# Exploring Thalassemia: A Computer Vision Framework for Automated Detection Through Haemoglobin Electrophoresis Pattern

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***Abstract-*** Thalassemia is a blood disorder and requires careful diagnosis to achieve appropriate treatment. Historically, the responsibility of analysing haemoglobin electrophoresis images has been carried out by highly proficient haematologists. This existing method is time-consuming and requires specialised knowledge. The study aims to develop a solution that employs machine vision techniques Artificial Intelligence etc. and is specifically designed for haemoglobin electrophoresis investigation. The process involves a systematic approach of resizing the images, enhancing their quality, and subsequently performing precise segmentation for eventual diagnosis. The efficacy of the suggested methodology was validated through experimentation on a substantial dataset comprising *72* strips and *576* test strip images These experiments highlight the importance of the technique implemented in this paper by showcasing its efficacy. The approach employed successfully fulfils the objectives of prompt treatment and enhanced patient thalassemia identification up to *97.36%* while constituting a notable technological breakthrough in diagnosing thalassemia.

***Index Terms-*** Thalassemia diagnosis, Machine Vision, Haemoglobin electrophoresis, medical technology

## I. INTRODUCTION

Thalassemia, a collection of hereditary blood illnesses that affect the generation of haemoglobin, poses a substantial worldwide health issue. Genetic changes that impact the production of haemoglobin result in the development of many types of thalassemia illnesses. Among these, beta thalassemia is a significant subtype distinguished by abnormalities in the beta-globin genes. The spectrum of symptoms ranges from a state of carrying the disease with mild anaemia (known as beta thalassemia trait) to a severe and life-threatening illness that requires regular blood transfusions (known as beta thalassemia major). In developing countries, a significant portion of the population is enrolled in thalassemia clinics, and precise and easily accessible diagnostic techniques, particularly Hb electrophoresis, have a crucial impact. Haemoglobin, a crucial component of red blood cells, helps oxygen move from the pulmonary system to body tissues. The adult HbA molecule has two alpha and two beta chains. In healthy individuals, *HbA2* constitutes less than *3.5%* of the total haemoglobin. Haemoglobin *A2* consists of two alpha chains and two delta chains. Genetic anomalies in the beta-globin genes are responsible for decreased synthesis or complete absence of adult haemoglobin. Beta thalassemia presents with a spectrum of symptoms, ranging from mild subclinical anaemia (known as beta thalassemia trait) to severe and life-threatening anaemia (known as beta thalassemia major). The severity of the symptoms and the requirement for frequent blood transfusions depend on the specific kind and severity of the genetic abnormalities. Previous research has investigated the commission of convolutional neural networks (CNN) for patient diagnosis. Some studies have utilized the measurement of blood distance as a foundation for their models, while a few have focused on diagnosing thalassemia by lane extraction. In *2018,* studies indicated that between 8 to 9k persons were enrolled in various thalassemia facilities in Pakistan [1], Children born to carriers of beta thalassemia trait have a 25% risk, hence screening for silent carriers is crucial. This risk is linked to severe transfusion-dependent thalassemia. Thus, proactive screening is necessary to identify carriers and manage genetic risk to prevent the severe form in future generations [2]. Clinicians utilize Hb Electrophoresis for screening and assessment and assessment of thalassemia for several decades. Even though PCR analysis and high-performance liquid chromatography (HPLC) could be employed to diagnose thalassemia in terms of cost-effectiveness, hematoxylophoresis is one of the most accessible techniques. Currently, an existing technique for routine clinical diagnosis in underdeveloped countries is Hb electrophoresis, due to the severity and severe impact of thalassemia on human life, accurate and efficient thalassemia diagnosis solutions are required. It requires the involvement of both medical experts and researchers to experiment and develop an automated solution for the identification of Thalassemia patients. The Hb electrophoresis test method is straightforward however it requires a few steps. In short, the process of lysing red blood cells releases the haemoglobin into a solution. The electrophoresis process is then carried out by applying this lysate to an appropriate electrophoresis medium (such as a cellulose acetate strip). As shown in Figure 1, Hb types travel varying lengths because of differences in ionic charge. To bring attention to the bands, this strip is subsequently dipped into a Ponceau staining solution. Images from haemoglobin electrophoresis tests show blood samples from up to eight patients on a single cellulose sheet. The most prevalent human haemoglobin tetramer, haemoglobin A *(HbA)*, sometimes referred to as adult haemoglobin or haemoglobin A1, makes up more than *97%* of the haemoglobin

found in red blood cells. The oxygen-binding protein haemoglobin, which is present in erythrocytes, is responsible for carrying oxygen from the lungs to the tissues. *HbA2*, which is made up of two a and two d chains, makes up only *2.5%* of the total haemoglobin in healthy adults and is a tiny part of the haemoglobin found in normal adult red blood cells. In patients with thalassemia, content is more than *3.5%*. Furthermore, during fetal life, HbF is the main type of haemoglobin in red blood cells. After birth, adult haemoglobin *(HbA) (97%)* mostly replaces *HbF*, which gradually declines to less than *1%* [3].

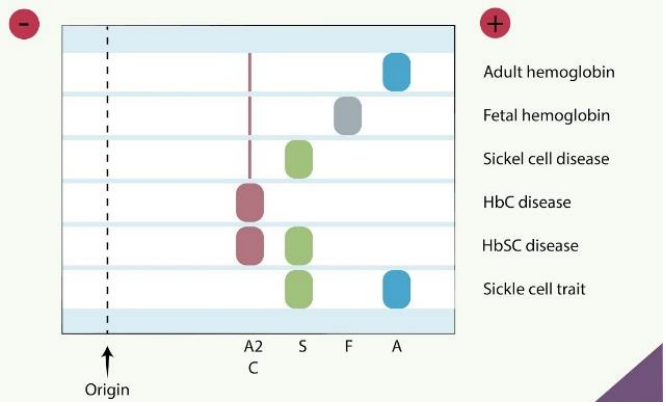


Figure 1: Drifting of Hb and Predicted Diseases [4]

The suggested methodology for automated diagnosis of Hb Electrophoresis comprises five sequential steps: image resizing, deployment of image enhancing techniques, variable-width sectioning, analysis of average pixel values, section categorization, and visualization. The initial stage is adjusting the size of gel pictures to a consistent dimension of *301 x 359* pixels, guaranteeing uniformity and employing effective preprocessing techniques. The second stage entails applying contrast stretching to enhance the distinction between the bright and dark regions of the gel image. The third stage involves enhancing the red hue, so accentuating significant regions of interest within the gel image. Variable-width sectioning is the fourth step of Hb Electrophoresis when the gel image is divided into accurate percentages along both the *x* and *y* sides to effectively handle its complicated structure. The fifth stage involves the categorization and visualization of sections, where sections are organized based on the *x-axis* and the findings are presented visually.

## II. LITERATURE REVIEW

The field of computer vision, picture processing, and pattern recognition has advanced significantly in recent decades. Medical imaging has gained prominence in recent years for its critical role in healthcare. Researchers have extensively documented the growth and healthcare applications of medical imaging through basic research and statistics.[5] The research showed encouraging results, however, dataset biases and the hunt for better diagnostic methods were limited. The atypical morphology of red blood cells (RBCs) in Thalassemia has detrimental consequences, impacting the growth and maturation of babies, and in certain instances, leading to early mortality soon after delivery. Thalassemia screening involves doing thorough tests such as Complete Blood Count (CBC) and haemoglobin electrophoresis. The CBC test is specifically deployed to identify the shape of red blood cells (RBCs). This literature review examines approaches for determining the morphology of Thalassemia blood cells, with a focus on the application of the active contour technique. The active contour approach, as evidenced by research employing 16 normal and pathological blood cell images, demonstrates a noteworthy accuracy of 90% in distinguishing Thalassemia blood cells from abnormal cell images. This literature emphasizes the significance of accurate morphological analysis in detecting Thalassemia. This research supports the listed initiatives by proposing a novel approach to diagnose Thalassemia from electrophoresis images [6]. Khan et al. [7] suggested an automated thalassemia detection method employing Hb electrophoresis strips. Commissioning electrophoresis images, their investigation reached a consensus on quality. Applying deep convolutional neural networks (CNNs) for image segmentation and binary classification, *InceptionV3* achieved *95.8%* accuracy. *MobileNetV2*, despite its shallow architecture, performed similarly with low latency. The research showed encouraging results, however, dataset biases and the hunt for better diagnostic methods were limited. In [8] Abeykoon at el. applied a 4 steps method to automate the analysing process of DNA and RNA samples which starts with enhancing the given images and then selecting lanes and bands. Seree et al. [9] generated GP-based classifiers employing a multilayer perceptron and two blood samples from an automated blood sample analyser. This study examines the issue of thalassemia categorization by utilizing blood data obtained from an automated blood cell analyser. The blood samples were categorized into *10 and 15* groups, with the second study specifically focusing on those who had iron deficiency. The selected classifiers included a multilayer perceptron and a decision tree created by genetic programming. The classification accuracy exhibited a negative correlation with the number of classes. In both cases, the multilayer perceptron with two hidden layers demonstrated superior performance compared to the decision tree. The performance of the GP-based decision tree is similar to that of the multilayer perceptron with a single hidden layer. In the first case study, *13* input features were utilized to achieve a classification accuracy of *90%*, whereas the second study achieved an accuracy of *82%* with *15* input features. Bajla et al. [10] proposed a *2D* manual image processing gel analysis method in which users can apply various window filters and analysis on gel images via Gel Master software. Helena et al. [11] proposed a technique of quality introducing lane extraction and median distortion to clarify the images. For the preprocessing of images, Devi et al. [12] employed OpenCV-Python to explore image geometric changes. Operand set dimensionality distinguishes planar and spatial transformations. The research also examines classifications based on these changes in features. Isometries preserve angles and distances, while displacements maintain distances and orientations.

## III. METHODOLOGY

The methodology follows a sequential procedure as shown in Figure 2, commencing with the loading and preprocessing of the image. Subsequently, it improves the image quality, identifies important areas, and visually represents potential regions of interest for thalassemia diagnosis through computer vision algorithms.

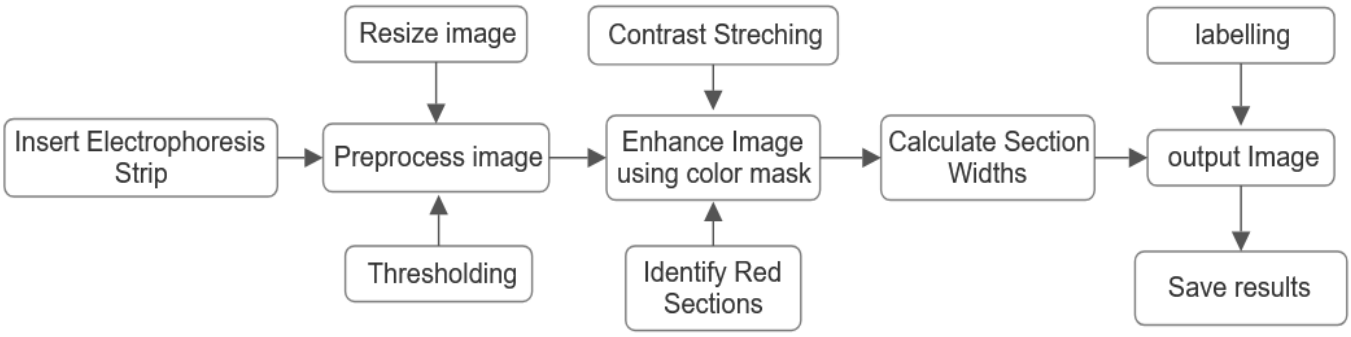


Figure 2: Block Diagram

The first stage involves loading the original electrophoresis strip image, which is a vital initial step to begin the analytical process. After the image is loaded, a sequence of preprocessing steps is carried out to standardize it, guaranteeing uniform dimensions for subsequent analyses. The image is resized to a specific dimension of *301x359* pixels, aligning it with the parameters necessary for the following stages of the methodology. To acquire these images research at Lady Reading Hospital Peshawar was a crucial endeavour in gaining a comprehensive understanding of the electrophoresis process, the intricate dynamics of haemoglobin drifts, and the diagnostic procedure. While immersed in the clinical environment, the idea was to actively engage in the electrophoresis process, gaining valuable insights into the intricacies and challenges of the diagnostic process. During the visit substantial dataset was acquired, comprising more than *70* electrophoresis strips. Each strip had a variety of data, including over *500* different samples. The focal point of this research lies in this diverse dataset, which provides a wide and diversified foundation for the development and assessment of automated diagnostic approaches. Their expertise was requested to manually discern a subset of the samples from the dataset. This manual diagnosis serves as a benchmark to assess the accuracy and efficiency of the automated system, ensuring that the results align with expert evaluations and enhancing the uniformity of the diagnostic approach. Moreover, the practical experience gained at Lady Reading Hospital facilitated a collaborative exchange of knowledge and insights with medical experts, while also enhancing the acquired dataset. This relationship exemplifies the interdisciplinary character of research, as it combines clinical expertise with technology breakthroughs to advance the field of Hb Electrophoresis diagnosis. In the next step, to identify red pixels within the image, a mask is created to isolate the essential features for diagnosing thalassemia.

$$M\,(x,y) = \int_{L(x,y)}^{U(x,y)} I(x,y)dx \qquad \text{(i)}$$

Equation (i) implies that, for every pixel, the binary mask is derived by integrating the image intensity values within the defined colour range. The integral bounds, *L (x, y) to U (x, y)*, define the range of colours that determine whether the pixel is included in the region of interest. This strategic step lays the foundation for focusing on specific characteristics that are indicative of the condition. Afterwards, the image is converted to grayscale, a process that simplifies its representation and readies it for the following stages of processing. The production of an improved image signifies a crucial point in the approach. Through the process of isolating red regions with the pre-existing mask, this enhancement step intensifies the visibility of characteristics that are relevant to the diagnosis of thalassemia. Simultaneously, a function computes variable section widths for both the *x and y* axes, offering flexibility through predetermined percentages. This adaptability is crucial in accommodating various image structures encountered in thalassemia diagnostic scenarios. To enhance the visibility of features, contrast stretching is utilized on the grayscale image[13]. This technique expands the spectrum of pixel intensities, thereby enhancing the distinction of image characteristics. The crucial step in the process is the detection of red sections, where a threshold, determined by the average pixel value of the enhanced image as shown in equation (ii), serves as a differentiating factor.

$$\mu = \sum_{i=1}^{n} a_i \qquad (ii)$$

Where $\mu$ = mean, a = pixel, i = number of pixels. Sections exhibiting pixel values below this threshold in a predefined area are deemed potential indicators of thalassemia-related characteristics. Bounding boxes are visually drawn around the identified red sections, and labels are assigned based on the column index. The addition of labels, such as the term "major," to specific sections enhances the visual representation, facilitating the identification of areas that may be of significance in diagnosing thalassemia. A predeveloped library is used to display the original image, enhanced grayscale image, and final output, which includes bounding boxes and labels, to facilitate additional analysis and documentation. This visual examination offers researchers and diagnosticians a concrete depiction of

possible areas of interest. The final step of the methodology is to save the enhanced image, which includes drawn bounding boxes and labels, as a JPEG file. The tangible output functions as a documented reference, containing the findings and visual representations obtained from the computer vision techniques deployed in the thalassemia diagnostic process. Essentially, the methodology encompasses a thorough process starting from loading and preprocessing images, then enhancing features, identifying them, and finally representing them visually. This process results in a tangible output that could be further analysed and referenced.

## IV. EXPERIMENTATION

The implementation process was performed by introducing a simulation environment and other associated libraries with various libraries. The Integrated Development Environment (IDE) utilized in the process is Microsoft Visual Studio Code. This IDE version was chosen due to its compatibility with Windows and the availability of documentation and up-to-date libraries that were required in the process. The process of diagnosing Thalassemia starts with importing the necessary dependencies. Furthermore, the option is provided to set a specific dimension of the image which is currently set to *301x359* pixels. In the subsequent critical stage, a binary mask is generated to detect red pixels falling within a specified colour range. The following steps aim to improve the image and isolate specific areas of interest. A contrast-stretching technique is utilized to emphasize particular characteristics, thereby facilitating the generation of an improved grayscale image. The experimental configuration involves establishing a threshold by utilizing the mean pixel value to differentiate areas that indicate the presence of thalassemia. In the next step predefined libraries were utilized, and the mean value of all the pixels was measured to define a threshold for the detection of the presence of blood on the strip. As previously discussed in section I blood drifts up to different positions on the strip marking various diseases. So, the image captured in the first step was divided into sections by imaginary lines depending on the drift of blood as shown in Figure 3.

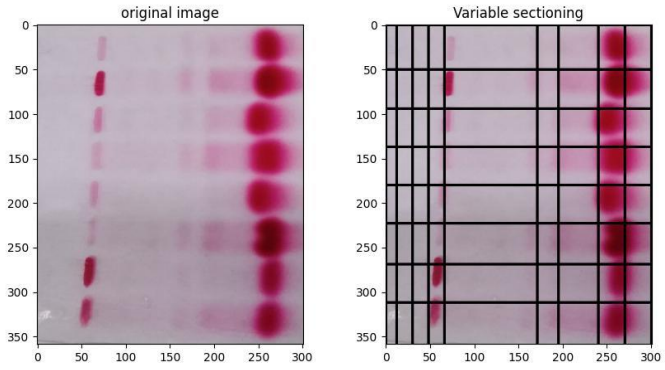


Figure 3: Variable sectioning

The experimentation progresses through a careful and thorough examination of various sections within the image. The algorithm sequentially examines predetermined section dimensions in both the horizontal and vertical directions. It identifies sections that contain predominantly red pixels by comparing the average pixel values to a specified threshold. The identified sections, which are sometimes designated as *major*, are visually indicated by bounding boxes.

## V. RESULTS AND DISCUSSIONS

During the testing phase, technicians and clinicians labelled certain images which were analysed by the program. The images were utilized to adjust all values, including the threshold value for masking the red colour and the average value of pixels after stretching. Subsequently, all the remaining images were labelled.

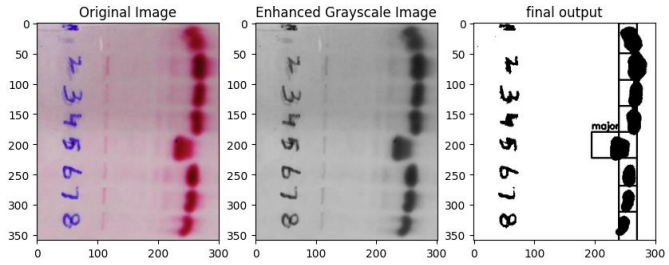


Figure 4: Labelled Images

Figure 4 depicts the diagnostic process on a single strip with eight distinct samples. Utilizing the adjusted values obtained during the testing phase, the prediction was made that sample number five corresponds to thalassemia major. In the final step iterative method was applied, to label all the images, and the corresponding answers were recorded in an Excel sheet to assess the accuracy and F1 Score.

As mentioned in Table 1, *108* strips were obtained from which 800 distinct samples were collected. Among these samples, *40* had already been labelled by doctors, while the remaining *760* were unlabelled. Subsequently, the *760* samples underwent the pipeline process to verify their accuracy.

Table 1: Data Set parameters

| **Parameters** | |
|---|---|
| No of Strips | 108 |
| No of Samples | 800 |
| Labelled Samples | 40 |
| Non-labelled Samples | 760 |
| Accuracy | 97.36 ± 0.2% |
| F1 Score | 0.98 |

Overall, employing the threshold and lane extraction technique, this model achieved a remarkable accuracy of 97.36% in distinguishing between thalassemia and non-thalassemia samples. In addition, it is worth mentioning that out of 480 non-thalassemia samples, only 12 strip images were classified incorrectly, and out of 240 thalassemia major samples, only 7 were misclassified.

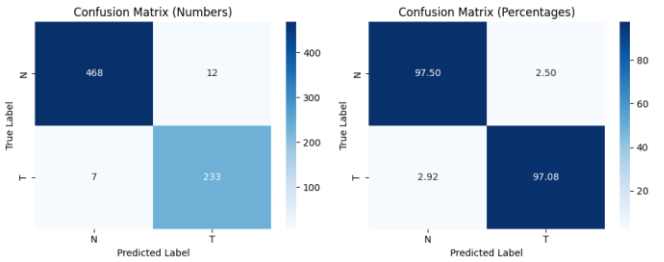


Figure 5: Confusion Matrix

In comparison with previous work, this paper achieved a remarkable result as shown in Table 2.

Table 2: Comparison with previous findings

| Reference | Technique | Accuracy |
|---|---|---|
| [6] | Active Contour | 90 % |
| [14] | Nayve Base and Decision Tree | 91.74 % |
| [7] | Inception V3 | 95.8 % |
| **Proposed Technique** | Threshold and lane Extraction | 97.3 % |

Overall, the findings indicate that the applied methodology shows potential as a reliable and effective tool for diagnosing Thalassemia in blood samples, which could lead to enhanced medical diagnostics and patient care. The developed method offers a cost-effective and accessible early-stage Thalassemia diagnosis method for developing nations with limited resources. The methodology's simplicity and utilization of common technologies make it suitable for resource-constrained healthcare settings.

## VI. CONCLUSION

The diagnostic method employed to identify Thalassemia in blood samples, which involves the utilization of both thresholding and lane extraction techniques, has shown remarkable efficacy. The methodology, implemented in this research demonstrates a remarkable accuracy of *97.36%* and an F1 score of *0.98*. Segmenting images into sections based on blood flow and conducting a meticulous analysis of pixel values was found to be successful in identifying sections affected by thalassemia-major. The model's proficiency in accurately categorizing samples was apparent in the low rates of misclassification for both thalassemia and non-thalassemia samples. The developed method demonstrates superior performance compared to previous techniques, surpassing methods such as Active Contour, Naive Base, Decision Tree, and even advanced models like *Inception V3*. This demonstrates the effectiveness of the thresholding and lane extraction method in Thalassemia detection. Future research is to develop a comprehensive portable hardware setup based on a smart portable system.

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