# **Computer Vision for Malaria Parasite Classification in Erythrocytes**

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## ABSTRACT

In this is paper, we introduce a new approach to represent a mathematical modeling technique by means of linear programming as an efficient tool to solve problems related to medical imaging problems especially Malaria Diagnosis through Microscopy Imaging problems .Two applications are approached: formulation of a linear programming based on the given data and solving the given problem using graphical method approach for detecting parasite. Also we applied some image processing techniques namely image segmentation, morphological operations. In the first application, just we have to develop mathematical model from the collected information and in second approach we have to solve problem by Graphical approach. We mark region infected with malaria from the original image leads to identifying parasite and also we classified different species of malaria by using graphical approach. By observation of graph we can predict whether the blood is infected by parasite or not. We can also classify the number of species of parasite infected the erythrocytes and parasite identification by labeling the infected area.

#### **INDEX TERMS**

Image processing, Microscopic imaging, Malaria Blood images, Red Blood Cells, Segmentation.

#### BACKGROUND

Malaria is a serious infectious disease caused by a peripheral blood parasite of the genus *Plasmodium*. According to the World Health Organization (WHO), it causes more than 1 million deaths arising from approximately 300– 500 million infections every year [1]. Although there are newer techniques, manual microscopy for the examination of blood smears (invented in the late 19th century), is currently "the gold standard" for malaria diagnosis. Diagnosis using a microscope requires special training and considerable expertise. It has been shown in several field studies that manual microscopy is not a reliable screening method when performed by non experts due to lack of training especially in the rural areas where malaria is endemic. An automated system aims at performing this task without human intervention and to provide an objective, reliable, and efficient tool to do so. But this work had done by other authors [2].

Microscopy diagnosis is performed by manual visual examination of blood smears[10]. The whole process requires an ability to differentiate between non parasitic stained components (e.g. red blood cells, white blood cells, platelets etc.,) and the malarial parasites using visual information. If the blood sample is diagnosed as positive (i.e. parasites present) an additional capability of differentiating species and life-stages (i.e. identification) is required to specify the infection. On light microscopic examination of the blood film the Morphological stage of the parasites can be reported (Fig.1.1).

In order to perform diagnosis on peripheral blood samples, the system must be capable of differentiating between malarial parasites and healthy blood components. The majority of existing malaria-related image analysis studies doesn't address these requirements. A brief introduction about the malaria parasite, its species and life-cycle stages is provided in the next section.



Figure 1.1: examples of infected red blood cells with distinct shapes



Figure 1.2: Non-infected malaria blood through microscope imaging

# MALARIA PARASITE

The genus *Plasmodium* has four species that can cause human infection: p.*falciparum*, p.*vivax*, p.*ovale*, and p.*malariae* [3]. During the life cycle in peripheral blood, the different species may be observable in the four different life-cycle stages which are generally morphologically distinguishable: ring, trophozoite, schizont, and gametocyte. The species differ in the changes of the shape of the infected cell, presence of some characteristic dots and the morphology of the parasite in some of the life-cycle-stages . The life-cycle-stage of the parasite is defined by its morphology, size and the presence or absence of malarial pigment . In malaria blood cell, the red corpuscles of vertebrates are infected by malaria parasites.

The WHO practical microscopy guide [7] for malaria provides detailed procedures for laboratory practitioners. Diagnosis initially requires determining the presence/absence of malarial parasites in the examined specimen. Then, if parasites are present two more tasks must be performed: identification of the species, life-cycle stages causing the infection and calculation of the degree of infection. However, these tasks are not necessarily performed separately.

Using a microscope, visual detection and identification of the *Plasmodium* [12] is possible . A popular stain, Giemsa, slightly colors red blood cells (RBCs) but highlights the parasites, white blood cells (WBC), platelets, and various artefacts . In order to detect the infection it could be sufficient to divide stained objects into two groups such as parasite/non-parasite and differentiate between them. However to specify the infection and to perform a detailed quantification, all four species of *Plasmodium* at four life-cycle-stages must be differentiated . Despite that the term 'artefact' is not very definitive, any stained object that is not a regular blood component or a parasite is referred here using this term: these include bacteria, spores, crystallized stain chemicals, and

particles due to dirt. It must be noted that other peripheral blood parasites and RBC anomalies are included in this artefact class definition. They could be examined in individual dedicated classes if their identification is also required.

A specimen for manual microscopy diagnosis can be prepared (on a glass slide) in two different forms: first one is a *thick blood film* (figure 2) enables examination of a larger volume of blood, hence it is more sensitive to detect parasites. However, the thick film preparation process destroys RBCs and thus makes identification of species difficult.



Figure 2: examples of Giemsa-stained (a) thin and (b) thick blood film smear images, (c) a concentrated (thick) field of a thin blood film smear [5]

# METHODS

## Describing linear programming methods:

Optimization models are defined by an objective function composed of a set of decision-making variables, subject to a set of restrictions, and presented as mathematical equations. The objective of optimization is to find a set of decision making variables that generates an optimal value for the objective function, a maximum or minimum value depending on the problem, and complies with a set of restrictions imposed by the model [9]. Such restrictions are conditions that limit the decision-making variables and their relations to assume feasible values. We have a model (fig.3) composed of an objective function, restrictions, decision-making variables and parameters [8].

The chart represented in figure 3 shows definitions and interactions among these components [6]. A solution of a problem is called optimal when the decision-making variables assume values that correspond to the maximum or minimum value of the objective function and complies with all restrictions of the model. An algebraic representation of a generic formulation of linear programming model could be presented as given below.

The objective function:

 $Z = c_1 x_1 + c_2 x_2 - \dots - (1)$ 

It is subject to restrictions:

$a_1 x_1 + b_1 x_2$	$\leq \mu_{1(2)}$
$a_2x_1 + b_2x_2$	$\leq \mu_2$ (3)
$a_3 x_1 + b_3 x_2$	$\leq \mu_{3(4)}$
$a_4x_1 + b_4x_4$	$\leq \mu_4$ (5)

with  $x_{i\geq 0}$  (i = 1,2)-----(6)



Figure 3: Linear programming model components

# Where:

(1) represents the mathematical function encoding the objective of the problem and is called objective function(Z) in linear programming, this function must be linear. (2)-(5) represents the linear mathematical function encoding the main restrictions identified based on the parasite species  $x_1$  and  $x_2$  values.

(6) non-negativity restriction, that is, the number of infected red blood  $cells(x_1)$  and non-infected red blood  $cells(x_2)$  may assume positive value or zero. Because negative value for these two categories not possible.

" $x_j$ " corresponds to the decision-making variables that represent the number of infected red blood cells(j=1) and number of non-infected red blood cells(j=2).

" $c_i$ " represents cost coefficients that each variable is able to generate or cost for parasite detection . " $\mu_i$ "represents the the species of parasite . we have four species of parasites described in the above sections.

'a<sub>i and</sub> b<sub>i</sub>' represents the quantity of resources each decision making variable consumes.

## RESULTS

The figure 4 shows that the original image along with parasite detection image and infected region is labeled. So we can say that directly the person infected with malaria.



**OBJECT DETECTION** 



Figure 4

The microscopic image in fig.5 depicts the image not infected with malaria so there is no line vertically in x-aixs and no region is labeled because there is no infected region.



If we find some of red blood cells infected with parasite and some of the blood cells not infected with parasite then the resultant graph by using this method is shown in figure 6. In this case we say that the blood is infected with malaria. Also we can see the labeling of infected region as shown in figure 6.



Figure 6

In some extreme cases the RBC may infected with more than one parasite species. The figure 7 depicts that the RBC infected with two species of parasite namely p2 and p4. Obviously we can say that the malaria is little bit severe when compared to the previous cases. The infected region is labeled (fig.7).





# CONCLUSION

There are different cases raised in this article for malaria parasite detection. Also we mark region infected parasite when compared with region not infected with malaria parasite. In addition, the difference between the infected and non-infected different parasite species results is emphasized. The complete automation techniques not explained in this article but we taken images based on the results.

## DISCUSSION

In this paper we consider all species of parasite as a single variable but we can consider four variables for four different species of parasite and can be implement using some other methods available in linear programming. This is an open problem for new researchers.,

#### ACKNOWLEDGEMENTS

I would like to express my thanks to Dr.Ivy Chakrabarty and Mrs.Amulya for their valuable suggestions and Support with this work.

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