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Detection and Analysis of Malarial Parasites Using Microscopic Images

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Abstract - Malaria is an infectious disease which is mainly diagnosed by visual microscopical evaluation of Giemsa stained blood smears. As it poses a serious global health problem, automation of the evaluation process is of high importance. The propose a set of features for distinguishing between non-infected red blood cells and cells infected by malaria parasites and evaluate the performance of these features on the set of red blood cells from the created database. The developed graphical user interface provides all tools necessary for creating a database of red blood cells. This approach proved to deliver good results on images with various qualitative characteristics resulting in only occasional over-segmented cells. The main part of this work is devoted to the extraction of features from the red blood cell images that could be used for distinguishing between infected and non-infected red blood cells. We propose a set of features based on shape, intensity, and texture and evaluate the performance of these features on the red blood cell samples from the created database using receiver operating characteristics. The results have shown that some of the features could be successfully used for malaria detection.

Keywords **- RBC Component, Microscopic images, Parasites, Feature Extraction, NN Classifier, SVM Classifier.**

1. Introduction

Malaria is a serious global disease and a leading cause of morbidity and mortality in tropical and sub-tropical countries. It affects between 350 and 500 million people and causes more than 1 million deaths every year. Yet, malaria is both preventable and curable. Rapid and accurate diagnosis which enables prompt treatment is an essential requirement to control the disease. The most widely used technique for determining the development stage of the malaria disease is visual microscopical evaluation of Giemsa stained blood smears. This process consists of manually counting the infected red blood cells against the number of red blood cells in a slide. The manual analysis of slides is, however, time-consuming, laborious, and requires a trained operator. Moreover, the accuracy of the final diagnosis ultimately depends on the skill and experience of the technician and the time spent studying each slide and it has been observed that the agreement rates among the clinical experts for the diagnosis are surprisingly low. In this context, the development of a mechanism that automates the process of evaluation, quantification and classification in thin blood slides becomes a high priority and the aim of this work was to contribute to improvement upon malaria microscopy diagnosis by removing the reliance on the performance of a human operator for diagnostic accuracy. A number of methods have been proposed for automatic parasite detection in Giemsa stained blood films based on different approaches.

In this work, we propose a set of features and evaluate the performance for a general problem of distinguishing between infected and non-infected red blood cells. Some of these features have already been used in other works but some of them may be new for the problem of malaria parasites detection. Exact definition of these features is provided, including description of the parameters controlling the generation of the transformed images and description of the preprocessing steps performed. Individual sets of features are evaluated on a created dataset of red blood cell samples using ROC curves for different parameters controlling the feature extraction. Evaluation is followed by a discussion on the effects of different preprocessing techniques and possible utilization of these features for more specific problems of distinguishing between different types of malaria parasites.

The important thing in human life is its life and health. So to make it Secure and to protect for different type of diseases using modern technology here I have develop certain algorithm which will help full in identifying serious diseases like Malaria. Identification of malaria at early stage will be helpful as its effect increases drastically and cause great harm to human life. The malaria is due to imbalance (increase) of amount of Malaria parasites in the blood of patient's which indicates the degree of its

infection. Plasmodium spp. Is a prominent blood parasite which causes malaria. It is nothing but recognition of Plasmodium spp and blood sample visual detection The staining process slightly colorizes the red blood cells (RBCs) but highlights Plasmodium spp parasites, artifacts, and white blood cells (WBC). RBCs in pink color and Giemsa stains nuclei, chromatin in blue tone. It has been shown in several field studies that manual microscopy is not a reliable screening method when performed by non-experts. Malaria parasites host in RBCs when it enter in blood stream. Manual counting of parasitemia is time consuming and tedious and need experts. So to achieve this I have developed an algorithm which will very helpful for identifying the diseases fast and accurate which will give accuracy about 96.72% and work efficiently and easy to use. In this technique I have use the blood cell images to find out whether the patient is malaria affected or not. For that here I have used the statistical characteristics of image like (Skewness, Standard deviation, kurtosis and Energy) which will overcome the problem of not clearly visible boundaries of cells. For the classification here I implemented two algorithms which on by discussed latter and have different advantages over increase in performance.

2. Literature Survey

In the past few years, many researchers have been working on the detecting of malaria using different techniques. An automated diagnostic method can be developed by understanding the diagnostic process and representing it by a specifically tailored image processing based algorithm. The image processing based algorithm should perform diagnosis more or less imitating the manual microscopy. The algorithm should be capable of operating in an unsupervised environment and needs to be robust with minimal false negatives (leading to high sensitivity). The unsupervised nature of the proposed procedure should reduce human intervention, and in so doing speed up the diagnosis process. The algorithm should also be sensitive enough to capture parasites at all stages particular at the early stages of their life cycle and do this without missing any parasites irrespective of image variations. In order to perform diagnosis, the method must be capable of differentiating between parasite and artefacts.

The majority of the image based diagnosis methods reported in literature does not address this requirement. The challenge to achieve this high degree of sensitivity to parasites with an ability to exclude artefact and debris in an unsupervised environment was carried out by developing a very novel and simple statistical method for image classification. The image classification problem performs the following steps: i) RBC enumeration, ii) potential parasite identification and iii) reports parasitaemia by counting the number of iRBC per every 1000 RBCs considering each image corresponds to a section of microscopic field. D. Ruberto et. al. follow morphological method for detection of parasites in Giemsa stained blood slides. Different objects in blood are identified using their dimensions and color. The parasites are detected by means of an automatic thresholding based on morphological approach, using Granulometrices to evaluate size of RBCs and nuclei of parasite. A segmentation method using morphological operators combined with the watershed algorithm.

3. Methodology

System architecture used for Malaria parasite detection involves following steps: Image Acquisition, Image Pre-processing, Feature Extraction, Database, Classification and Result. General block diagram of malaria detection system is shown in Figure1.

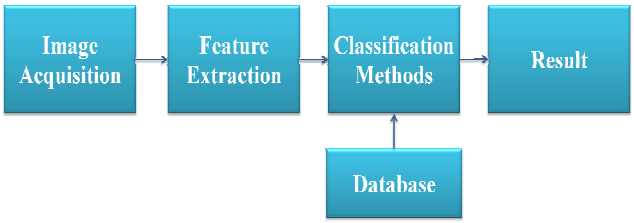
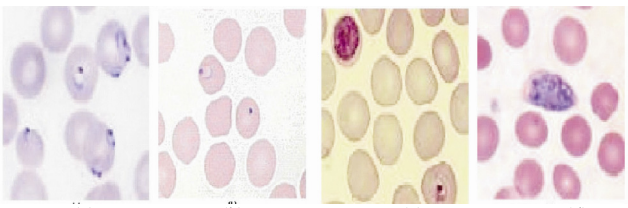


Figure 1: Malaria detection system.

3.1 Image Acquisition

Thin blood film images were obtained from laboratory. The samples obtained mostly had low number of parasites in early stages (rings) of their life cycle. The samples were stained using a fast Giemsa protocol to highlight the parasites and Slide images were acquired using a charge coupled device (CCD) camera with different range of magnification. In total 70 cases were analyzed i.e. 35 positive cases and 35 negative cases obtained from laboratories. Some input images are shown in Figure 2 which is malaria parasites in blood sample or infected by malaria & Figure 3 shows normal blood sample or not infected by malaria.



(a) (b) (c) (d)

Figure 2: (a) P. Falciparum (b) P. Vivax (c) P. Malariae (d) P. Ovale.

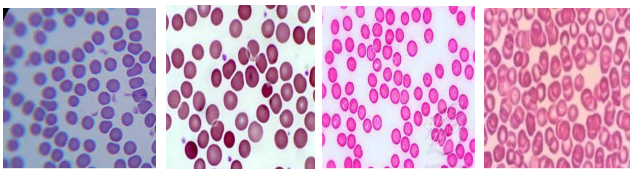


Figure 3: Non infected input images.

3.2 Feature Extraction

Since the chosen features affect the classifier performance, selection of feature which is to be used in a specific data classification problem is as important as the classifier itself. The features which give predominant difference between normal and infected cells are identified and used for training purpose. The selected features are geometrical, color and statistical based. The mathematical morphology provides an approach to the processing of image based on shape. The set of parameters corresponds to the geometrical features are as follows:

1. Phase -: It computes the complex vector.

2. Mean -: Mean is average or mean value of array.
Here, mean is in r, g, b plane.

$$S_M = \overline{b} = \sum_{b=0}^{L-1} bP(b) \qquad (1)$$

3. Skewness -: The coefficient of Skewness is a measure for the degree of symmetry in the variable distribution. It's normal distribution is zero.

$$S_S = \frac{1}{\sigma_b^3} \sum_{b=0}^{L-1} (b - \bar{b})^3 P(b) \qquad (2)$$

4. Kurtosis -: The coefficient of Kurtosis is a measure for the degree of peakedness/flatness in the variable distribution. Here, kurtosis normal distribution is 3.

$$S_K = \frac{1}{\sigma_b^4} \sum_{b=0}^{L-1} (b - \bar{b})^4 P(b) - 3 \qquad (3)$$

5. Standard Deviation -: Standard Deviations normalize by n-1 where n is the sample size.

$$S_D = \left[\sum_{b=0}^{L-1} (b - \bar{b}) \right]^{-\frac{1}{2}} \qquad (4)$$

6. Energy -: The Energy is derived by using Gray Level Co-occurrence Matrix (GLCM). Energy is 1 for a constant image.

$$S_N = \sum_{b=0}^{L-1} P(b)^2 \qquad (5)$$

P(b) is the first-order histogram estimate, Parameter b is the pixel amplitude value, b is the mean of x, σ is the standard deviation of x. L is the upper limit of the quantized amplitude level. The above parameters are used for feature extraction. The statistical features use gray level histogram and saturation histogram of the pixels in the image and based on such analysis, the mean value; angular second momentum, Skewness, Standard deviation, Kurtosis are treated as the features and calculated using above equations.

Table 1: Parameter Values

Img No.	Phase	Mean	Skewness	Kurtosis	Standard Deviation	Energy
1	-14.152	191.54	-0.5826	2.3798	0.0822	0.3070
2	-5.1976	187.54	-0.6091	2.3606	0.1237	0.2101
3	21.173	233.85	-1.2430	4.2072	0.0620	0.5844
4	-7.7442	161.88	-0.0469	1.7473	0.1016	0.2447
5	6.3109	216.59	-0.5131	3.0235	0.0752	0.4382
6	-1.6942	223.05	-0.8626	3.0001	0.0864	0.4865
7	-11.376	206.67	-0.0013	2.5529	0.0932	0.2890
8	-3.4268	195.54	-0.5136	3.0233	0.1924	0.3148
9	-25.160	229.09	-0.9576	3.2825	0.0763	0.5010
10	21.298	198.04	-0.6258	2.1234	0.1279	0.2553
11	-2.8634	133.91	-0.4669	1.8473	0.2356	0.1547
12	-32.003	218.82	-1.0028	3.6523	0.1115	0.4520
13	6.4918	172.63	-0.4922	1.8365	0.2564	0.2800
14	13.877	184.33	-0.7551	2.4295	0.1910	0.2645
15	95.774	222.70	-1.6234	6.4954	0.1408	0.4526
16	62.521	222.38	-0.9417	3.5287	0.1167	0.4094
17	16.859	150.16	-0.1509	2.8820	0.0899	0.2670
18	46.368	218.83	-0.8857	3.9442	0.0984	0.4035
19	17.722	154.51	-0.2869	2.7399	0.1641	0.1299
20	11.738	134.64	-0.4183	1.9369	0.1212	0.2819

3.3 Classification

The classification techniques utilized are as follows:
1. Neural Network.
2. Support Vector Machine.

These techniques will describe in detail later with their performance aspect. The developed algorithm gives good accuracy with Neural Network and Better with Support Vector Machine.

3.3.1 Neural Network

Artificial Neural Network (ANN) has been employed together with image processing techniques to automate the assessment of these blood disorders using the morphological features of erythrocytes in the blood. Prior to training, the first necessary step is to preprocess the giemsa stained blood sample images acquired from using a high resolution digital camera mounted on a microscope.
An Artificial Neural Network (ANN) is an information processing paradigm that is inspired by the way biological nervous systems, such as the brain, process information.

The key element of this paradigm is the novel structure of the information processing system. It is composed of a large number of highly interconnected processing elements (neurons) working in unison to solve specific problems. ANNs, like people, learn by example. An ANN is configured for a specific application, such as pattern recognition or data classification, through a learning process. Learning in biological systems involves adjustments to the synaptic connections that exist between the neurons.

Neural networks consist of simple elements & they work in parallel. Biological nervous systems inspire these elements. There is cordial relationship between elements which decide the network function. For performing a specific, you can train a neural network by adjusting the values of the connections (weights) between elements. We should adjust and train the neural networks, and give a particular input so that it will leads to a specific target output. Training has been given to Neural networks to perform complex functions in various fields, such as classification, pattern recognition, identification, and control systems and vision, speech. Training can be given to neural networks to solve problems which are troublesome to human beings or conventional computers. ANNs are computational networks which attempt to simulate the networks of neurons. This simulation is neuron by neuron simulation. A neural network system consists of many simple processing elements with operate in parallel and whose function is decided by connection strengths, network structure, and the processing performed at computing elements modes.

The terminology of artificial neural network has developed from biological model of brain. The ANN processes information in parallel with a large number of processing elements called neurons and uses large interconnected networks of simple and non linear units. Neural networks consist of the connected cells: The neurons. The neuron receives impulses from either input cells or other neurons and performs some kind of transformation of the input and transmits the outcome to other neurons or to output cells. The neural networks are build from layers of neurons connected so that one layer receives input from the preceding layer of neurons and passes the output to the subsequent layer. ANN includes three groups or layers of units such as input, hidden and output. They are interconnected with one another. The input units give raw information which is fed the network.

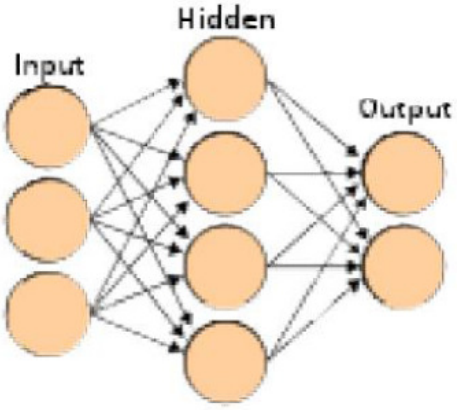


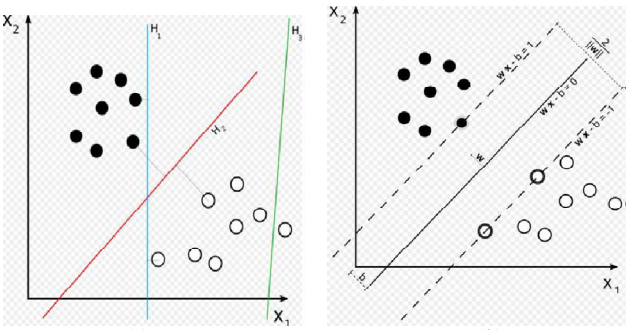
Figure 4– Artificial neural network interconnected groups.

The activity of input unit and the weights on the connections between the input and the hidden units determine the activity of each hidden unit. The behavior of the output units relies on the weight between output unit and activity of the hidden units. It is interesting as the hidden units are free to build their own representations of the weights between the hidden units and input units determine when hidden unit is active by making proper modification of these weights, a hidden unit can select what it represents below figure 4.

3.3.2 Support Vector Machine

Support vector machine (SVM), which is based on Statistical Learning Theory (SLT), has shown much better performance than most other existing machine learning methods which are based on traditional statistics. Support vector machine is widely used for data analyzing and pattern recognizing. The algorithm was invented by Vladimir Vapnik and the current standard incarnation was proposed by Corinna Cortes and Vladimir Vapnik.

SVM is based on structural risk minimization (SRM) principle rather than empirical risk minimization (ERM) principle which is employed by conventional neural networks. It is originated from statistical learning theory (STL) which aims to learn patterns from a small sample set and has some attractive features such as generalization and high empirical performance. Classifying data has been one of the major parts in machine learning. The idea of support vector machine is to create a hyper plane in between data sets to indicate which class it belongs to. The challenge is to train the machine to understand structure from data and mapping with the right class label, for the best result, the hyper plane has the largest distance to the nearest training data points of any class.



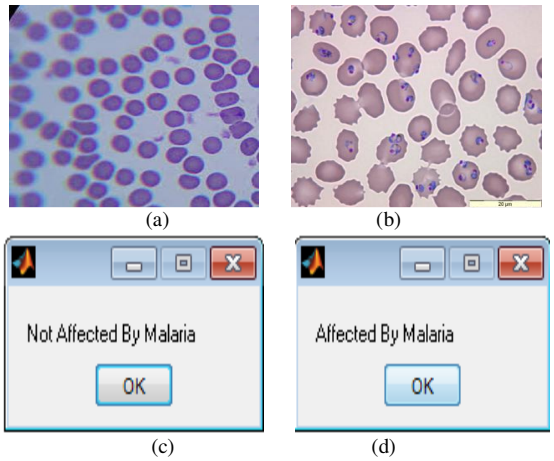
(a) (b)

Figure 5– Hyper Plane

(As we can see from figure 5, H3 does not separate the two classes while H1 separate the two class with a small margin, only H2 gives a maximum margin between two classes, therefore it's the right hyper plane used by support vector machine) However, instead define a function for the hyper plane itself; we define the margin in between the two classes. From figure 5, we can see that the position of our hyper plane is depend on the value of W.

3.4 Results

We took 70 images from different laboratories and did the testing. The aim is to distinguish between negative and positive cases of malaria using thin or thick smear blood slide images. It does require minimum supervision of human interference and it enhances the speed of whole process of diagnosis.



(a) (b)

(c) (d)

Figure 6: (a) Non-affected image, (b) Affected Image, (c) Non affected image Output & (d) Affected image output.

Table 2: Classifier Comparison

Algorithms	Accuracy (%)	Computational Time(ms)
Neural Network	88.57	6.58
Support Vector Machine	94.28	3.852

4. Conclusions

This project addresses how the identification of malaria diseases is possible using image processing by effectively analyzing various parameter of blood cell image by using GLCM as Energy and other like Skewness, Kurtosis, and Standard Deviation. The experimental results indicate that the proposed approach is a valuable approach, which can be significantly support an accurate identification of malaria diseases in a little computational effort. There can be mistake in counting manually the number of RBC & WBC (process of Giemsa) as the boundaries are not clearly defined or visible which lead us to the error in wrong decision. So to solve this problem the developed algorithm be more helpful the other techniques. As this system can meet the real time application requirements, so we can easily have the standalone working version of this system. Support vector machine gives good accuracy as compared to neural network.

References

[1] Yashasvi Purwar, Sirish L Shah, Gwen Clarke, Areej Almugairi and Atis Muehlenbachs, "Automated and unsupervised detection of malarial parasites in microscopic images", Purwar et al. Malaria Journal 2011, 10:3641,Department of Chemical and Materials Engineering, University of Alberta, Edmonton, Canada.

[2] Pallavi T. Suradkar, "Detection of Malarial Parasite in Blood Using Image Processing", International Journal of Engineering and Innovative Technology (IJEIT) Volume 2, Issue 10, April 2013A.

[3] S.Abdul Nasir, M.Y.Mashor and Z.Mohamed, "Segmentation Based Approach for Detection of Malaria Parasites Using Moving K- Means Clustering", Department of Medical Microbiology & Parasitology, School of Medical Sciences, Health Campus, Universiti Sains Malaysia, IEEE EMBS International Conference on Biomedical Engineering and Sciences, Langkawi, 17th - 19th December 2012.

[4] S.Kareem, I.Kale and R.C.S Morling, "Automated Malaria Parasite Detection in Thin Blood Films:- A Hybrid Illumination and Color Constancy Insensitive, Morphological Approach", IEEE Trans.on Applied DSP and VLSI Research Group University of Westminster London, United Kingdom, 2012.

[5] Saowaluck Kaewkamnerd, Apichart Intarapanich, Montri Pannarat, Sastra Chaotheing, Chairat Uthaipibull and Sissades Tongsima, "Detection and Classification Device for Malaria Parasites in Thick- Blood Films" The 6th IEEE International Conference on Intelligent Data Acquisition and Advanced Computing Systems: Technology and Applications 15-17 September 2011, Prague, Czech Republic.

[6] Sriram R., Meenalochani Chandar and Kota Srinivas, "Computer Aided Malarial Diagnosis for JSB Stained White Light Images Using Neural Networks", International Journal of Advanced Research in Computer

Science and Software Engi-neering, Volume 3, Issue 8, August 2013, CSIR-CSIO, Chennai, India.

[7] Isha Suwalka, Ankit Sanadhya, Anirudh Mathur and Mahendra S Chouhan, "Identify Malaria Parasite Using Pattern Recognition Technique" Geetanjali Institute of Technical Studies Dabok, Udaipur, India,2011.

[8] Matthias Elter, Erik Haßlmeyer and Thorsten Zerfaß Fraunhofer, "Detection of malaria parasites in thick blood films", Institute for Integrated Circuits IIS Image Processing and Medical Engineering Department Am Wolfsmantel 33, 91058 Erlangen, Germany, 33rd Annual International Conference of the IEEE EMBS Boston, Massachusetts USA, August 30 - September 3, 2011.

[9] D. Anggraini, A. S. Nugroho, C. Pratama, et al., "Automated status identification of microscopic images obtained from malaria thin blood smears," in 2011 International Conference on Electrical Engineering and Informatics (ICEEI), Bandung, Indonesia, 2011.

[10] Amit Kumar, Manjunatha M, J Chatterjee and Ajoy K Ray, "Segmentation of Blood Smear Images using Normalized Cuts for Detection of Malarial Parasites" Dept. of Electronics & Electrical Communication Engineering, Annual IEEE India Conference (INDICON) 2010.