Malaria Parasite Diagnosis Using Computational Techniques: A Comprehensive Review

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Abstract. Malaria is a very serious disease that caused by the transmitted of parasites through the bites of infected Anopheles mosquito. Malaria death cases can be reduced and prevented through early diagnosis and prompt treatment. A fast and easy-to-use method, with high performance is required to differentiate malaria from non-malarial fevers. Manual examination of blood smears is currently the gold standard, but it is time-consuming, labour-intensive, requires skilled microscopists and the sensitivity of the method depends heavily on the skills of the microscopist. Currently, microscopy-based diagnosis remains the most widely used approach for malaria diagnosis. The development of automated malaria detection techniques is still a field of interest. Automated detection is faster and high accuracy compared to the traditional technique using microscopy. This paper presents an exhaustive review of these studies and suggests a direction for future developments of the malaria detection techniques. This paper analysis of three popular computational approaches which is k-mean clustering, neural network, and morphological approach was presented. Based on overall performance, many research proposed based on the morphological approach in order to detect malaria.

Keywords: Review, Malaria, K-mean Clustering, Neural Network, Morphological

1. Introduction

One of the most significant current discussions in biomedical technology is a malaria detection. Malaria is a serious global health disease caused by a blood parasite named plasmodium spp. According to the World Health Organization (WHO), more than 300-500 million malaria cases and almost 1 million deaths per year [1]. This disease became a big issues especially in areas of Africa, Asia, and South America [2]. Based on ranking, the malaria is the second most dangerous after tuberculosis [2]. The disease is generally diagnosed by examining properly stained peripheral blood smear as the malarial parasite particularly invades red blood corpuscles (RBC) of the circulatory system [3]. Traditionally, this condition is diagnosed by examining a properly stained blood smear. In this situation, the detection part is frequently left to an untrained hand, particularly in backward rural areas where malaria is prevalent and all modern medical amenities have not yet reached. In such an age-old diagnosis method, the human error component becomes an obvious key issue. To avoid this, introducing software to identify disease in pathological laboratories could be a good alternative to the current situation. Unfortunately, no such work has been conducted out to yet to use engineering science concepts to the diagnosis of malaria [3]. In recent years, there has been an increasing amount of literature on discussed about automated malaria parasites detection technique [4–7]. Now, the automated detection technique is more reliable and effective compared to the traditional technique using microscopy screening [8,9]. Besides, the result of automated technique also faster and high accuracy. In this paper, a comprehensive
review and analysis on four popular automated malaria detection methods was explained. This review concentrates on the K-mean Clustering, Neural Network, and Morphological Approach. The objective of this paper is to explore the advantages and drawbacks of automated malaria detection techniques. This paper is organized into three sections. Section 2 explains the literature review of different types of malaria detection techniques. Section 3 describes the summary of the work.

2. Review Technique

There is a large volume of published studies describing a new method in order to detect the malaria parasites. The review and analysis of three selected approaches which is K-mean clustering, neural network, and morphological approach was elaborated as below;

2.1 K-Mean Clustering

In 2013, Aimi et al. [10] published a paper in which they described a new technique using k-means clustering in order to detect the malaria parasite. This method involved a few steps which is; (1) enhanced the cell image using partial contrast stretching, (2) different RGB, HSI, and C-Y colour model colour components were analysed to identify colour components that can provide significant segmentation performance, and (3) median filter and seeded region growing area extraction algorithms were used to smooth the image and remove any unwanted regions, respectively. They also make a comprehensive research and analysis on Moving k-Means (MKM), Fuzzy c-Means (FCM), and Cascaded MKM and FCM [11]. The proposed method was experimented on 125 cell image from Hospital Universiti Sains Malaysia (HUSM). A few assessment evaluation was applied in order to prove the effectiveness of each methods. The result performance based on sensitivity, specificity, and accuracy was shown in table 1.

| Method              | Sensitivity | Specificity | Accuracy |
|---------------------|-------------|-------------|----------|
| MKM                 | 73.00       | 99.50       | 98.64    |
| FCM                 | 82.13       | 97.64       | 97.14    |
| Cascaded MKM and FCM| 78.23       | 99.48       | 98.80    |

Based on the qualitative findings provided in the previous section, it can be seen that the proposed cascaded clustering algorithm is able to segment the infected cell areas from its blood cells background, especially in the case of overlapping RBCs. In addition, Sivakumar and Ramesh [12] showed that K-Means clustering technique is effective in order to detect the White Blood Cell in malaria sample images. This process involved a few steps such as using median filter to eliminate noise, image conversion, enhanced the image based on adaptive histogram and segment the nucleus and cytoplasm using K-mean clustering. The research study by Haryanto et al [13] also found that to identify the malaria virus, the K-means clustering approach can be used with a segmentation technique. The findings of blood that is infected will be directly identified using K-Means clustering segmentation approaches capable of giving identification automation with Giemsa staining of malaria. The diagnosis of malaria is done by various methods which include thick and thin smear method, rapid diagnostic test, antigen detection etc. The limitations of these methods includes false positive rate. This paper presents a methodology to identify the malarial parasites so that the false positive rate is reduced. The above finding is consistent with the study by [12] and [13]. Padmapriya et al. [14] examined the color based discrimination is one of the most feasible methods as it shows greater accuracy and efficiency. The K-means clustering technique is followed for color based discrimination. The segmented malarial cell from K-means clustering is further subjected to morphological operations to extract the feature for classification. The results show that the proposed method helps in the detection of infected red blood cells thus improving decision-making for malaria diagnosis. With the same objective, Savkare et al. [15] proposed a method of K-Mean clustering was used to segment blood cells automatically. For image acquisition by a high resolution camera, Giemsa stained thin blood slides are utilised. Preprocessing,
segmentation, separation of overlapping blood cells, and evaluation of segmentation results are all part of the processing process. On 60 image, the proposed algorithm is put to the test. The photographs in the database are of various magnifications and situations. The accuracy of segmentation attained is 98.89 percent. In another study, Muda and Salam [16] found a better method for combining K-means and Median-cut segmentation algorithms for colour blood cells images. After comparing the best results from Fuzzy c-means, K-means, and Meanshift, the median-cut strategy used. They employed blood cell image infected with malaria parasites as cell images. The proposed strategy yields a better result in terms of object segmentation for the subsequent feature extraction phase. The K-means clustering technique is followed for color based discrimination. The segmented malarial cell from K-means clustering is further subjected to morphological operations to extract the feature for classification. The results show that the proposed method helps in the detection of infected red blood cells thus improving decision-making for malaria diagnosis [14].

2.2 Neural Network

The researchers focused on understanding and visualizing the model to understand it by utilizing customized CNNs to distinguish between parasitized and unaffected cells to help malaria screening. They evaluated the performance of each customized CNN [17]. Rajaraman et al. [18] employed a pre-trained CNN model to extract features and classify smear cell images automatically into infected and uninfected cells. He optimized the model layers experimentally for feature extraction purposes. For Malaria microscopic diagnosis, the researchers exploited deep learning beside convolutional neural network (ResNet34) using Malaria cell images dataset with parasitized and uninfected images. That makes identifying patients’ conditions infected or uninfected an easy task by enabling open-source artificial intelligence [19]. Besides, Kumar et al. [20] used malaria blood smear images to detect the presence and absence of malaria by utilizing a customized convolutional neural network. His proposed model consists of various deep learning layers such as convolutional layer, max-pooling layer, batch normalization layer and fully connected layer. His robust model was applied on 27558 single cell images with achieving an accuracy of 99.71% for training and 98.23% for test data. Automated malaria detection using deep learning algorithms needs human experts to label the images and huge datasets. Therefore, to overcome these challenges, Manescu et al. [21] proposed a novel approach. It leverages routine clinical microscope labels from their quality-controlled malaria clinics to train CNN and obtain an automated malaria diagnosis system. The proposed system provides total malaria parasite and white blood cell counts. His system achieves 92% accuracy and 90% specificity. This system aims to scale up malaria diagnosis in urban regions where the assessment of thousands of specimens is required. Because the existing machine learning models are insufficient for feature extraction and generalization ability. Shi et al. [22] used an ensemble neural network to automatically classify and learn more accurate malaria image attributes. He introduced an adaptive threshold control method for cell segmentation, followed by using the cell as the centre of image extraction to acquire the training dataset, which eliminates the noise problem caused by sliding window cutting. The goal of applying transfer learning is to address the issue of a lack of training data. He used his proposed method to recognize malaria images and got a score of 94.58 percent. The experimental results suggest that the model is resilient and generalizable, and that it is a reliable data processing method for clinical malaria fast diagnosis.

The automated process increases the speed of diagnosis and reduces the treatment cost. Chowdhury et al. [23] exploited a convolutional neural network to count blood cells on blood smear images and detect the presence or absence of malaria pathogen. He obtained 95% precision when he compared the results with the ground truth and 100% accuracy for predicting the malarial infection. His software is ported to microcomputers for rapid prototyping. With the same objective, Cruz et al. [24] proposed a new CNN architecture with the name FideNet for malaria detection purposes. This state-of-art model achieves 98.53 sensitivity, 98.88 accuracy and 99% precision. The research study by Hu et al. [25] also found the image sharpening and histogram equalization method to enlarge the differences between parasitized regions and other areas. He proposed a new CNN structure with five layers and dropout technology to reduce the overfitting in the network. In the paper, he compared his model with the pre-trained CNNs and other traditional algorithms. His model achieves 99.98% accuracy. The proposed model can assist clinicians in diagnosing the malaria disease accurately. In contrast, Zhao et al. [26] The endemic of malaria in Africa, as well as the socioeconomic constraints that accompany it, were discussed. He designed an automated mobile phone screening system that takes into account the
advantages of available resources. He used an SSD multi-box object identification architecture to isolate images of individual red blood cells with 90.4 percent average precision from thin blood smears collected using light microscopy. The FSRCNN model, which upscales low-resolution images to high-resolution images from 32x32 to 128x128 with a PSNR of 30.2 compared to the baseline of 24.2 using bicubic interpolation, was then implemented. Finally, with a 96.5 percent accuracy, he used VGG16 CNN to identify between infected and uninfected blood cells. These sequential models establish a streamlined screening platform by revealing the number of malaria-infected red blood cells in a particular sample to the healthcare professional. This model is compatible with low-end smartphone hardware and does not require a high-speed internet connection.

Employing computer-aided diagnosis with the employment of pre-trained convolutional neural networks such as GoogleNet and ShuffleNet V2 with transfer learning. The accuracy of GoogleNet is 93.89% and 95.2% in ShuffleNet [27]. Banerjee's aim is to detect malaria in real-time images. Therefore, he proposed a Deep Convolutional Neural Network (DCNN) called "Falcon" to detect malaria from blood smear slide images of a malaria screener. He obtained trustworthy accuracy of 95.2% for malaria's presence or absence compared with existing CNN models [28]. To minimize the human inputs to diagnose malaria, Pundir exploited deep learning methods to extract features from data and classify them automatically. That leads to improving the efficiency of the pathologists and reducing pathologists' necessity in rural villages [29]. In 2021, Ragb et al. [30] employed a deep convolutional neural network with a mixture of machine learning algorithms, such as transfer learning, cyclical, constant learning, and ensemble methods to identify parasitic cells from red blood smears images. 14 networks pre-trained from the ImageNet database are employed with various machine learning algorithms to classify 27558 images. 80% of the images are training, and the remaining are 10% for test and 10% for validation. He obtained the best test accuracy among other state-of-the-art methodologies.

2.3 Morphological Approach

Malaria is an epidemic health problem that necessitates prompt and correct diagnosis in order to provide effective treatment. Pathologists typically diagnose malaria by visually inspecting blood stained slides. This type of visual evaluation, however, is subjective, error-prone, and time-consuming. To address the challenges, a number of automatic malaria diagnosis approaches have been presented thus far [31–33]. In recent years, there has been an increasing interest in Histogram Equalization approach in order to diagnosis malaria disease. A method using first localizes leukocytes by color component combination and adaptive histogram thresholding (AHT), and crops sub-image corresponding to each leukocyte were investigated by Zhou et al. [34]. To extract the complete leukocyte, clever edge detection is used. As a result, by eliminating the nucleus from the leukocyte, cytoplasm is obtained. As a result, the approach produces more accurate segmentation results than their equivalents. In addition, according to Bhattacharya et al. [35] extracting hue, saturation, and intensity planes, followed by histogram equalisation, improves the malaria image. To remove the noise from the image, a median filter is used. After preprocessing, k-means clustering is used to partition the malaria parasite to obtain a clear vision of the region of interest. Following clustering, region increasing area extraction is used to remove undesirable areas from the segmented image. Research finding by Mushabe et al. [36] also points towards The red blood cells are extracted using histogram-based thresholding. To break clumped red blood cells, boundary curvature computations and Delaunay triangulation are utilised. The RGB pixel values of the stained parasites are used as features in a Bayesian classifier to classify them. The results demonstrate that contaminated red blood cells may be detected with 98.5 percent sensitivity and 97.2 percent specificity. Similarly, Aggarwal et al. [37] found green channel and histogram equalisation are used to improve the images, while background subtraction is used to acquire a clear view of the region of interest. A median filter is used to remove noise from the images after preprocessing. After that, Otsu's segmentation approach is applied to the filtered images. This study makes use of a database from the World Health Organization. The studies show promising results, with an accuracy of up to 93%. Summary, Awasthi et al. [38] presented a comprehensive review of systematic comparison is made with six such prominently used methods, namely Contrast Limited Adaptive Histogram Equalization (CLAHE), RIQMC-based optimal histogram matching (ROHIM), modified L0, Morphological Varying (MV)-Bitonic filter, unsharp mask filter and joint bilateral filter as shown on figure 1. Based on comparison, the image enhanced using the GF methodology resulted in better
segmentation accuracy (up to 50% improvement over native images) and visual quality, with no change in colour tones.

![Figure 1](image)

**Figure 1.** (A) The images within a focal stack of healthy RBCs in a blood smear, after processing with, (B) CLAHE [39], (C) ROHIM [40], (D) modified Lo [41], (E) MV-Bitonic [42], (F) unsharp mask [43], (G) joint bilateral filter (BF) [44] and (H) guided filter (GF) [38].

Furthermore, manual inspection necessitates the pathologist's undivided attention and is a difficult and time-consuming method of detecting malaria. As a result, the development of automated technologies is critical for the rapid and accurate identification of malaria. It can lower the rate of false negatives and aid in the early detection of disease, when it can be properly treated. In 2021, S. Chatterjee and P. Majumder [45] proposed a new called “Information Padding” used lightweighted and easily implementable in terms of time and space complexity. Also, it has a training accuracy of 97.98% and a validation accuracy of 97.6%. Salamah et al. [46] uses intensity slicing and morphological operations to segment blood components, blood component classification using a rule based on parasite candidate features, and parasite candidate formation. It lowered misclassification error by 2.6 percent and relative foreground error by 45.5 percent, respectively. The addition of properties to the blood component classification improved the system's precision. This method's average precision, recall, and F-measure were all 86 percent. It has been demonstrated that the proposed approach is suitable for detecting malaria parasites.

Another studies by Nugroho et al. [47] proposed a detection method based on adaptive thresholding, colour segmentation between green channel (G) with hue channel (H) from HSV colour space, and some morphological operation techniques. The data used are digital microscopic images of thin blood smear. This research achieves the sensitivity level of 91.6% and positive predictive value (PPV) of 89.1%. It shows that performance of the proposed parasite detection method is reliable to assist doctor and contributes for developing the computer aided detection in Plasmodium cases. Sharma et al. [48] found differences suggesting that used a Otsu thresholding as a main component. Otsu's thresholding and morphological filtering are used to separate the erythrocyte areas from the other blood components in the smears. The clump erythrocytes are segmented using the inherent geometrical
property of the clump's concavity point detection, which is unaffected by any geometrical deformation or image acquisition faults. The segmented erythrocytes are then analysed using a thresholding technique based on the "pseudo-valley" idea to identify contaminated erythrocytes. The proposed approach is tested on three different databases. The accuracy of erythrocyte segmentation was found to be 97.95 percent, with improvements of 8.76 percent and 0.87 percent when compared to the classical watershed and marker controlled watershed segmentation techniques, respectively. Furthermore, the contaminated erythrocyte was identified with a precision of 88.57 percent. The above finding is consistent with the study by Nugroho et al. [49]. The author examined a saturation channel is retrieved from HSV. There are three distinct groupings of images that have been segmented in various ways. Plasmodium is segmented using Otsu thresholding and morphological image processing. There are 124 cropped images in the data set. The accuracy, sensitivity, and specificity of the evaluation results are 97.99 percent, 82.23 percent, and 99.33 percent, respectively. The proposed method is suitable to help the development of CAD in malaria diagnosis, based on these high evaluation values.

Furthermore, Hendrawan et al. [50] proposed using the color-based cascading method to segment and detect malaria parasite-infected microscope images. Color normalisation is the first step, then gamma correction, noise reduction, exposure compensation, edge enhancement, fuzzy c-means clustering, and finally morphological processing. In 574 photographs, we employed the approach to detect malaria infection in four Plasmodium types and three stages of malaria development. The method's sensitivity, specificity, and accuracy were found to be 97.91 percent, 98.61 percent, and 98.26 percent, respectively. The research study by Varma and Chavan [51] also found demonstrated classifying blood smears into thin and thick blood smears using the local binary pattern (LBP) technique is effective. Infected cells are counted using morphological operations and k-means clustering algorithms, as well as intensity patterns within the cells. For thick and thin blood smear images, the tests are run on standard datasets utilising segmentation and morphological techniques. The suggested algorithm's performance is measured using a confusion matrix. Sensitivity and specificity are used to compare the results. Interestingly, Mustafa et al. [52] presents a morphological approach to image segmentation in order to automate the detection of malaria parasites in malaria images. This method use a mix of image filtering and the morphological operator. By comparing the suggested image segmentation approach to existing segmentation techniques such as Otsu, Niblack, local adaptive, and Feng approaches, the effectiveness of the proposed image segmentation methodology has been determined. Overall, the experimental findings show that the proposed morphological technique gave the best segmentation results, with 98.52 percent segmentation accuracy and 99.62 percent specificity.

A new approach for morphological filtering of blood image as a segmentation pre-processing tool. On blood image, traditional morphological closure removes undesirable components but also loses vital information. The suggested morphological filtering preserves foreground component information while reducing noise and artefacts. This method could be tweaked to work with other pathological images as well, such as tissue analysis and cell differential analysis [53].

3. Conclusion

Malaria is a severe public health problem that kills millions of people each year. Because light microscopy is the most common approach for diagnosing malaria, well-trained microscopists are required. A huge amount of blood may be analysed quickly and easily using a thick blood smear. The following is a summary of the primary finding: (1) this study discovered that the appearance of infected red blood cells (RBCs) and their morphological characteristics are critical for detecting the presence of malaria parasites. Due to the non-standard preparation of blood slides, which results in colour variations in different slides, it is difficult to determine the presence of malaria parasites as well as observe their morphological characteristics. (2) There are several methods for detecting malaria parasites. When compared to conventional diagnostic procedures, the automated parasite identification algorithm provides a number of advantages. It avoids the drawbacks of quick methods, such as species specificity and high per-test costs, while keeping many of microscopy's conventional advantages, such as species discrimination. This paper could be utilised to research and create a novel malaria detection and classification technique in the future.
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