., Zheng, H. [6]) uses evolutionary convolutional deep networks. It can work with keras, it automatically generates a good neural architecture. It can be called as sub domain of AutoML. The data used used here is by NIH. Around 28000 images of both infected and uninfected cells. Pre processing of dataset included sample purification, image rescaling and data enhancement. The final accuracy of the model is 99.98 percent. Further work includes testing accuracy of model on different datasets, improving mobility and testing with better network architectures.

CNN-Based Image Analysis for Malaria Diagnosis (Liang, Zhaohui and Powell, Andrew and Ersoy, Ilker and Poostchi, Mahdieh and Silamut, Kamolrat and Palaniappan, Kannappan and Guo, Peng and Hossain, Md Amir and Sameer, Antani and Maude, Richard James and Huang, Jimmy Xiangji and Jaeger, Stefan and Thoma, George [7]) looks into normal CNN models and transfer learning models. The CNN model is 17 layers and gives an average accuracy of 97.37%. The transfer learning model gives an accuracy of 91.99% on the same dataset. The dataset used here has been acquired from Chittagong Medical College Hospital, Bangladesh. It contains 27578 images of infected and uninfected cell. The dataset is perfectly balanced. The training-testing split used here is 90%-10%. The results indicate that the new CNN model is more accurate than the transfer learning model (by around 7%). The limitation is that accuracy is relatively lower than models in other papers.

In Image Classification of Unlabeled Malaria Parasites in Red Blood Cells (Zhang, Z., Ong, L. S., Fang, K., Matthew, A., Dauwels, J., Dao, M., Asada, H. [8]), HOGs features extracted and classifier trained offline. Viola-Jones object detection is implemented. Model out-performs PCA feature classification by 50% and Hugh transform

algorithms by 24%.. Accuracy achieved with model is 93%. Limitations are that red blood cells which were shriveled up were not detected. Also, the processing time is very high at 3.3 seconds with a margin of error of 0.4 seconds.

FPGA Implementation of CNN Algorithm for Detecting Malaria Diseased Blood Cells (Sağlam, S., Tat, F., Bayar, S. [9]) implements FGPA (Field Programmable Gate Array) for CNN. The average computation time is 174 microseconds. Dataset was taken from US National Library of Medicine site. Testing contained 200 images. 90 diseases, 90 healthy and 20 invalid. Experimental accuracy was 94.76% (189 of the 200 were correctly classified). Uses VHDL language for high efficiency (low energy usage and low use of embedded circuit platform hardware). Limitations are that the dataset used is very small having only 200 images. Also, accuracy is quite low when compared to other models at 94.76%.

Automatic White Blood Cell Detection and Identification Using Convolutional Neural Network (Novoselnik, F., Grbić, R., Galić, I., Dorić, F. [10]) uses image segmentation for detection of white blood cells. These cells are then classified using a CNN into 5 different classes. Dataset used for this was attained by medical staff of Faculty of medicine at Clinical Medical Center Osijek, Croatia. The dataset contains 412 images. Resolution is 2560x1920. Dataset is extremely unbalanced. The classifications are 'Eosinophils', 'Lymphocytes', 'Monocytes', 'Neutrophils' and 'Unknown'. Modified LeNet-5CNN was used. It is a 7 layer CNN. ReLU is used as the activation function. Accuracy attained was 81.11%. Limitation is that accuracy is low and the dataset used is highly imbalanced.

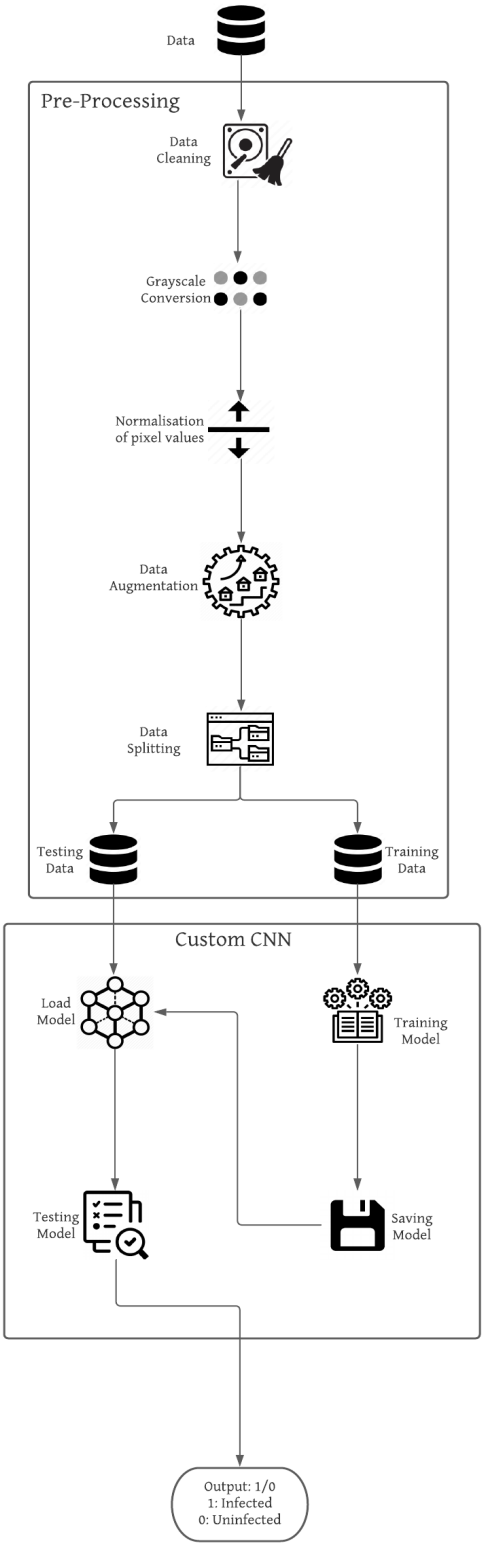
There have been several attempts at solving this problem of detecting malaria cells from a given cell sample. There are 2 main approaches. The first one being segmenting the image to extract the cells first and the second would be to run the CNN directly on the image. However the first step to both these approaches is heavy pre-processing. As the images are of cell slides we need to get a clear image of the cells preset. To achieve this a variety of techniques have been employed. A few of them being passing a low pass filter to adjust difference in luminescence and even using a pixel classifier to determine whether a pixel belongs to the foreground or background. The first method we found to be used in previous papers was to first run segmentation algorithms on the images. Various methods were deployed for this, a few of them being binary thresholding and specialized mathematical functions. A unique method we found was using an open source module called CellProfiler which identified the cell boundaries of various types of cells from erythrocytes to white and blood cells. These identified cells are then run through a CNN or a KNN algorithm to identify any malaria cells. The second method is to run a classification algorithm directly on the image. The CNN's had

several layers with most of them having RELU and SIGMOID as activation functions. Another method being used was the Faster R-CNN architecture. Overall this method lowered the accuracy as there was a higher presence of false positives. All the work that we have reviewed is focused on developed countries that have access to premium hardware. These regions are already equipped to combat malaria to their fullest capabilities. As mentioned above, Africa was home to 94% of the total world's cases. Taking in other factors (such as technological infrastructure and Healthcare facilities), it is of paramount importance to ensure that the model to be run is computationally efficient. Our work focuses mainly on designing a computationally efficient model which can run on older hardware as these regions are impoverished and don't have access to the most cutting edge hardware. This would allow hospitals in more impoverished regions, that do not have cutting edge hardware, to also implement our software and help save lives.

4 Proposed System

We plan to achieve our goal using a 2 stepped process. The first step being to run and test a few pre-trained models like VGG-19 [16], ResNet50 [17] and InceptionV3 [18].The accuracy F1 score would be noted down to be used later in our system. Another major parameter that would be noted down would be the time to run that particular model. This is essential as our aim to create a lightweight model would only be achieved if the run time is lesser compared to the already tested pre-trained models.
VGG-19 is a pre trained network that is 19 layers deep. It normalizes and reduces dimensions - to keep scale centralized - in terms of when we will perform Convolutions later on. The reason this is important, it is to bring everything "down in line" in a normalized, streamlined and orderly fashion - so we have some sense of normality. As in we want the general structure of what we are parsing to be normalized and centralized so that we have a pre-defined boundary that we are being relative towards. The majority of the layers are MaxPooling ones or use ReLu as the activation function.
ResNet50 is another pre trained network that has 48 convolution layers 1 MaxPool layer and 1 Average Pool layer giving us a total of 50 layers. This plain network was inspired by VGG neural networks, with the convolutional networks having 3×3 filters. However, compared to VGG nets, ResNets have fewer filters and lower complexity.
InceptionV3 that started out from Googlenet intends to allow deeper neural networks without increasing the number of parameters. It replaces bigger convolutions with smaller convolutions which definitely leads to faster training. Say a 5 × 5 filter has 25 parameters; two 3 × 3 filters replacing a 5 × 5 convolution has only 18 (3*3 + 3*3)

parameters instead. In addition smaller auxiliary CNN's are added between layers during training.



What we are striving to achieve is to maintain the same level of accuracy as the above mentioned models as well as keep the model computationally cheap. We aim to do this by running a simple CNN on our images. The first step would be to pre-process our images in particular convert them to grey-scale and adjunct the pixels. On these images we would run a simple CNN to detect the malaria cells. We plan to use the concept of depthwise separable convolutions [19] in order to achieve this goal.

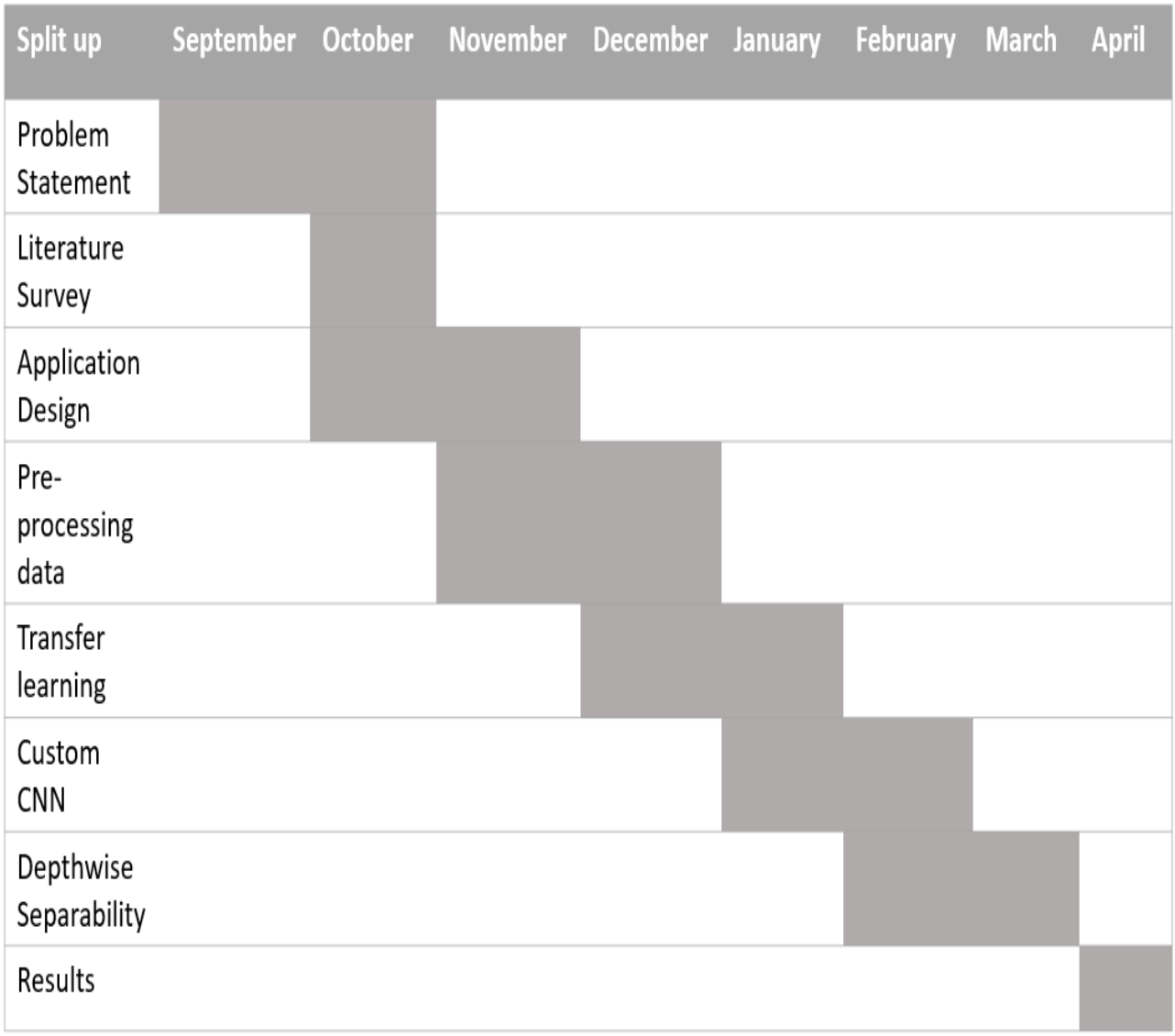
5 Module Split-up

Phase 1 : Pre-processing the dataset of images
This includes grayscale conversion, normalization of pixel values to a predefined range, data augmentation such as flipping (both horizontal and vertical), rotation, cropping, shearing and more, image standardization and more techniques.
We also shift the image pixels both horizontally and vertically to provide a wider range of images.We also increase and decrease the brightness, contrast and other features of the image for the above reason.
Phase 2 : Pre-trained models
In phase 2, we will implement the concept of transfer learning as we will start working on pre-trained models such as VGG19, ResNet50, InceptionV3 (so far) and more. We will explore the structure of these CNNs and the algorithms behind them. We will note down the accuracy, F1 score and all other metrics for every model so that we can quantitatively compare all the pre-trained models.
Phase 3 : Designing our own CNN, training and testing
In phase 3, we will start designing our own CNN, based on how the pre-trained models performed. We will attempt to create a CNN which is simple and lightweight so that it can be run on limited hardware, since the regions that are most affected by malaria are impoverished regions. We use depth-wise separable convolutions in order to achieve the lightweight goal Then we will train and test our model on the dataset.
Phase 4 : Iteratively changing CNN structure until optimal results are obtained
In phase 4, we will keep repeatedly redesigning the CNN until the results obtained are optimal while also making sure to keep the CNN simple.

6 Feasibility

This project is highly feasible. A lightweight Convoluted Neural Network with several layers can be employed to detect the malaria cells. Alongside several existing pre-trained neural networks can be used to perform the same task and can also be used for comparison to our custom CNN. The aim of our model would be to achieve a high level of accuracy. The aim is to deploy a system that is lightweight enough so that it can be run on limited hardware which is available in impoverished regions.

7 Estimated Timeline



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