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RECOGNITION AND CLASSIFICATION OF MALARIA PARASITES OF THIN BLOOD SMEARS

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ABSTRACT:

The project comprises of an image processing system that identifies the malaria parasites in the blood cells of our human body. To detect the malaria parasites, various methods are used in this system. The functioning of this system is categorized into two parts. In the first part of the system, morphological processing technique is used to extract the Red Blood Cells (RBC). The regions in the blood cells will be detected, so does the parasitic images in the blood. Through this detection, classification of affected and non affected red blood cells can be known including the count of RBCs. The second part of the system uses the cross correlation function to categorize the parasite into one of the four species namely, Plasmodium falciparum, Plasmodium vivax, Plasmodium ovale. Accurately, the system detects 95% of the parasite occurance in the blood.

KEYWORDS : Image processing, malaria parasite detection, standardized cross-correlation. Diagnosis of malaria.

INTRODUCTION :

Malaria may be a fatal parasitic disease found widely, especially in tropical and subtropical countries. The parasite undergoes a posh life-cycle within the physical body , utilizing red blood cells (RBCs) as hosts. Malaria infections are diagnosed manually by pathologists who examine microscopic images of blood clots on glass slides and count the infected blood. Based detection using digital image processing techniques produces better results than manual malaria medical imaging. The aim of this work is to develop a detection and arrangement for the accurate detection of malaria parasites present in thin-blood images and for the excellence of parasite species. Digital image processing techniques are utilized in the pre-processing phases to get high-quality medical images.

LITERATURE REVIEW :

Various techniques for the pre-processing phase are proposed within the literature.
[1] Deepa. A. Kurer et al. proposed a replacement approach to low-level image processing-SUSAN (Smallest Unvalued Segment Assimilation Nucleus) Theory performing Edge and Corner detection. Image features are generated supported the colour , texture and geometry of cells and parasites, also as features that make use of them. A two-stage tree classifier distinguishes between true and false positive, then recognizes the four sorts of infection. The algorithm identifies parasite species with a sensitivity of 99 percent and a positive predictive value of 90-92 percent.
[2] Daniel MaitethiaMemeu et al. suggested a way for the identification of plasmodium parasites from photographs of thin blood coagulation . the tactic is predicated on the synthetic Neural Network (ANN) test for the presence of plasmodium parasites in thin images of the blood coagulation . Pre-processing, extraction features are applied and a diagnosis was made on the idea of features extracted from the pictures . 95.0 per cent accuracy within the detection of infected erythrocytes was achieved with reference to the results obtained by expert microscopes.
[3] S. Kareem et al. proposed a completely unique idea to spot the entire number of red blood cells (RBCs) also as their location within the Giemsa thin film images. the tactic uses basic knowledge of the cell structure and therefore the brightness of the components thanks to the Giemsa staining of the sample and detects and locates the RBCs within the image. For malaria detection, this study posed an easy approach supported the form and size of every RBC by estimating its roundness using the acceptable threshold. Classification of malaria parasites is conducted out using an NCC that doesn't require training like the ANN.

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METHODOLOGY:

the strategy of functioning of the project comprises of 4 parts namely Image acquisition, Pre-processing, Detection and counting of RBCs and Classification of Malaria parasites.

1)**IMAGE ACQUISITION:**

A complete of 160 Images of Giemsa stained thin blood smears were collected from the middle for Disease Control and Prevention (CDC). All Images were prepared using oil immersion views (10×1000) of Giemsa stained blood films captured employing a light microscope mounted with a camera .Matlab is employed for reading each of the pictures . These images have different magnification and size characteristics. Pictures selected withprecision (180×240) during this experiment.

2) **PRE-PROCESSING :**

The aim of pre-processing is to get rid of unwanted objects and noise from the image so as to facilitate image segmentation into meaningful regions. Matlab functions are wont to perform the subsequent steps:
Converting the coloured images to a grayscale presentation,.
Estimating the background using the morphological opening technique.
Subtracting the background image from the first image.
Photo contrast enhancement and conversion of grayscale images into binary presentation by thresholding methods,
Transforming images into negative presentation.

3) **DETECTION AND COUNTING OF RBCs :**
The hematologist must detect infected RBCs and skills many RBCs are infected. It became therefore essential to determine a counting algorithm. Knowledge of the dimensions and position of RBCs is additionally needed to separate agglomerated RBCs. After preparing the pictures within the pre-processing stage presented within the previous section, the subsequent morphological processing algorithm is employed to extract and modify information on the form and structure of the RBCs within the image. it's applied to negative binary images. Morphological image processing is administered in three stages, beginning with removing ground noise in thin blood slide images and filling the gaps, then identifying and counting the RBCs within the image. Based on the pictures utilized in this technique , RBC areas were found to be larger than 100 pixels. we'd like to get rid of all small objects containing but 100 pixels to detect RBCs within the image. this is often done using the Matlab function, bwareaopen) (as follows. bw = bwareaopen(bw,100).
To fill the holes within the RBC binary image, the imfill role of Matlab is employed to detect the boundary of the cell. This function extracts regional datum that aren't sure to the image boundary.
A new algorithm is made on the idea of the form and size of every RBC by measuring its roundness using the suitable threshold.
metric = 4*pi*area/perimeter^2.

4) **CLASSIFICATION OF PLASMODIUM SPECIES :**

Four species of Plasmodium are known to infect humans for an extended time. May include: Plasmodium falciparum (P.F), plasmodium (P.V), Plasmodium ovale (P.O) and Plasmodium malariae (P.M). Indeed, all of them endure an equivalent life stages in peripheral human blood (Ring, T.zoitesS.izonts, G.cytes). it's therefore sometimes challenging to discriminate between species at an equivalent stage of life, especially within the early stages.
The classification technique is predicated on the NCC Normalized Cross Correlation function, which is that the standard method of estimating the degree to which two sets of numbers relate. One set of pixels of the image, often mentioned as a mask, slides past the reference set of pixels of the second image and therefore the sum of the products calculated at each position. the height of the cross-correlation function shows where the 2 sets are identical and therefore the low values are different.
The peak of cross-correlation function is specifically designed to accurately diagnose malaria if it's found. This arrangement for plasmodium species in patients ' blood samples includes two groups of images, reference images and test images. Reference images are a group of infected images containing all kinds and stages of malaria parasites.

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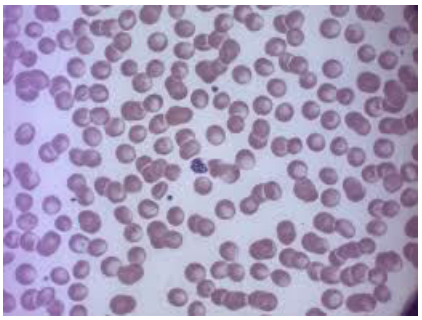


Fig 1: Human malaria parasite

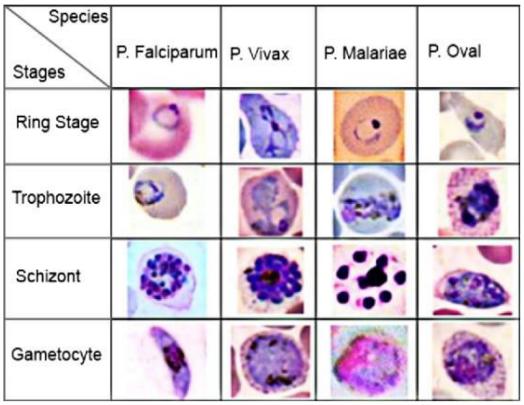


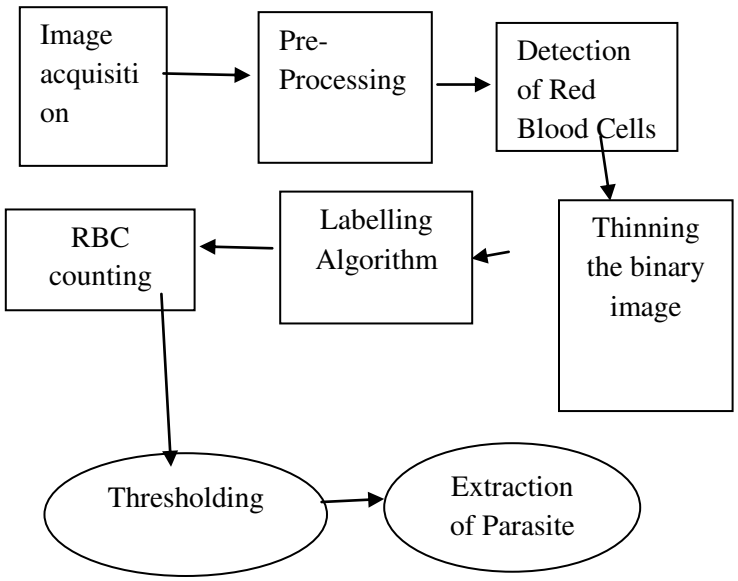
Fig 2: Automatic diagnosis of malaria parasite.

The existing 160 images are used as test images. All images utilized in this technique are converted to a gray scale. The classification technique is predicated on the NCC Normalized Cross Correlation function. Perfect matching (max c) is that the maximum value of the NCC.

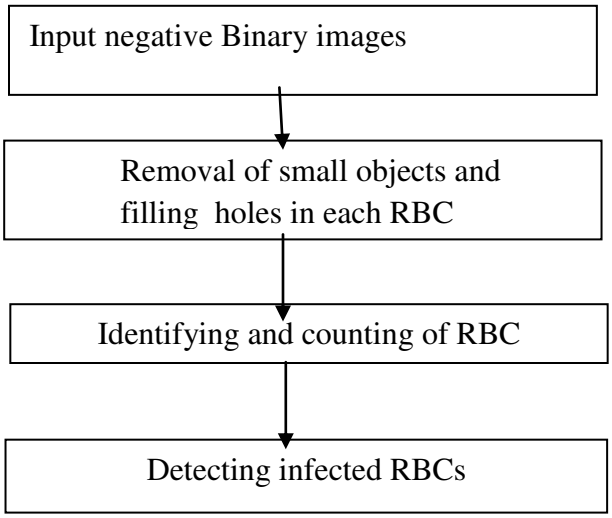
If the worth of max c is bigger than or adequate to 0.7, the infected blood is present and therefore the sort of parasite and its stage is identified and registered. The optimal matching outcome is one. Otherwise, the results of the diagnosis isn't malaria. The experiment is administered with reference images of the dimensions (27x27) and therefore the test image of the dimensions (240x180).

The NCC comparison is predicated on a search for a correlation between the grey scale test and therefore the reference picture. Perfect matching (max c) is that the maximum value of the NCC. If the worth of max c is bigger than or adequate to 0.7, then the infected blood and therefore the sort of parasite and its stage are identified and registered. The optimal matching outcome is one. Otherwise, the result's not malaria.

BLOCK DIAGRAM :



Flow Chart :



RESULT :

Two systems are presented during this work. the primary may be a plasmodium detection and RBC count system. It classifies erythrocytes as infected or uninfected supported the form and size of RBCs by calculating their roundness using the acceptable threshold. The results of this proposed system were compared to the manual leads to order to work out the accuracy of the proposed system. The difference between the 2 results is taken into account to be a percentage error of the system. the typical of all errors is calculated to work out the accuracy of the

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system. the typical error is 5.03 supported the results.This means that the accuracy of the study is 94.97 percent.

Images		Manual approach		Proposed approach		Difference in %
	Total of RBCs	RBCs States		RBCs States		
		Normal RBC count	Abnormal RBC count	Normal RBC count	Abnormal RBC count	N & abn
P.V_R	15	7	8	15	8	6.2
P.V_T	25	9	14	4	14	7.4
P.V_S	40	17	26	6	12	4.1
P.V_G	36	8	25	3	16	2.0
P.O_R	35	15	18	22	19	3.6
P.O_T	26	8	13	14	23	6.3
P.O_S	9	1	6	23	20	9.5
P.O_G	12	5	5	8	6	4.6
P.F_R	27	8	18	24	12	9.0
P.F_T	28	11	8	6	7	7.1
P.F_S	28	14	20	12	14	6.2
P.F_G	24	8	20	18	8	8.0
P.M_R	25	14	12	15	8	2.0
P.M_T	18	6	15	7	24	0.0
P.M_S	48	8	18	8	18	1.2
P.M_G	15	12	34	8	20	3.2
AVG						5.025

Table : Results of RBC Count and its states

Images for the P.O's ring stage have an NCC equla value of 0.5 which is less than 0.7 and are not perfectly matched to the target image due to the image's rotation. This result is removed from the final outcome. All other images tested that gave NCC values greater than or equal to 0.7 are perfectly matched to the plasmodium images extracted. The uninfected images will be those whose NCC values are less than 0.5.

TYPE	RING	T zoites	S izonts	G cytes
P.V	0.5	0.9	0.9	0.9
P.O	0.7	0.9	0.9	0.9
P.F	0.7	0.8	0.9	0.6
P.M	0.6	0.8	0.9	0.9

Table : Malaria species NCC values

CONCLUSION :

This paper presents two malaria detection and classification image processing systems. the primary is that the detection system for RBCs, and therefore the second may be a malaria arrangement that classifies malaria together of its four types.

The detection system for malaria is predicated on morphological processing for state detection and RBC counting. supported the form and size of every RBC, a replacement algorithm is developed because the parasite deforms the RBC into an irregular shape and increases the dimensions in various stages.

that specialize in each RBC's external boundary, an algorithm is developed to live the region and perimeter of the RBC and a RBC roundness test function is employed supported an inexpensive threshold (0.90). This method diagnoses the RBCs as cells that are infected or not infected within the picture.

Method results showed excellent performance with approximately 95 percent accuracy for malaria detection compared to manual results. The second system classifies one among the four known species because the parasite. this technique uses the standardized cross-correlation function to match templates within the spatial field of image signals.

In practice, so as to avoid an uneven background within the correlation image, the pictures may have to be normalized to an equivalent intensity range. a drag affecting matching is that correlation is neither rotational nor scale invariant and therefore the process won't work well unless the template is that the same size because the reference image feature and is similarly oriented. there's no rotation or scaling of the image utilized in this. The

leads to the advanced stages of the parasite were more accurate. The coefficient values for max cross-correlation indicated an ideal match (100 percent) of plasmodium extracted with the target images.

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Fig 1, Human malaria parasite, https://www.google.com/search?q=detection+of+malaria+parasite+in+thin+blood+smear&rlz=1C1CHBF_enIN883IN883&source=lnms&tbm=isch&sa=X&ved=2ahUKEwj4q9GswJrnAhXDH7cAHeaKCawQ_AUoAXoECA4QAw&biw=866&bih=588&dpr=1.5

Fig 2, Automatic Recognition of malaria parasites, https://www.google.com/search?rlz=1C1CHBF_enIN883IN883&biw=866&bih=588&tbm=isch&sa=1&ei=vPopXszNE9u6rQHWpoWYAg&q=automatic+diagnosis+of+malaria+parasites&oq=automatic+diagnosis+of+malaria+parasites&gs_l=img.3...30528.60213..60883...10.0..0.901.6076.44j4j5-2j1.....0....1..gws-wiz-img.....0j0i131j0i67j0i10j0i10i24j0i5i30j0i8i30j0i24.ak37RLIRRs8&ved=0ahUKEwjMm7DxwJrnAhVbXSsKHVZTASMQ4dUDCAc&uact=5