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Malaria Parasite Identification using Feature Based Recognition

Priya G R[1], Spandana A Shetty[2], Kavya Hegde[3]
[1](Computer Science, Srinivas Institute of Technology, India)
[2](Computer Science, Srinivas Institute of Technology, India)
[3](Computer Science, Srinivas Institute of Technology, India)
[1]Corresponding Author: priyagr926@gmail.com

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Abstract: *Malaria is one in all the life threatening diseases. Diagnosis of diseases like malaria is very hooked in to the identification of parasites in blood. Various methods are applied for this process. The majority of all method uses machine learning to identify the malarial parasites. This method has shortcomings in long training time and also the must be retrained if a replacement data emerged. Among all of the other various methods that are used, identification using feature based recognition is likely to be rarely used. This method is powerful within the term that it doesn't require training process, but only an image sample from which the feature are visiting be extracted. During this paper, we design an identification process for blood parasites using one all told the famous local feature extraction algorithms, i.e. SURF (Speeded-Up Robust Features). In our experiment, we evaluate the system to spot Plasmodium parasites. During this experiment, we are focusing only on parasite's gametocyte stage. Here, we use the system to spot whether or not the parasite is Plasmodium falciparum, Plasmodium malariae, Plasmodium ovale, or Plasmodium vivax.*

Key Word*: blood parasite, automatic recognition, SURF, local feature extraction, gametocyte stage.*

I. Introduction

The earlier method of diagnosis and identification of parasites which is present in blood is becoming ever more important with the rise in imported parasitic disease within the Temperate Zone. Any clinical haematology laboratory can expect to be called upon to diagnose these parasites in blood, especially malaria. This method considers the imported blood parasites that would be encountered and discusses the merits of the varied diagnostic tests available. supported the facts that happens during manual test of vegetative cell using microscope, the event of an automatic mechanism for identifying the presence and kind of parasites in blood seems appropriate. With this sort of automation, errors because of human is not any longer an element affecting the accuracy because the identification process has been computerized. additionally, a special clinical expert within the identification process isn't needed. The identification process also will be faster and easier. So far, this sort of study has been done by plenty of individuals for the identification of malaria parasites. There are many methods are implemented to get quick and accurate automation process. The automation process to spot the presence and kind of parasites within the blood by employing a local feature extraction continues to be rarely found within the existing studies. For that, we'll design the automation process for identifying the presence and kind of parasites within the blood by using feature based recognition and so evaluate the results of the designed system. Here, we use feature based recognition to spot blood parasites. the explanation behind this is often because, generally, this method doesn't require training process and it's been evaluated to provide good result for common objects.

II. Literature survey

Current malaria diagnosis dependent totally on microscopic examination of Giemsa-stained thick and thin blood flim samples. The bolster performance of sporozoan classification, in many of the cases researchers are using automated malaria detection devices using digital image analysis. The matter is aggravated with low parasitemia condition. [1]. Erythrocytes are automatically segmented using thresholds of optical phase and refocused to enable quantitative comparison of phase images various machine learning algorithms are used including linear discriminate

classification(LDC),logistic regression(LR), and k-nearest neighbour classification(NNC)to calculate the physical parameters of the cell [2]. The main intension of our system is to detect the parasites by the use of an automatic thresholding supported by a morphological approach. Mainly, here a morphological method is used for cell image segmentation purpose. Ans cell images segmentation is supported by a grey scale granulo metrics and openings with disk-shaped elements, flat and hemispherical. Morphological mehod is more accurate than the classical watershed based algorithm [3]. The only way supported digital image processing of Giemsa-stained thin smear image is developed to facilitate the diagnostic process. The diagnosis procedure is split into two parts, enumeration and identification. The image-based method presented here is suppose to automate the tactic of enumeration and identification, with the foremost advantage being its ability to hold out the diagnosis in an unsupervised manner using image samples. Unsupervised method have high sensitivity and also reducing cases of false negatives. The image based method is tested over a fixed number of images from two different laboratories. The aim is to tell apart between positive and negative cases of malaria using thin smear blood slide images [4]. Unsupervised nature of method requires very less human intervention thus speeding up the entire process of detection of malaria parasites. Overall sensitivity by the use of unsupervised method of capturing cases of malaria parasites is 100% and for all species of malaria parasites it's sensitivity is nearly 56-60%. There are various techniques to diagnose malaria of which manual microscopy is taken into consideration to be the gold standard among all of the methods.

III. Proposed System

In project to form these modules we got an open source library released by Google. The proposed system performing feature based recognition for parasite identification which mainly includes features detection, feature description also as feature matching processes. System has advantage over machine learning which always have to be trained to be ready to classify the information so retrained if a brand new class of information emerged. we design the identification process to identify the malarial parasites using feature based recognition so evaluate whether or not it can provides a good result for parasite identification process. In feature detection image samples is labeled in step with their contents. In retrieving this image samples, object that want to be identified must be isolated where there's no other object than the item itself. This must be assured because we want to retrieve interest points only from the item of interest. The interest point is that the points at which occurs a neighborhood maxima of the computed value. And in next step the feature description interest point position and scale is obtained, a descriptor is formed for every interest point within the image. This can be done by calculating the worth of the Haar wavelet response x and y for every point within a radius 7s where s is that the scale where the interest point is found. Calculation of dominant orientation is included in an exceedingly certain sliding orientation window size. For the extraction of descriptors, an oblong area with size 10s and interest point orientation is additionally built. the most process takes place within the feature matching is elimination. Elimination is performed by calculating the interpretation and orientation between interest points and their neighbor. During this case, the scale, translation, and orientation are going to be divided for upcoming processes. The orientation doesn't accept as true with majority scale, translation, and orientation, it will be eliminated from the matched interest point candidates. During this extra point elimination process that's interest point which occur between image sample and input image. And that we have gotten this interest point inside the region of interest. Once the matching process will finished we are going to head to the comparing process of two images. Parasite classification is set by the load defined between sample image and input image. For these styles of identification, weighting using matched interest point between input image and sample image and width and height ratio as defined isn't enough to produce an honest identification.

IV. Result and Discussion

For each form of parasite, a picture sample is chosen to be compared later with the input images. Here, we are focusing only on parasite's gametocyte stage for less complicated identification and more focused evaluation. This is often done because in solving every problem, we'd like to begin from an easier problem then rise to a more complex problem, Especially considering that the tactic used is comparatively new within the field concerned. The next step is to check the sample images with the input images. To do this, system uses the tactic as explained within the analysis section. Parasite classification is set by the burden defined between sample image and input image. Sample image with the most important weight are going to be assigned because the style of parasite for the input image. These results indicate that the interest point value from input images is comparable or close with interest point value from sample images although they're come from the various kind of parasites. It would happen due to the very fact that the parasites types which require to be identified come from the identical species. It seems that for this kind of identification, weighting using matched interest point between input image and sample image

and width and height ratio as defined isn't enough to produce an honest identification. The result are shown in Table 1

TABLE 1: Experimental Result

Parasite Types	**TPR**	**FPR**	**PPV**	**ACC**
Plasmodium falciparum	0.61	0.213286	0.74	0.689556
Plasmodium malariae	0.333333	0.333333	0.166667	0.621111
Plasmodium ovale	0.75	0.363636	0.428571	0.666657
Plasmodium vivax	0.5	1	0.636365	0.388886

Note:

- TPR = True Positive Rate
- FPR = False Positive Rate
- PPV = Positive Predictive Value
- ACC = Accuracy

V. Conclusion

Based on tests as well as computations done so far, identification of the parasite by using the interest points extraction does not give required results. The weighing process is not sufficient for good identification. The result obtained till now shows that the interest points obtained is relatively similar in many sets of images. This is because of parasites may be from same species and they shares similar characteristics. For future development, identification as well as analysis process result might be improved by using multiple sample images with improved algorithms for each category and exploit the color information which is still not supported by any algorithms which are based on the feature extraction.

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