Malaria Detection using Machine Learning

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Abstract

Malaria is a life-threatening spread by infected Anopheles mosquito bites. Existing means of diagnosis include light microscopy and rapid diagnostic tests, which are used in conjuction to provide accurate results. However, the costs associated with them, in terms of human capital and time required, are immense.

We seek to provide a complementing approach to infection classification using machine learning, which is fast and inexpensive. By training different algorithms like logistic regression, boosted decision trees, support vector machines and convolutional neural networks on images of varying sizes and using image transformations to augment the dataset, we conduct a comprehensive study on model accuracy and inferencing time.

1. Introduction

Malaria is an infectious disease caused by 5 species of the Plasmodium parasite: *Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium malariae*, *Plasmodium ovale* and *Plasmodium knowlesi*, spread by bites of the Anopheles mosquito. An estimated 241 million infections and 627,000 deaths occurred in 2020-21 [1].

1.1. Testing Methods

The infection can be detected using microscopy tests, Rapid Diagnostic Tests (RDTs) and serological tests.[2]

Microscopy tests involve collecting and dyeing a thin or thick blood specimen with Giemsa or Wright's stain to detect infections visually and ascertain the percentage of infected to uninfected cells.

RDTs indicate whether the patient is infected with one of the species of the malaria-causing *Plasmodium* and provide results in about 15 minutes. However, they fail to indicate a premature infection and negative RDT results need further evaluation. Using microscopy is also advised with positive results, so that the proportion of parasitized to uninfected

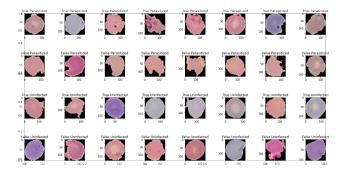


Figure 1. True and false parasitized and uninfected images.

cells can be determined.

Serological tests examine whether antibodies for the infection are present. They are mostly used for screening blood donors, testing for questionable diagnosis accompanied with treatment.

2. Literature Survey

3. Methodology

4. Dataset

The dataset used was publicly available, courtesy of images were taken at Chittagong Medical College Hospital, Bangladesh.[3]

4.1. Dataset Description

The dataset contains 13,799 parasitized and 13,799 uninfected image samples containing 3 colour dimensions for a total of 27,588 images. The images are of varying sizes. The maximum height and width was 385 and 394 pixels respectively. The minimum height are width was 40 and 46 pixels respectively. The mean height and width was 133 and 132 pixels respectively. The median height and width was 130 pixels. The mean aspect ratio of the images is 1.0138.

Out of the 27,588 images, 647 parasitized and 750 unparasitized images were misclassified [4].

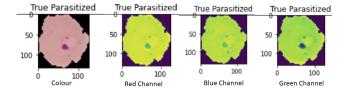


Figure 2. Comparison between various colour channels for a true parasitized cell.

4.2. Exploratory Data Analysis

In order to determine which colour channel was the clearest with respect to the identification of the chromatin dot characteristic to the parasitized cell, we plotted the images in different colour channels and in grayscale.

Out of the plotted images, the green channel showed the maximum isolation of the chromatin dot. We also visualised inverted images and noticed that the green channel had isolated the chromatin dot the most.

4.3. t-SNE visualisation

To visualise the images, we used the t-SNE algorithm to reduce dimensions

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[1] Removed for blind review

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An analysis of the frobnicatable foo filter.

In this paper we present a performance analysis of the paper of Smith *et al*. [1], and show it to be inferior to all previously known methods. Why the previous paper was accepted without this analysis is beyond me.

[1] Smith, L and Jones, C. "The frobnicatable foo filter, a fundamental contribution to human knowledge". Nature 381(12), 1-213.

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1968] didn't handle case B properly. Ours handles it by including a foo term in the bar integral.

•••

The proposed system was integrated with the Apollo lunar lander, and went all the way to the moon, don't you know. It displayed the following behaviours which show how well we solved cases A and B: ...

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 \conf_a \conf_a \conf_a \conf_a \conf_a See The TpXbook, p165.

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\setcounter{page}{4321}
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Method	Frobnability
Theirs	Frumpy
Yours	Frobbly
Ours	Makes one's heart Frob

Table 1. Results. Ours is better.

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