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Generalized Simulation Model for the Comparative Study on Anaemia Detection

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ABSTRACT: Anaemia is a kind of haematological disorder affecting approximately one-fourth of our wold population. It can either be termed as lowering of haemoglobin in blood or be described as decreased ability of blood to carry oxygen to the entire body. The conventional method of manual counting, identification and further detection of anaemia is a tedious process and also error prone one. So many processes related to detection of anaemia using image processing methods were proposed by different scientists. Various transform methods, segmentation procedures and different counting algorithms were applied on those techniques to make the detection process an accurate one. It also leads to an efficient procedure to make detection process easier and also time consuming one. So in this paper we have two techniques for anaemia detection. The first objective of this paper is based on counting technique in which it automatically detects and count the red blood cell numbers in blood sample and finally making detection on it. The second objective is based on convolution neural network method in which it identifies which type of anaemia the specified blood sample belongs to.

KEYWORDS: Anaemia detection, Image processing, Transform methods, Segmentation, CNN.

I. Introduction

Human blood mainly consists of 3 different types of blood cells namely red blood cells, white blood cells and platelets. A person's overall health maintenance, evaluation, diagnosis and its balance is determined by making a test on blood count in specifies blood sample. That is a complete blood count checkup is carried out in each one's body to determine different blood disorders including anemia. Any variation in count from its normal value indicates that the person is having some kind of medical unbalanced issues in his body.

Red blood cells also known as erythrocytes are the main blood cell in the blood. It mainly helps in carrying and distributing oxygen to each and every cells in our body and also giving red pigment to the blood. Its shape is defined by either minute disc or round shaped. Automated detection and counting of red blood cells is one of the major step for the diagnosis of several diseases. Convection method that the hematologists do is counting each and every blood cells manually through microscope. But this procedure for the identification, counting and further detection of anemia is an error generating one and also time consuming task. So a solution to this problem was introduction of image processing techniques to count and detect RBC's to analyze the presence of anemia which is automotive, cost effective and also an efficient one.

II. RELATED WORK

In this section we will implement the proposed system as two objectives. Objective One method using the RBC counting algorithm method and connected component labelling method. Objective two method using the convolutional neural network method and finally the features extraction.

The primary objective of the paper i.e. a generalized stimulation model for anaemia detection is to be modelled since the manual location, identification and further counting of red blood cells is a tedious, time consuming and also an error prone Procedure. So here firstly based on counting algorithm method i.e., both normal RBC counting algorithm and water- shed transform to separate overlapping blood cells through the connected component labelling method. The count value obtained from the counting algorithm together with the volume of the blood taken can be used to decide whether the person is anaemic or not.



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Normal RBC count range (per cubic millimetre of blood) for humans of different age groups are given below:

New-borns: 4.8-7.2 million
Adult male: 4.6-6.0 million
Adult female: 4.2-5.0 million

We know generally the dimension of a microscopic slide is 2.5×7.5 mos. the volume comes out to be 3.75 sq.cm. Therefore, a normal person's microscopic slide can accommodate approximately 500 RBC's. So lesser then 500 RBC'S present per microscopic slide is found to an an anaemic person's one. This the basis for detection of anaemic persons based on blood counting algorithm along with the combination of watershed segmentation. The series of steps involved in detection and finally estimating the number of RBCs are input image capture, image pre-processing and enhancement, RBC segmentation, post processing and finally the counting of red blood cells. The systematic representation of objective 1 procedure is depicted in flowchart fig.1 as follows:

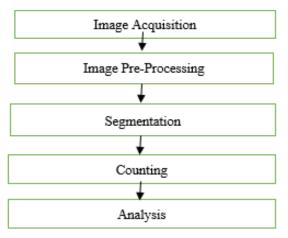


Fig. 1. Flow Chart

The input image is the microscopic view of blood smear image of the person who has to be tested for anaemia. The next step is image pre-processing and enhancement procedure. Pre-processing is done to improve the quality and contrast of the image for the later stages. Image enhancement is done to improve the brightness and hue specifications of the image and finally helps in a clear cut segmentation procedure in later stages. Segmentation is the process of separating the region of interest that we required from the background portion. Here we prefer the much more advanced water segmentation process. It finds catchment basins and watershed ridge lines in an image and considering it as a surface where light pixels are high and dark pixels are low.

The counting using Connected Component Labelling (CCL) is implemented, bwconncomp returns the connected components found in the binary image. The functions label and bwlabeln also compute connected components for specified binary images. They use significantly less memory and is s faster than the other functions. The basic steps in finding the connected components are searching for the next unlabelled pixel p and then uses a flood fill algorithm to label all the pixels in the connected component containing preheat above steps until all the pixels are labelled. Finally, the number of red blood cells present in the microscopic slide is founded.

In the Fig.2, the number of red blood cells detected is about 82 which is lesser than 500, the normal threshold value. This indicates that the given blood sample is about anaemic i.e., abnormal.



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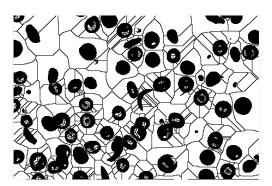


Fig. 2. Abnormal

In the Fig.3, the number of red blood cells detected is about 633 which is greater than 500, the normal threshold value. This indicates that the given blood sample is not anaemic i.e., normal.

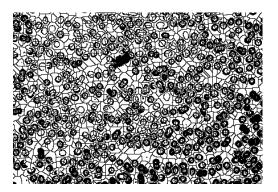


Fig. 3. Normal

III. CNN ARCHITECTURE

Here we developed an automated, high throughput RBC shape classification framework that consists of 5 classification classes. They are sickle cells, dacrocytes, elliptocytes, abnormal, and normal classes. So here we employ deep convolution neural networks to realize those classifications. Furthermore, we also identify their features namely metric value and aspect ratio., and thereby arrives at most accurate result that which type of anemia is possesed by the patient.

The images used for creating the training, testing and validation datasets are obtained from five different database sections namely sickle cells, elliptocytes, dacrocytes, abnormal and normal classes. In sickle classes we have sickle shaped cells instead of normal or biconcave RBC cells. In elliptocytes elliptical or oval shaped cells. While other type of deviated shaped cells from from normal shape is included in abnormal sections.



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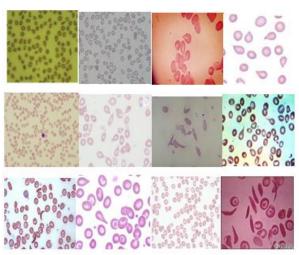


Fig. 4. Dacrocyte Dataset

IV. TRAINING AND TESTING

Firstly, here we are loading the data as an image data store object. The data store contains 40 altogether images of digit from 0 to 9. The mages are generated by applying random transformations to digit images created with different resizing features or fonts. Each image is 255 by 255 in pixel quality. Divide the data store so that each category in the training set has 8 images each and the testing images makes the rest of the images from each label. Image input layer creates an image input layer which inputs images to a network and applies data normalization.

A ReLu layer performs a threshold operation to each element of the input. It will not change the size of the inputs. Max pooling layer performs down sampling and divides the input images into rectangular pooling regions and finally compute the maximum of each region. The softmax layer applies a softmax function to the input. The classification layer computes the cross entropy loss for multi class classification problems with mutually exclusive classes that it holds. We will start the training with an initial learning rate of 0.0001 and maximum number of epochs at 20.

V. FEATURES EXTRACTION

Here we are extracting mainly 2 features namely aspect ratio and metric value. Metric value is a measure of an object's roundness. It is represented by:

$$Metric value = \frac{4*pi*area}{perimetre^2}$$

The metric value for a perfect circle is 1, reducing to 0 with decrease in the roundness of an object. As healthy RBCs are circular in shape, the metric value for a healthy RBC is equivalent to 1. Similarly, Aspect ratio RBCs is the ratio of the major axis to minor axis of the cell. The aspect ratio of a circle is 1 and as the circularity of the shape decreases the aspect ratio increases. It is given by:

Aspect ratio=
$$\frac{major\ axis}{minor\ axis}$$

Table -1 Feature Comparison Table

	Aspect ratio	Metric value
Normal RBC	1.291	0.775
Sickle cell	1.495	0.297
Elliptocyte	1.518	0.229
Dacrocyte	1.478	0.409



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VI. RESULTS AND DISCUSSION

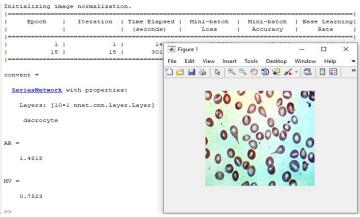


Fig. 5. CNN Result

The Findings of both normal and abnormal people's test report finded using counting algorithm method in objective 1 results that the patients sample count above the threshold limit 500 is Normal and less than the threshold limit is Anemic.Similarly Resulted output of image tested using CNN shown in fig 4. infers that the tested image belongs to dacrocyte class and the aspect ratio and metric value is found to be 1.4015 and metric value to be 0.7523. This infers that the given image specifications are belonging to dacrocyte class itself which is already given as per the table I feature comparison table.

VIII. CONCLUSION

Detection RBC counting algorithm method is found to be very accurate and also less time consuming task. Different types of distorted cells require a highly trained pathologist, as there are a large number of variable features making it difficult to distinguish these cells. The segmentation of different objects in the image helps in improving the efficiency of the algorithm as features are extracted for only the selected cells rather than the entire group of erythrocytes present. There is no existing combined methodology that detects sickle cell anemia and thalassemia causing abnormalities in human blood sample. Detection based on convolution neural network gives much more advanced way of finding the types or different classes of anemia present in each patients. Finally extracting it's features and comparing it with normal values proves that it is very efficient and also very accurate procedure.

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