

A Review on Computer Vision based Classification of Sickle Cell Anemia in Human RBC

Diksha R. Tembhurne and Dr. R. M. Deshmukh

Department of Electronics & Telecommunication Engineering

Dr. Rajendra Gode Institute of Technology & Research Amravati, Maharashtra, India

dikshagrim333@gmail.com

Abstract: Anemia is a disease which is caused by the deficiency of red blood cells. The shape of red blood cell changes to sickle or crescent shape in sickle cell anemia disease. Sickle Cell Disease is a blood disorder which results from the abnormalities of red blood cells and shortens the life expectancy to 42 and 48 years for males and females respectively. It also causes pain, jaundice, shortness of breath, etc. Sickle Cell Disease is identified by the presence of sickle cells and other abnormal cells like ovalocyte, echinocytes are detected and classified in different classes it helps to find out reason of abnormalities. Given a two-dimensional image, a computer vision system must recognize the present objects and their characteristics such as shapes, textures, colors, sizes, spatial arrangement, among other things, to provide a description as complete as possible of the image. This paper presents computer vision based classification of sickle cell disease. In their an artificial neural network(ANN) is a computational model that uses a network of a function to understand and translate a data of one form into a desired output. In this paper we have summarized for we reviewed the various techniques to get the sickle cell identification or sickle cell classification. The artificial neural network technique is used to train and classify the microscopic images into sickle cell.

Keywords: Red blood cell, sickle cell anemia Computer Vision, Classification, artificial neural network.

I. INTRODUCTION

RED BLOOD CELL (RBC) has a significant role in the gaseous interchange of external environment and the living tissue. Haemoglobin is the protein in RBC that works as a carrier of oxygen. Usually haemoglobin A dominates throughout the life after six weeks of age. It contains two alphas and two beta chains. Sickle cell disease (SCD) is found when a person receives two abnormal copies of haemoglobin genes, one from each parent. That means a healthy haemoglobin (HbA) is replaced by sickle haemoglobin (HbS). We say a person has sickle cell traits if he/she contains single abnormal genes, which means HbS replaces half of the HbA. Blood is a vital fluid in which RBC is the prime component. Red blood cell's shape is biconcave. The red blood cell lives usually 120 days. Normally red blood cells are round and move flexibly in vessels of blood. Because of SCA, the RBC's shape becomes like C shape. Sickle cell anemia is a blood disease which reshapes the hemoglobin in red blood cells. These cells are inflexible and sticky. The sickle cells live 10 to 20 days after that they fall apart. These distorted and irregular shaped cells block or slow down the blood flow in vessels of blood and deliver less oxygen to the different parts of the body. The normal person has hemoglobin A, but sickle cells person carry hemoglobin S due to abnormal change in gene. In low oxygen condition, formation of non-covalent hemoglobin due to the absence of polar amino acid then convert red blood cell into sickle cells As shown in fig.1 these type the normal red blood cell and sickle red blood cell.

For diagnosis of some specific diseases like malaria, leukemia and different types of anemia, normal blood cells detection and counting are the most important steps. The counting of RBCs manually in microscopic images is an enormously tiresome and also time consuming which gives incorrect results. To perform faster and more accurately, automatic analysis of microscopic blood images is very important. These problems are solved by applying different quantitative digital image analysis on microscopic blood images for classification of normal cell and abnormal cell as shown in fig.2.

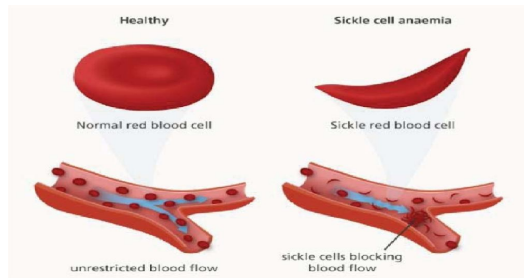


Figure 1: Normal Red Blood Cells and Sickle Red Blood Cells

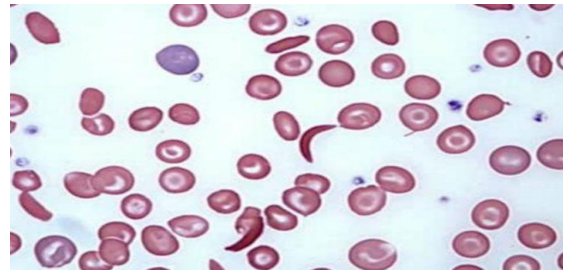


Figure 2: Microscopic image of blood sample

In this research, we used an advanced neural network algorithm for medical data classification based on machine learning for the purpose of utilizing intelligent techniques for analysing the huge amount of Sickle Cell Disease (SCD) datasets. It is important to understand that computer vision accomplishes much more than other fields such as image processing or machine vision, with which it shares several characteristics. Machine learning (ML), an area of computer science, offers us data-driven prediction in various applications, including image analysis, which can aid typical steps of image analysis (i.e., preprocessing, segmentation, feature extraction, and classification). Algorithms based on deep learning, an emerging subfield of ML, often show more accurate performance compared with traditional approaches to computer vision-based tasks, including red blood cells identification, such as sickle cell. Moreover, ML-based algorithms often provide discriminative features associated with outputs extracted through their training process, which may enable us to dissect complex traits and determine visual signatures related to traits in sickle cells. Neural Network approaches is considerably used within classification techniques for medical fields. This is attributed to their features of parallel processing tools, self-organization, self-learning methods, and non-linearity. Then, we also address recent challenges in computer vision-based microscopic image analysis and the typical image analysis process (e.g., segmentation, feature extraction, and classification), as well as its applications

II. LITERATURE REVIEW

This section presents a deep of works related to the different methods .Sickle cell classification various methods and performance analysis of various method we describe of this review paper is useful to attract researchers working in this area follows as, Intisar Shadeed Al-Mejibli et.al.[1] proposed an integrated system model, which offers the services of testing, following-up and monitoring patients with (SCD). The proposed system uses support vector machine SVM, which is supervised machine learning approach to analyze the collected data of a specific patient and takes the appropriate action such as send alert message to the healthcare staff. To perform the classification process, four methods are applied with SVM algorithm, which are Sequential Minimal Optimization SMO, Rules JRIP, Tree Decision Stump and Naive Bays for comparative analysis. In this paper, many experiments were implemented based on the four machine learning algorithms to determine patients of SCD from normal patients. The results were promising as they show 99% classifications were accurate when using SMO algorithm.

Ahmad Sabry Mohamad et.al.[2] presented image processing technique has been used to produce automated detection of Sickle Cell Anemia. A Laplacian of Gaussian (LoG) edge detection algorithm computed to detect sickle cells diseases at the early stage in diagnosing patient. A MATLAB software able to demonstrate the abnormalities of the human Red Blood Cell (RBC) in the single shapes and quantities of sickle cells present in each dataset. A data samples of sickle cells from government Ampang Hospital has contributed this study to validate the results.

Sagar Yeruva et.al.[3] proposed approach tackles the limitations of manual research by implemented a powerful and efficient MLP (Multi-Layer Perceptron) classification algorithm that distinguishes Sickle Cell Anemia (SCA) into three classes: Normal (N), Sickle Cells(S) and Thalassemia (T) in red blood cells. This paper also presents the precision degree of the MLP classifier algorithm with other popular mining and machine learning algorithms on the dataset obtained from the Thalassemia and Sickle Cell Society (TSCS) located in Rajendra Nagar, Hyderabad, Telangana, India.

Manuel Gonzalez-Hidalgo et.al.[4] implemented code library, the confusion matrices with the raw data, and we used the public erythrocytesIDB dataset for validation. We also defined how to select the most important features for classification to decrease the complexity and the training time, and for interpretability purpose in opaque models. Finally, comparing the

best performing classification methods with the state-of-the-art, we obtained better results even with interpretable model classifiers.

Mohammed AbdulaheemFadhel et.al.[5] presented, RBC has circular shape in front view and biconcave shape in side view. RBCs take the sickle shape with person infected with cell anemia. Based on such different shapes, the work objective is to count the numbers of normal and abnormal RBC cells using two image processing techniques; circular Hough transform and watershed segmentation. Such counting is practically important in assessing the level of anemia disease danger. The processing Code of this technique is done on MATLAB 2015a.

Hamid Falah Dheyab et.al.[6] implemented a various kinds of machine learning models to classify the dataset of sickle cell patients. Artificial intelligence techniques have served to strengthen the medical field in solving its problems and providing rapid technical methods with high efficiency instead of traditional methods that can be subject to many problems in diagnosis and to determine the appropriate treatment. The main objective of this study to obtain a highly qualified classifier capable of determining the suitable dose of the SCD patients from 9 classes. Through examining the techniques used in our experiment based on performance evaluation metrics and making sure that each model performs. We applied numerous models of machine learning classifiers to examine the sickle cell dataset based on the performance evaluation metrics. The outcomes obtained from all classifiers, show that the Naïve Bayes Classifier obtained poor results compared to other classifiers. While Levenberg-Marquardt Neural Network during the training phase obtained the highest performance and accuracy of 0.935222, AUC 0.963889. The test phase obtained an accuracy of 0.846444, AUC 0.871889.

Russell Keenan et.al.[7] ANN showed that the proposed network produces significant improvements using the different evaluation methods. In our experiments, The MLP algorithm produced the best result in terms of the lowest error rates compare with other techniques. The Mean Square Error, Root Mean Square Error, Mean Absolute Error, and Mean Absolute Percentage Error achieved 17887.55, 133.74, 90.20 and 0.1345, respectively.

Chayashree Patgiri et.al.[8] introduced a detection technique to detect normal and abnormal red blood cells have been detected using Niblack's thresholding technique from microscopic blood images of sickle cell anemic patient. The process involves preprocessing of microscopic blood smear and segmenting the preprocessed image using Niblack's thresholding algorithm. Then using geometrical features of blood cells a metric (form factor) is calculated to classify normal red blood cells and abnormal cells.

Yaima Paz-Soto et.al.[9] artificial neural networks-based classifiers, trained with the characteristics obtained from integral geometry-based functions, to classify erythrocytes into normal, sickle, and other deformations classes. Our proposal achieves accuracy of 98.40%. This result is superior to those of previous studies concerning the classes of greatest interest. Also, our approach is computationally more efficient than previous works, making it suitable for supporting medical follow-up diagnosis of sickle cell disease.

Suvinol Sangkatumvong et.al.[10] demonstrate that cardiovascular autonomic response to hypoxia is substantially more sensitive in SCA than in normal controls. We also developed a model to compensate for the confounding effects of respiration on the HRV spectral indices by using the corresponding respiration signal to compensate for the respiratory correlated part of the HRV. This technique improved the resolution with which the effect of hypoxia on changes in HRV could be measured.

Bheem Sen et.al.[11] In this research Idb1 erythrocytes microscopic photographs of blood smears obtained from patients infected with sickle cell, and the dataset is divided into test and train for each classis which are circular, elongated and others. For the classification task five pre trained model are used which are VGG16, VVG19, ResNet50, ResNet101 and Inception V3. Proposed models' efficiency is shown by the results of the work, which offers better accuracy of the classification.

Vishwas Sharma et.al.[12] The proposed method involves acquisition of the thin blood smear microscopic images, pre-processing by applying median filter, segmentation of overlapping erythrocytes using marker-controlled watershed segmentation, applying morphological operations to enhance the image, extraction of features such as metric value, aspect ratio, radial signature and its variance, and finally training the K-nearest neighbor classifier to test the images. The algorithm processes the infected cells increasing the speed, effectiveness and efficiency of training and testing. The K-Nearest Neighbour classifier is trained with 100 images to detect three different types of distorted erythrocytes namely sickle cells, dacrocytes and elliptocytes responsible for sickle cell anaemia and thalassemia with an accuracy of 80.6% and sensitivity of 87.6%.

Dr. Bikesh Kumar Singh et.al.[13] In this study Long short-term memory (LSTM) and Extreme learning machines (ELM) are used for the classification of dosage of HU in case of SCD patients. Also, the performance of two methods has evaluated and compared. The study is conducted on pathological attributes of SCD patients consist of 12 pathological features for predication and single target variable i.e. HU dosage in milligrams discretized into 3 bins: low dose, moderate dose, and high dose. The dataset comprises 1128 sample points. The experimental results show that LSTM performs better than ELM in terms of class wise and overall accuracy for the given dataset.

Dimitrios P. Papageorgiou et.al.[14] The proposed framework can successfully classify sickle shape RBCs in an automated manner with high accuracy, and we also provide the corresponding shape factor analysis, which can be used synergistically with the CNN analysis for more robust predictions. Moreover, the trained deep CNN exhibits good performance even for a deoxygenated dataset and distinguishes the subtle differences in texture alteration inside the oxygenated and deoxygenated RBCs.

Mo Zhang et.al.[15] Results show that dU-Net can achieve highest accuracy for both binary segmentation and multiclass semantic segmentation tasks, comparing with both unsupervised and state-of-the-art deep learning based supervised segmentation methods. Through detailed investigation of the segmentation results, we further conclude that the performance improvement is mainly caused by the deformable convolution layer, which has better ability to separate the touching cells, discriminate the background noise and predict correct cell shapes without any shape priors.

III. PROPOSED METHODOLOGY

Methodology of proposed work shows the following steps:

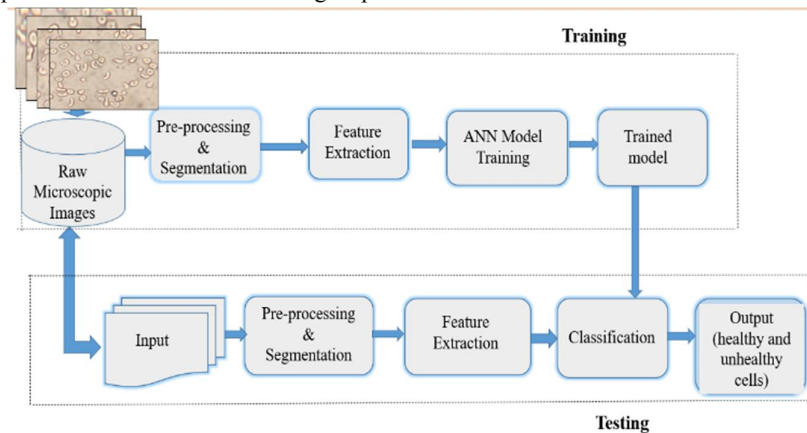


Figure 2: Block diagram of Methodology

3.1 Raw Microscopic Images

The data set is collected from standard benchmark dataset, erythrocytesIDB (<http://erythrocytesidb.uib.es/>). The erythrocytesIDB contains images of peripheral blood smears samples taken from patients with Sickle Cell Disease in Special Hematology Department of the General Hospital ‘Dr. Juan Bruno Zayas Alfonso’ from Santiago de Cuba.

3.2 Pre-processing and Segmentation

In the image pre-processing step, we pre-processed our images to enhance the image quality by erasing small pieces of noise for the exact detection of the wanted areas of skin. We get an image as an input and resize the image, then we use median filter to cast off the noise and makes the image noise free. The middle filtering system improves the strength value of the image by exchanging the strength value of the nearby pixel that may have sounds. Then we improved the contrast of the image for finding the better lesion part of the image. The microscopic image is converted to gray image, median filter is used to eject the noise from the Gray scale image. Final step in data pre-processing is enhancement of the image in this the small objects are removed and sharpening of the image is done to get a better-quality image. Otsu thresholding technique is used to separate the three class, this method is one of the best thresholding methods is to detach object from the image. Otsu select the threshold that reduce the interclass variance of the threshold black and white pixels. Further, Morphological

operation is to reject the undesirable objects from the image. In this the holes of the object are covered; borders of the image are cleared and small objects are eliminated from the image.

3.3 Feature Extraction

Feature extraction is the preliminary step in image classification. Sometimes the input data size is too large, which is tremendously hard to procedure in its raw form. For solving this, the input data can be transformed into a set of features. Feature extraction is the method by which unique features of skin lesion images are extracted. This method reduces the complexity in classification problems. The purpose of feature extraction is to reduce the original data set by measuring certain properties, or features, that distinguish one input pattern from another. We will use the two groups of features: GLCM (Texture features), Shape or geometrical features.

3.4 ANN Model Training and Classification

For experimental evaluation, we used total 'n' microscopic images. After that we have to split the dataset into 70-30% ratio for training and testing set of images. Classifier is used to classify healthy or unhealthy cell images from input microscopic images. To classify feature data into a given number of classes, we have used machine learning technique. In this project, Artificial Neural Network classifier, are used to train the microscopic images. Classifier takes set of images, create trained model and predicts for each input image belongs to which of the two categories of unhealthy or healthy cell classes.

IV. CONCLUSION

Based on survey, different methods of detecting sickle cells in blood smear using machine learning techniques with different state-of-art network models were studied. The original images are pre-processed and refined to remove unwanted objects using computer vision based medical image processing techniques to reduce complexity and improve the training process. Detection of sickle cells from RBC within a shortest time correctly is the most challenging task. In this paper, an automated system presents which can be used for detection and classification of sickle cell anemia. It is hoped that proposed system would prove helpful in medical sectors and save lives of people with high accuracy and high sensitivity.

V. FUTURE WORK

In future, other cells like RBC, platelets and WBC count can also be automatically detected efficiently, making the job of pathologist easy and more number of patients can be benefitted within a short span of time by early diagnosis of disease. Sickle cells can be treated with gene editing method called CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats). It has been implemented successfully for a patient. In future Deep learning can be used in genomics called Deep Crispr to detect other RBC abnormalities in blood sample. It needs huge amount of data to train so that efficiency can be improved.

REFERENCES

- [1]. Dhafar Hamed Abd, Intisar Shadeed Al-Mejibli ., "Monitoring System for Sickle Cell Disease Patients by Using Supervised Machine Learning", 2017 2nd -AL-Sadiq International Science Conference on Multidisciplinary in IT and Communication Science and Technologies -2nd- AIC – MITC – Baghdad – IRAQ.
- [2]. Ahmad Sabry Mohamad Nur Syahirah Abdul Halim , Muhammad Noor Nordin , Roszymah Hamzah ,Jameela Sathar " Automated Detection of Human RBC in Diagnosing Sickle Cell Anemia with Laplacian of Gaussian Filter. " 2018 IEEE Conference on Systems, Process and Control (ICSPC 2018), 14–15 December 2018, Melaka, Malaysia.
- [3]. Sagar Yeruva M. Sharada Varalakshmi , B. Pavan Gowtham , Y. Hari Chandana , PESN. Krishna Prasad. " Identification of Sickle Cell Anemia Using Deep Neural Networks." Available online at www.ijournalse.org Emerging Science Journal (ISSN:2610-9182) Vol. 5, No. 2, April, 2021.
- [4]. Manuel Gonzalez-Hidalgo, Natasa Petrovi , Gabriel Moya-Alcover, Antoni Jaume-i-Capo. "Sickle-cell disease diagnosis support selecting the most appropriate machine learning method: Towards a general and interpretable approach for cell morphology analysis from microscopy images." SCOPIA research group. University of the

- Balearic Islands. Dpt. of Mathematics and Computer Science. Crta. Valldemossa, km 7.5, E-07122 Palma, Spain
rXiv:2010.04511v1 [cs.LG] 9 Oct 2020.
- [5]. Mohammed AbdulraheemFadhel, AmjadJalilHumaidi , Sameer RazzaqOleiwi "Image Processing-Based Diagnosis of Sickle cell Anemia in Erythrocytes. " Annual Conference on New Trends in Information & Communications Technology Applications-(NTICT'2017) 7 - 9 March 2017.
 - [6]. Hamid Falah Dheyab, Osman Nuri UCAN , Mohammed Khalaf "Implementation a Various Types of Machine Learning Approaches for Biomedical Datasets based on Sickle Cell Disorder". Authorized licensed use limited to: University of Prince Edward Island. Downloaded on June 08,2021 at 11:00:36 UTC from IEEE Xplore. 978-1-7281-9090-7/20/\$31.00 ©2020 IEEE.
 - [7]. Russell Keenan, Mohammed Khalaf, Abir Jaafar Hussain1, Dhiya Al-Jumeily, Robert Keight1, Paul Fergus, and Ibrahim Olatunji Idowu "Applied Difference Techniques of Machine learning Algorithm and Web-based Management System for Sickle Cell Disease." 2015 International Conference on Developments of E-Systems Engineering 978-1-5090-1861-1/15 \$31.00 © 2015 IEEE DOI 10.1109/DeSE.2015.18.
 - [8]. Chayashree Patgiri, Amrita Ganguly .Department of Electrical Engineering, Assam Engineering College, Guwahati 13, India chayashreepatgiri21@gmail.com aganguly.ele@aec.ac.in . "Red Blood Cell and Sickle Cell Detection from Microscopic Blood Images of Sickle Cell Anemic Patient." 978-1-5386-9279-0/19/\$31.00 c 2019 IEEE.
 - [9]. Yaima Paz-Soto, Silena Herold-Garcia, Leandro A. F. Fernandes and Saul D'iaz-Matos Engineering and Thecnical Science Faculty Universidad de Guantanamo, Gu antanamo, Cuba Email: ysoto@cug.co.cu Universidad de Oriente, Santiago de Cuba, Cuba Email: silena@uo.edu.cu, saul.diaz@estudiantes.uo.edu.cu Universidade Federal Fluminense, Niteroi, Brazil Email: laffernades@ic.uff.br. " Automatic Classification of Erythrocytes Using Artificial Neural Networks and Integral Geometry-Based Functions ." Authorized licensed use limited to: UNIVERSITY OF WESTERN ONTARIO. May 27,2021 at 00:02:55 UTC from IEEE Xplore.
 - [10]. Suvimol Sangkatumvong , Michael C.K. Khoo, and Thomas D. Coates." Abnormal Cardiac Autonomic Control in Sickle Cell Disease following Transient Hypoxia". 30th Annual International IEEE EMBS Conference Vancouver, British Columbia, Canada, August 20-24, 2008.
 - [11]. Bheem Sen, Utter Pradesh, India senbheem1998@gmail.com Shubhra Dixit,Utter Pradesh, India sdixit@amity.edu Adarsh Ganesh adarshganesh130@gmail.com Anupama Bhan abhan@amity.ed. "Deep Learning based diagnosis of sickle cell anemia in human RBC ." 2021 2nd International Conference on Intelligent Engineering and Management (ICIEM).
 - [12]. Vishwas Sharma, AdhirajRathore, Garima Vyas Department of Electronics & Communication Engineering Amity University, U.P, Noida-201303 sharma.vishwas1995@gmail.com,adhirathore21@gmail.com,gvyas@amity.ed." Detection of sickle cell anaemia and thalassaemia causing abnormalities in thin smear of human blood sample using image processing ".
 - [13]. Dr. Bikesh Kumar Singh Dept. of Biomedical Engineering NIT, Raipur India bsingh.bme@nitrr.ac.in Hardik Thakkar Dept. of Biomedical Engineering NIT, Raipur Raipur, India hardikthakkar1710@gmail.com "Hydroxyurea Dosage Classification for Sickle Cell Disease Patients". Proceedings of the Sixth International Conference on Inventive Computation Technologies [ICICT 2021] IEEE Xplore Part Number: CFP21F70-ART; ISBN: 978-1-7281-8501-9.
 - [14]. Mengjia Xu,Dimitrios P. Papageorgiou, Sabia Z. Abidi, Ming Dao, Hong Zhao, George Em Karniadakis," A deep convolutional neural network for classification of red blood cells in sickle cell anemia ". PLOS Computational Biology | <https://doi.org/10.1371/journal.pcbi.1005746> October 19, 2017.
 - [15]. Mo Zhang, Student Member, IEEE, Xiang Li, Member, IEEE, Mengjia Xu, and Quanzheng Li, Member, IEEE Joint first authors, " Automated Semantic Segmentation of Red Blood Cells for Sickle Cell Disease ". University of London July 13,2020 at 00:41:54 UTC from IEEE Xplore.