Automated Dengue Recognition and Analysis through Image Processing and Machine Learning

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Abstract—Detecting dengue fever using image processing techniques typically involves the analysis of medical images such as blood smears or tissue samples. Dengue is a viral disease transmitted by Aedes mosquitoes, and its diagnosis primarily relies on clinical symptoms, serological tests, and molecular assays. Image processing can be used as a complementary tool to assist and identify the dengue virus or related disparities in the body. Dengue fever, alternatively known as break-bone fever, is a lifethreatening arboviral disease caused by the DENV virus. It is a major global health concern with an increasing incidence worldwide. The existing clinical methods for diagnosing dengue are manual, requiring significant time and labor. The present work aims to develop an automated system using machine learning and digital image analysis to detect dengue infection from blood smear images. The custom algorithms are designed to extract platelets, red blood cells, and white blood cells, and train a feature vector. By automating the analysis of blood smear images, aids healthcare professionals detect cases of dengue more efficiently, allowing for early treatment and potentially saving lives. However, it is crucial to address data quality, algorithm selection, validation, interpretability, and ethical considerations throughout the development process.

Keywords—Dengue, DENV, pixel intensity, edge detection, Hough transform, histogram thresholding, CIELab space

I. INTRODUCTION

Dengue fever, commonly known as break-bone fever, is a severe and potentially life-threatening arboviral disease caused by the DENV virus. It poses a significant global health concern, with its incidence on the rise across the world. Early and accurate diagnosis of dengue is crucial for effective management and timely treatment of patients. Dengue fever poses a substantial burden on public health systems worldwide, particularly in humid and semitropical regions where the disease is endemic. World Health Organization (WHO) reports, nearly 39 billion dengue infections occur annually, with around 96 million of those resulting in symptomatic illness. Severe cases of dengue can lead to Dengue Hemorrhagic Fever (DHF) or Dengue Shock Syndrome (DSS), which can be life-threatening if not promptly diagnosed and treated. The current clinical methods for diagnosing dengue often rely on manual examination of blood smears, which is a time-consuming and labor-intensive process. To address these challenges, this work aims to design and develop an automated method that utilizes machine learning and digital image analysis techniques to detect dengue infection from microscopic images of human blood smear. Timely and accurate diagnosis is essential for effective management and treatment of dengue fever. Traditional diagnostic methods involve laboratory tests such as polymerase chain reaction (PCR) and enzyme-linked immunosorbent assay (ELISA) to detect the presence of the dengue virus or antibodies in the patient's blood. While these methods are effective, they can be time- consuming, expensive, and require specialized laboratory facilities. To address the challenges posed by traditional diagnostic methods, researchers and healthcare professionals have been exploring alternative approaches. One promising avenue is the use of machine learning and digital image analysis techniques to automate the recognition of dengue infection from human blood smear microscopic images [1]. By leveraging advanced algorithms and training models on extracted features from images of human blood smear, this automated method aims to streamline the diagnostic workflow and provide accurate results in a timely manner. This can significantly improve the efficiency of the diagnostic process, enabling healthcare providers to identify dengue cases early and initiate appropriate treatment promptly. Early detection of dengue infection is crucial for managing the disease effectively [2]. With timely intervention, healthcare professionals can closely monitor patients, provide supportive care, and take necessary measures to prevent complications associated with severe dengue. Additionally, early diagnosis allows for effective vector control strategies to be implemented, reducing the spread of the disease within communities. The primary objective of this automated system is to improve the detection of dengue cases and enhance the Complete Blood Count (CBC) testing process. By automating the investigation of images of human blood smear, the method streamlines the diagnostic workflow, leading to more efficient and accurate results. Early detection of dengue infection is crucial for prompt medical intervention and effective management of the disease [2]. By combining the power of machine learning and image analysis, this work offers the potential to revolutionize the diagnosis of dengue fever. It not only reduces the manual effort required for diagnosis but also enhances the accuracy and efficiency of the diagnostic process.

II. LITERATURE REVIEW

In the field of blood cell analysis techniques, traditional manual counting using a hemocytometer is known to be laborious, time-consuming, and susceptible to errors due to overlapping cells and inconsistent visual perception. However, the emergence of digital image processing techniques offers a promising alternative that minimizes errors and reduces stress overload on technicians.

Mayfong Mayxay et al [3] demonstrated a strap test that yielded results with sensitivity 33.5%-34.0%, specificity 84.0%- 91.0%, and precision ranging between 85.0%-90.0% and recall value 32.5%-34.0%. The method results in low sensitivity, relatively small value in diagnosis of prospectus dengue cases. Earlier works used digital image processing and segmentation methods to categorize white blood cells (WBC) based on the edge energy of the cell structures.

The emphasis is to select features and classification method. Alfred RJ. Katz et al [4] examined the five major

methods to classify the type of WBCs and proposed the top performing supervised learning technique neural network. Ms Joshi et al [5] studied WBC detection and classification of acute Leukemia by image of human blood smears. The classifier K-Nearest Neighbor (KNN) is employed to observe the result with 93.0% of precision. Madhukar Monica et al [6] worked to recognize acute lymphoblastic leukemia through decision support tools. The authors used K-means Clustering procedures of the Lab color model for image segmentation at accuracy of 93.5%. Ilyas K et al [7] proposed morphology-based segmentation operation and Blob processing. The method successfully extracts the blood cells with an accuracy of 91.7%. Prabakaran K et al [8] worked on improving image resolution method to aid the evaluation of human blood smears slides under microscope. Reddy VH [9] worked with feature extraction using a series of pipelined techniques to count blood cell. It is a time optimized result. Pooja RP et al [10] combined Otsu thresholding algorithm, morphological operation. This was to fill the holes of blood components to aid their detection and count using thresholding technique and labelling. The proposed method resulted at an accuracy of 94.58%. Alomari YM et al [11] recommended and designed the serialized operations to segmentation and extract features. A Randomized Circular-shape Detection algorithm (RCD) was proposed to observe an accuracy of 97.5%. Tandon R et al [12] proposed a time and cost effective and efficient algorithm for segmentation. Lazuardi L et al [13] calculated the kappa coefficient of 0.6 through statistical analysis. The method adopted the series of image processing techniques. Dey R et al [14] used color-based segmentation and morphological operations. The method employed L*a*b channels of the image were extracted and used to performed morphological operation to extract platelets. Khan S et al [15] performed segmentation using Otsu threshold algorithm flowed by Morphological operation. The proposed work generated an accuracy of 95.0% relative to the traditional approach. Burduk R et al [16] proposed platelet extraction, the approach included the Watershed algorithm and thresholding technique to achieve segmentation. The classifier used to test the features was Support Vector Machine (SVM). Acharya V, et al[17] employed labelling algorithm with HT. the authors proposed further enhancement of the work through texture and shape descriptors.

III. METHODOLOGY

A. Pre-processing

The Input module is designed to

a. Read the microscopic images and normalize it for next stage without any distortion or artifacts introduced in the images.

b. Denoising of the normalized image. Empirically, several kernels were designed and test to find the best fit kernel to eliminate the noise.

B. Custom algorithm designed to segment Platelet

Step-1: Load the input image

Step-2: Convert the RGB image to CIELab color space.

Step-3: Extract the chromatic channel 'a' from the image: chromatic channel 'a' provides more information and contributes to the intensity distinction. Values of 'a' is larger as compared to 'L' and 'B' for platelet as in above figure 1a,

whereas for non-platelets all the three values are equally contributing as depicted in figure 1b.
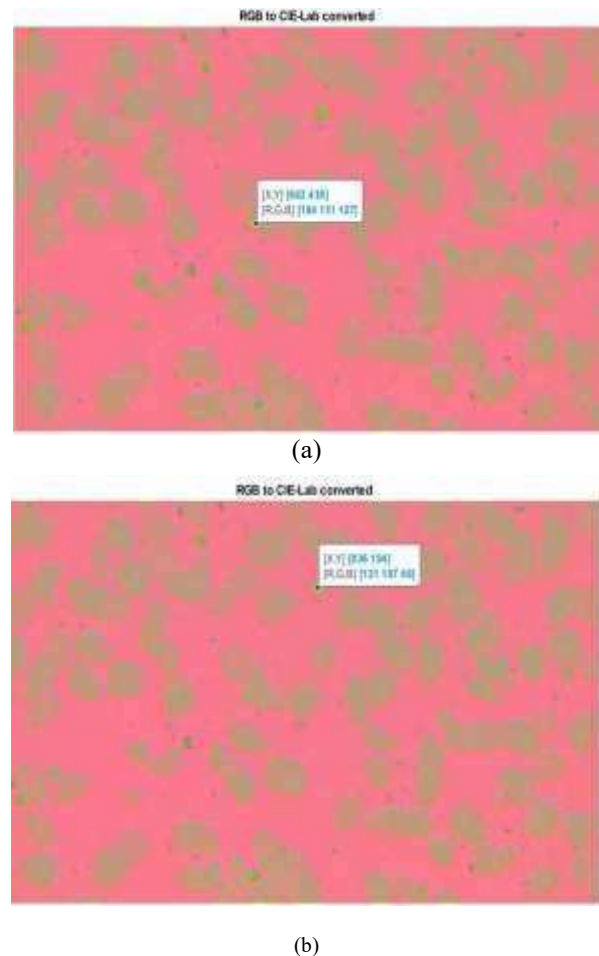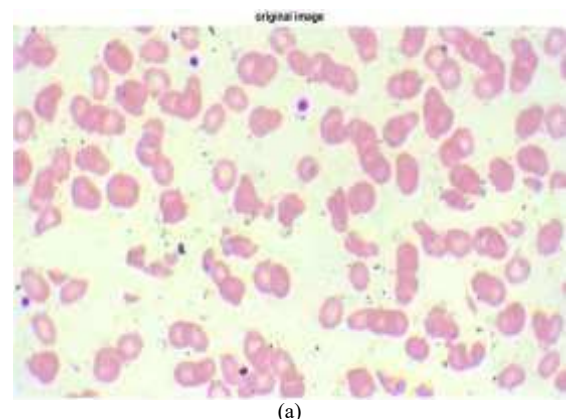

(a)

(b)

Fig. 1. (a) Intensity values for platelet regions , (b) Intensity values for non-platelet regions

Step-4: Binarization using the threshold intensity value of the platelets

Step-5: Removal of smaller particles from the image, mean radius of a platelet is considered for noise removal.
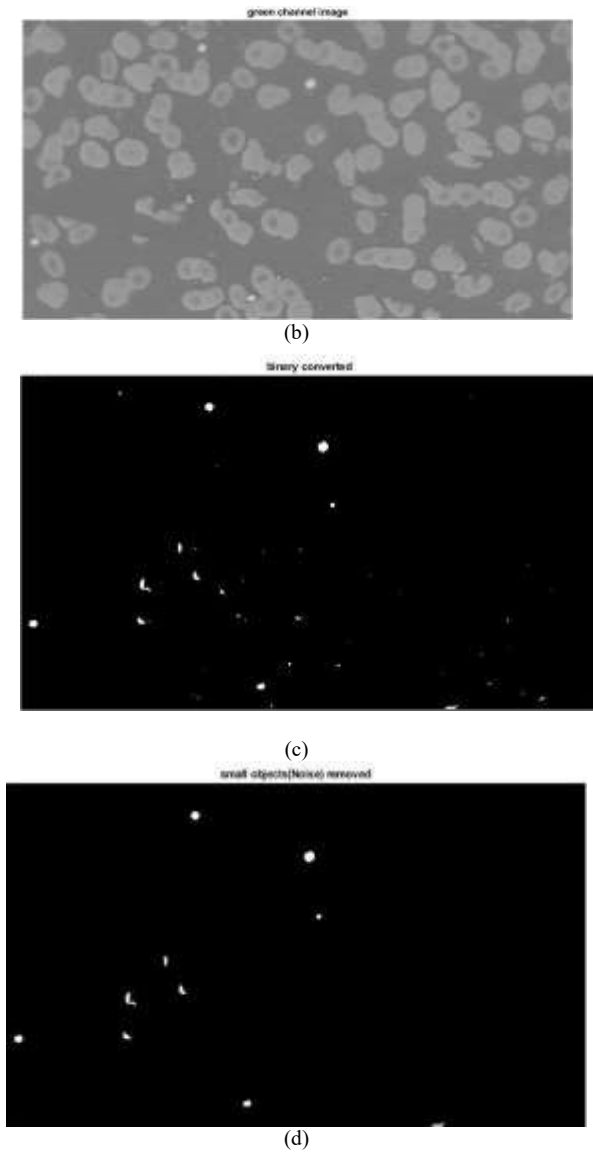

(a)

(b)

(c)

(d)

Fig. 2. (a) Original Image Figure , (b) green channel extracted image, (c) Segmented Image in Binary, (d) Result Image with only Platelets

C. Custom algorithm designed for extraction of RBCs

Algorithm DetectRBCs(input_image):

Step 1: Convert the colored input image into a grayscale image The values used are empirically derived as show below:

gray_pixel = 0.299 * red + 0.587 * green + 0.114 * blue

Step 2: Edge detection using Sobel edge detector edge_image

= sqrt(Gx^2 + Gy^2) for a kernel size 3, Gx and Gy are gradients in respective direction

Gx = (1 * P1 + 2 * P2 + 1 * P3) - (1 * P7 + 2 * P8 + 1 * P9) for the x-direction

Gy = (1 * P1 + 2 * P4 + 1 * P7) - (1 * P3 + 2 * P6 + 1 * P9) for the y-direction

Step 3: Binary morphological operation erode to connect the broken edges eroded_image(x, y) = min(I(x + i, y + j) for all (i, j) in SE) where SE is structuring element

Step 4: Binary fill operation to minimal overlapped RBCs dilated_image(x, y) = max(I(x + i, y + j) for all (i, j) in SE)

Step 5: Remove smaller particles considering them as noise filtered_ image

=Dilate (Erode (filled_image,structuring_element), structuring_element)

Step 6: Segment the resultant image to contain only the region of interest segmented_image= ExtractRegionOfInterest(connected_components, label)

Step 7: Create the colored mask over segmented image colored_mask = AssignColors(segmented_image, color_map)

def CreateColoredMask(segmented_image, color_map):

colored_mask = np.zeros_like(segmented_image, dtype=np.uint8) for label, color in color_map.items():
colored_mask[segmented_image == label] = color return colored_mask
# Step 8: Apply the mask on the input image to detect the RBCs and mark them

output_image(x, y) = input_image(x, y) * colored_mask(x, y)+background_color*(1 - colored_mask(x, y))

Def ApplyMask (input_ image, colored_mask, background_color = (0, 0, 0)): output_image = input_image. copy() for channel in range(input_image.shape[2]):

output_image[:, :, channel] = (input_image[:, :, channel] * colored_mask) + (background_color[channel] * (1 - colored_mask)) return output_image
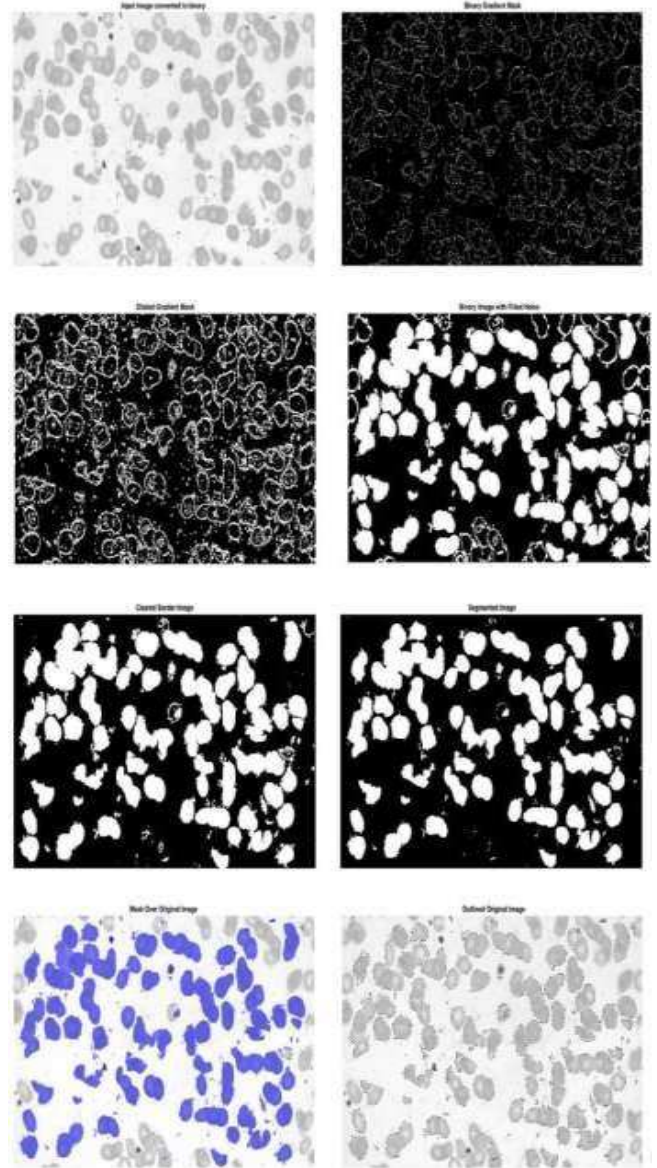

Fig. 3. Stagewise results for RBC Extraction

The pseudo code to detect the RBC's shows all the image processing techniques sequenced to achieve the extraction of RBC's. A 3X3 kernel was designed empirically to achieve the desired boundary extraction. The boundaries extracted are discontinuous, hence the image reconstruction is performed through morphological operations. A colored mask is created on the observed reconstructed image to superimpose it on the original images to map the pixels belonging to RBC's.

IV. EXPERIMENT RESULT AND ANALYSIS

A. The experimental results demonstrate the potential of image processing for dengue diagnosis

1) High Accuracy: the features extracted have contributed to achieve an overall accuracy of 94% in distinguishing between dengue-infected and non-infected blood samples using KNN classifier and SVM classifier. This high accuracy indicates the effectiveness of our approach.
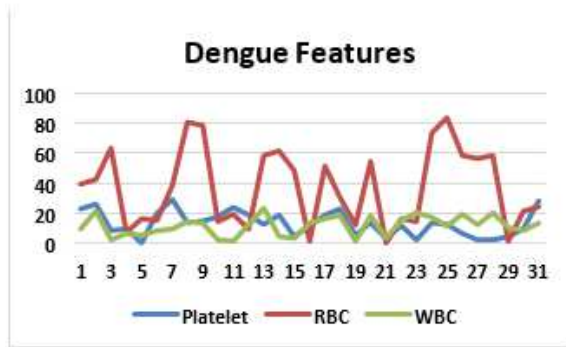

Fig. 4.   Feature Mapping for Dengue

2) Recall and precision: The recall value of features was 91% for negative and 97% for positive implying its ability to correctly identify dengue cases. Precision values were 97% and 91% showcasing the model's capability to avoid false alarms for non-dengue cases.

TABLE I.   MATRIX FOR RESULT ANALYSIS FOR DENGUE

	Precision	Recall	F1- score	support
No-Dengue	0.97	0.91	0.94	7142
Dengue	0.91	0.97	0.94	7330
Accuracy	----	----	0.94	16832
Macro avg	0.94	0.94	0.94	16832
Weighted avg	0.94	0.94	0.94	16832

3) ROC Curve Analysis: The ROC curve exhibited a steep rise and an Area Under the Curve (AUC) of 0.95, further confirming the model's capacity to discriminate between the two classes.
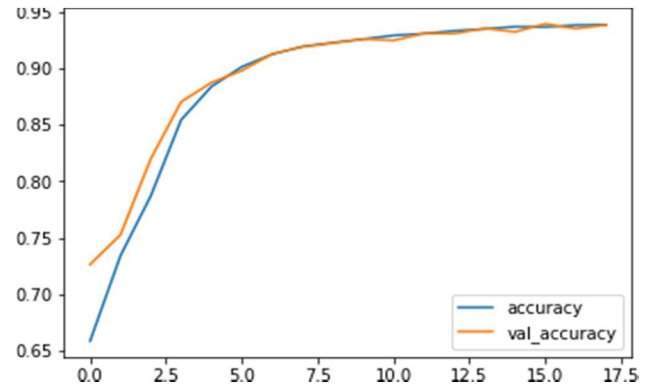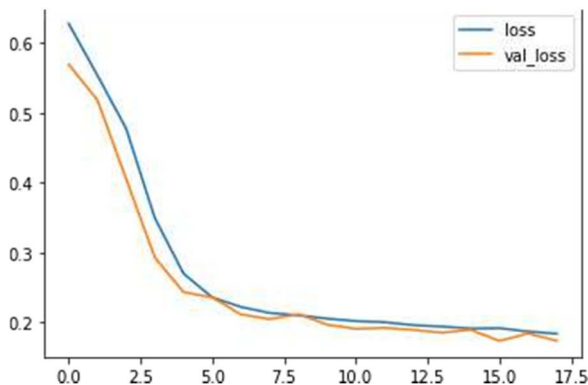

Fig. 5.   ROC Curve Analysis

4) Comparative analysis: The earlier approaches suggested by various researches are all based on shape descriptors, texture descriptors which fail when overlapping RBCs are encountered. The proposed method overcome such disadvantages.

TABLE II.   COMPARISION OF PARAMETER USAGE FOR PLATELET, WBC AND RBC DETECTION

Authors	Parameters	Remarks
Fatimah AlHafiz et al [18]	Thresholding & canny edge detector	Fails to detect the overlapping RBCs, WBCs and platelets
K T Kavya et al [19]	HIS color space, adaptive histogram equalization & active contour segmentation	Achieved extraction of overlapping RBC & WBC but with a lower accuracy of 89.6%
Siddharth Verma et al [20]	Dark Contrast Algorithm and KMedoid Clustering	Clustering approach leads to higher time complexity

5) Practical Implications: The results of our research suggest that image processing techniques can significantly contribute to early and accurate dengue diagnosis. This can lead to timely treatment and improved disease management, particularly in regions where dengue is endemic.

V. CONCLUSION AND FUTURE WORK

In conclusion, our study highlights the potential of image processing techniques for dengue detection through the analysis of blood samples. The high accuracy, sensitivity, and specificity of our classifier indicate its efficacy as a valuable tool in dengue diagnosis. These results hold promise for the development of automated, rapid, and accurate diagnostic systems for the early detection of dengue fever, ultimately contributing to better public health outcomes.

Future research in this domain may focus on expanding the dataset, incorporating additional image analysis techniques, and exploring the integration of this technology into real- world clinical settings.

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