A Survey on Blood Cell Segmentation

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Abstract – Blood Cell count is a preliminary process in major applications related to disease diagnosing and medical research. This seeks transparent perfection in cell counting as they witness the strength of candidate’s health. The conventional process of cells counting was practiced with microscopic visualization and was subjected to expertise of an individual. The automated methods ease the efforts of human and loaded the significant calculations and observations on algorithms and computational calculations. This paper reviews about the recent research work done against blood cell segmentation.

Keywords – CSF, GM, GMIs, HSV, K-means, LIM, MCP, MRI, NRBC, PDE, ROC, WM.

I. INTRODUCTION

Naturally, the human health is the most important of all the things in our lives. The positive affect of technology of any form on it is undoubtedly the most essential one. There are always more patients than it can be looked after and more healthy people to be followed up in order to minimize the risk of being ill. So, for performing required tasks in health sector, intelligent systems are always needed.

One such application is differential count in blood and bone marrow analysis. In most of the phases of medical diagnostic and screening, a person’s blood is routinely analyzed. Any kind of contribution in this analysis is appreciated greatly since it reduces the workload of medical experts. Automation of peripheral blood cell differentials has been available since the early 80’s. However, automation of bone marrow morphological assessment has not been successful enough to be accepted and used widely. Peripheral blood differential automation is mostly in cell suspension, which is based on either electrical conductivity or granularity (internal complexity) assessments. Since there are difficulties in obtaining fluent cell suspension of bone marrow cells, the previous methods are not as convenient. Automation based on the morphological assessment is the required methodology.

II. PREPROCESSING

In any pattern recognition system, the preparation of the input data is a crucial step affecting the system performance. Thus, it is clarifying to give the basic ideas behind constructing and selecting the input patterns.

In some applications, data acquired by an input device could directly use in recognition system. However, most of the time, the input signal needs to be processed to achieve reasonable system performance.

In preprocessing, generally, a priori information is utilized to simplify the task of the classification system. For example, if it is known that an input signal is affected by noise, a proper filtering stage can be designed to reduce the noise that significantly eases the task of the recognition system.

III. IMAGE SEGMENTATION PROCESS

Segmentation is the procedure by which an image is divided into meaningful and disjoint (non-overlapping) regions whose union defines the complete image. A region is connected set of pixels in which all pixels have some common properties.

In computer vision, image segmentation is the process of partitioning a digital image into multiple segments (sets of pixels, also known as super pixels). The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyze. Image segmentation is typically used to locate objects and boundaries (lines, curves, etc.) in images. More precisely, image segmentation is the process of assigning a label to every pixel in an image such that pixels with the same label share certain visual characteristics.

The result of image segmentation is a set of segments that collectively cover the entire image, or a set of contours extracted from the image. Each of the pixels in a region are similar with respect to some characteristic or computed property, such as colour, intensity, or texture. Adjacent regions are significantly different with respect to the same characteristic.
General segmentation procedures tend to follow the following rules:

1. Regions of image segmentation should be uniform and homogenous with respect to some characteristic or feature, such as gray level or texture.
2. Region interior should be simple and without many small holes.
3. Adjacent regions of segmentation should have significantly different values with respect to the characteristic or feature on which they are uniform.
4. Boundaries of each segment should be simple, not ragged, and must be spatially accurate.

**Image Segmentation Methods**

- **Thresholding**
  The simplest method of image segmentation is called the thresholding method. This method is based on a clip-level (or a threshold value) to turn a gray-scale image into a binary image. The key of this method is to select the threshold value (or values when multiple-levels are selected). Several popular methods are used in industry including the maximum entropy method, Otsu's method (maximum variance), and k-means clustering.

- **Clustering methods**
  The K-means algorithm is an iterative technique that is used to partition an image into K clusters. This algorithm is guaranteed to converge, but it may not return the optimal solution. The quality of the solution depends on the initial set of clusters and the value of K.

**Preprocessing Using Digital Morphology**

Morphology means study of form and shape. On this basis digital morphology means topology or structure of objects on a given image. Practically, an operator is 2D matrix that is also called as structuring element in digital morphology.

Originally, morphological processing was defined mathematically by considering the image and the structuring element as the sets in two-dimensional Euclidean space. Therefore, in its original form, morphological processing theory is constructed on the bimodal (binary) images.

Common approaches for color image segmentation are clustering algorithms such as k-means [1] or Mixture of Principal Components (MCP) [2]; however these algorithms do not take spatial information into account. Furthermore, clustering algorithms require prior information regarding number of clusters, which is a difficult or ambiguous task, requiring the assertion of some criterion on the very nature of the clusters being formed. Some progress has been made on this issue, however much experimentation still needs to be done [3].

An alternative set of algorithms exists which uses color similarity and a region-growing approach to spatial information [4]. Region growing is based on the following principles. The algorithm starts with a seed pixel, examines local pixels around it, determines the most similar one, which is then included in the region if it meets certain criteria. This process is followed until no more pixels can be added. The definition of similarity may be set in any number of different ways.

Region growing algorithms have been used mostly in the analysis of greyscale images; however, some significant work has been completed in the color realm by Tremeau et al. [5]. They discuss the segmentation of color regions which are homogeneous in color (i.e., no illumination effects are considered) thus restricting the application domain. They use a set of thresholds when calculating whether a color pixel is part of a region or not, and the Euclidean distance is used as the measure of similarity between two color vectors. It is well established [6] that the human perception of color similarity is poorly modeled by the Euclidean distance.

**Region Growing Algorithm**

A new region growing algorithm is proposed in this paper based on the vector angle color similarity measure and the use of the principal component of the covariance matrix as the "characteristic" color of the region, with the goal of a region-based segmentation which is perceptually-based. The algorithm is presented as follows:

1. Select seed pixels within the image.
2. From each seed pixel grow a region:
   a. Set the region prototype to be the seed pixel;
   b. Calculate the similarity between the region prototype and the candidate pixel;
   c. Calculate the similarity between the candidate and its nearest neighbor in the region;
   d. Include the candidate pixel if both similarity measures are higher than experimentally-set thresholds;
   e. Update the region prototype by calculating the new principal component;
   f. Go to the next pixel to be examined.
This algorithm presents several advantages over other color image segmentation algorithms. First, it is based on the concept of color vector angle. As was shown in the case of MPC [7], the vector angle is a shading-invariant color similarity measure, implying that intensity variations will be discounted in the region growing process, which is clearly not the case when using the Euclidean distance. Secondly, since spatial information is taken into account, regions having a slightly different color, but still spatially distinct, should appear as separate regions due to the region growing process.

Clearly a significant disadvantage of this approach to color image segmentation algorithm is need for seed pixels, and careful consideration needs to be given to the selection of those pixels. Ikonomakis et al. [8] gave an algorithm for selecting such pixels based on the hue values in the HSI space. Alternative approaches include finding those pixels in the color image with the greatest intensity, or to use the MPC algorithm to select the seeds based on the clustering result.

- **Compression-based methods**
Compression based methods postulate that the optimal segmentation is the one that minimizes, over all possible segmentations, the coding length of the data. The connection between these two concepts is that segmentation tries to find patterns in an image and any regularity in the image can be used to compress it. The method describes each segment by its texture and boundary shape.

- **Histogram-based methods**
Histogram-based methods are very efficient when compared to other image segmentation methods because they typically require only one pass through the pixels. In this technique, a histogram is computed from all of the pixels in the image, and the peaks and valleys in the histogram are used to locate the clusters in the image. Color or intensity can be used as the measure.

One disadvantage of the histogram-seeking method is that it may be difficult to identify significant peaks and valleys in the image.

- **Edge detection**
Edge detection is a well-developed field on its own within image processing. Region boundaries and edges are closely related, since there is often a sharp adjustment in intensity at the region boundaries. Edge detection techniques have therefore been used as the base of another segmentation technique.

The edges identified by edge detection are often disconnected. To segment an object from an image however, one needs closed region boundaries. The desired edges are the boundaries between such objects. Segmentation methods can also be applied to edges obtained from edge detectors.

- **Region-growing methods**
The first region-growing method was the seeded region growing method. This method takes a set of seeds as input along with the image. The seeds mark each of the objects to be segmented. The segmentation results are dependent on the choice of seeds. Noise in the image can cause the seeds to be poorly placed. Unseeded region growing is a modified algorithm that doesn't require explicit seeds.

- **Split-and-merge methods**
Split-and-merge segmentation is based on a quadtree partition of an image. It is sometimes called quad-tree segmentation. This method starts at the root of the tree that represents the whole image. The node in the tree is a segmented node.

- **Partial differential equation-based methods**
Using a partial differential equation (PDE)-based method and solving the PDE equation by a numerical scheme, one can segment the image. Curve propagation is a popular technique in this category, with numerous applications to object extraction, object tracking, stereo reconstruction, etc.

- **Parametric methods**
Lagrangian techniques are based on parameterizing the contour according to some sampling strategy and then evolve each element according to image and internal terms. Such techniques are fast and efficient, however the original "purely parametric" formulation, is generally criticized for its limitations regarding the choice of sampling strategy, the internal geometric properties of the curve, topology changes (curve splitting and merging), addressing problems in higher dimensions, etc.

- **Watershed transformation**
The watershed transformation considers the gradient magnitude of an image as a topographic surface. Pixels having the highest gradient magnitude intensities (GMIs) correspond to watershed lines, which represent the region boundaries. Water placed on any pixel enclosed by a common watershed line flows downhill to a common local intensity minimum (LIM). Pixels draining to a common minimum form a catch basin, which represents a segment.

IV. LITERATURE REVIEW
Venkatalakshmi [9] attempted the process of red blood cell counting through Hough Transform. The pre-processing stages include capturing of an image
via camera featured with microscope. However, this input is available on web for research applications. For image saturation the author implemented conventional HSV transformation but this technique does not consider non-linear characteristics of the capturing device. N. Valliammal [10] segmented the leaf image using morphological operations and wavelet transformation. Pulse coupled neural network for blood cell segmentation and counting was proposed by Vinod V. Kinbahune et al. [11]. The technique was used to denoise the image and clipping of some parameters that were considered as hindrance in blood cell counting.

Counting of white blood cells in image processing is analysed by Farnoosh Sadeghian et al. [12] using microscopic images. The property of white blood cells is optimized under various digital image processing algorithms for 20 images. S. Chinwaraphat et al. [13] used modified fuzzy clustering for white blood cell count. The research proposes a segmentation of nucleus and cytoplasm of white blood cell slides. The segmentation is performed firstly by using a standard FCM clustering technique to classify the image of blood sample slide into 4 primary groups as white blood cell nucleus, white blood cell cytoplasm, plasma and red blood cell. FCM which modified in order to eliminate a scattering or false clustering due to an unclear or color pixel similarity between cytoplasm and plasma background was implemented again iteratively until those errors were minimized. The minimization in each iteration loop was accomplished by using a neighboring color pixel of its scattering as a reference.

Morphological operations were used for the counting and segmentation of blood cells by Y. D. Ma et al. [14]. It is based on the feature of cell’s logical and morphological information. By using of mathematical morphological logical operation and laplacian filter, the method is realized with the MATLAB 5.10.

G.P.M Priyankara et al. [15] on white blood cell count research also studied white blood cells in deep prior to their research. The authors described the role of Hough Transform and Neural Network in this segment. The research is basically a broad survey of various blood counting techniques that are endorsed in various researches.

In other works of image transformation, S. Beucher [16] used watershed transformation. The author described the applications of image transformations to gradient images and problems related to over-segmentation. The authors also described various methods of image segmentation based on their definitions and implementation in developer’s work. Finally the watershed is described in details followed by respective applications.

Diabetic retinopathy detection from digital fundus images was carried out by S. Saheb Basha [17]. The images were segmented via morphological operations to identify the regions showing signs of diabetic retinopathy such as hard exudates, soft exudates and the red lesions: micro aneurysm and hemorrhages. Various color space values of the segmented regions are calculated. A fuzzy set is formed with the color space values and fuzzy rules are derived based on fuzzy logic reasoning for the detection of diabetic retinopathy.

Segmentation is the low-level operation concerned with partitioning images by determining disjoint and homogeneous regions or, equivalently, by finding edges or boundaries. The homogeneous regions, or the edges, are supposed to correspond to actual objects, or parts of them, within the images. Thus, in a large number of applications in image processing and computer vision, segmentation plays a fundamental role as the first step before applying to images higher-level operations such as recognition, semantic interpretation, and representation. Until very recently, attention has been focused on segmentation of gray-level images since these have been the only kind of visual information that acquisition devices were able to take and computer resources to handle. Nowadays, color imagery has definitely supplanted monochromatic information and computation power is no longer a limitation in processing large volumes of data. The attention has accordingly been focused in recent years on algorithms for segmentation of color images and various techniques, often borrowed from the background of gray-level image segmentation, have been proposed. L. Lucchese and S. K. Mitra [18] provide a review of methods advanced in the past few years for segmentation of color images.

Segmentation becomes more important while typically dealing with medical images where pre-surgery and post-surgery decisions are required for the purpose of initiating and speeding up the recovery process [19] Computer aided detection of abnormal growth of tissues is primarily motivated by the necessity of achieving maximum possible accuracy. Manual segmentation of these abnormal tissues cannot be compared with modern day’s high speed computing machines which enable us to visually observe the volume and location of unwanted tissues. A well-known segmentation problem within MRI is the task of labeling vowels
according to their tissue type which include White Matter (WM), Grey Matter (GM), Cerebrospinal Fluid (CSF) and sometimes pathological tissues like tumor etc. M. Masoor Ahmed and Dzulkifli Bin Mohamad [20] described an efficient method for automatic brain tumor segmentation for the extraction of tumor tissues from MR images. It combines Perona and Malik anisotropic diffusion model for image enhancement and K-means clustering technique for grouping tissues belonging to a specific group. The proposed method uses T1, T2 and PD weighted gray level intensity images.

Hanson-Lundberg [21] conducted a study on 1561 newborns to investigate nucleated red blood cells as a marker of acidemia in term neonates. The mean nucleated red blood cell count per 100 white blood cells was 9.2 +/- 18.1 (range, 0-327). Nucleated red blood cell counts were higher in infants with pH <7.20 (P =.001). Elevated nucleated red blood cell counts were associated with presence of meconium (P = .020) and neonatal intensive care unit admission (P =.024). The authors concluded that elevated nucleated red blood cell counts are associated with fetal acidemia, meconium, and neonatal intensive care unit admission.

Saracoglu et al. [22] conducted a study on 77 singleton pregnancies to investigate the variations of nucleated red blood cell (NRBC) counts in acute and chronic fetal hypoxia and to examine if it could be possible to establish a cutoff value for the number of NRBCs for prediction of fetal acidosis. The mean NRBC counts in chronic fetal distress group was higher than acute fetal distress. NRBC counts were found to be correlated with umbilical cord pH (r=-0.57; P<0.001). The cutoff value predicting fetal acidosis was determined as 14/100 leukocytes (sensitivity 87%, specificity 81%) by using ROC analysis. The authors concluded that the duration and the severity of fetal acidemia may be predicted by the number of NRBCs per leukocyte.

In another study by Ghosh et al. [23], a total of 75 cases were studied. Levels of NRBC per 100 WBC in umbilical venous blood were compared between 26 asphyxiated newborns (group I) and 49 non-asphyxiated newborns (group II). A statistically significant negative correlation existed between NRBC level and markers of acute intrapartum asphyxia, Apgar score and umbilical arterial pH (r=-0.50, P<0.001 and r=-0.48, P<0.001, respectively). Positive correlation was demonstrated with evidence of chronic ante partum asphyxia, presence of pregnancy induced hypertension and intrauterine growth restriction (r=2.66, P=0.02). A high NRBC count in umbilical blood correlated with poor early neonatal outcome. The authors concluded that the level of NRBC per 100 WBC correlates both with acute as well as chronic ante partum asphyxia. Further, it was also concluded that it can be used as a reliable index of early neonatal outcome.

Ferns et al. [24] conducted a study on 56 asphyxiated and 56 normal newborns value of nucleated red blood cells in predicting severity and outcome of perinatal asphyxia. There was a significant increase in the number of nucleated red blood cells in cases as compared to controls. Low Apgar, cord blood pH and neonatal outcome correlated well with nucleated RBC counts. The authors concluded that nucleated red blood cell count at birth is a useful predictor of severity and short-term outcome of perinatal asphyxia.

McCarthy et al. [25] conducted a study on 57 newborns to determine the umbilical cord blood nucleated red blood cell count in uncomplicated pregnancies delivered by elective caesarean section or delivered vaginally. The mean +/- standard deviation (S.D.) for nucleated red blood cell per 100 white blood cells (nRBC/100WBC) from the elective caesarean section group was 7.8 +/- 7.4. The vaginal delivery group had a mean value of 9.3 +/- 10.5, which was not significantly different. The authors concluded that although chronic hypoxia is associated with elevated nRBC, the stress of uncomplicated labor does not change the level. This adds credence to its use as a marker for hypoxia preceding labor and delivery.

Phelan et al. [26] conducted another case control study on 129 newborns to determine whether a relationship exists between the presence of nucleated red blood cells, hypoxic ischemic encephalopathy, and long-term neonatal neurologic impairment. The group of neurologically impaired neonates was separated into the following subgroups: group I, persistent nonreactive fetal heart rate pattern from admission to delivery (n = 69); group II, reactive fetal heart rate on admission followed by tachycardia with decelerations and absent variability (n = 47); group III, reactive fetal heart rate on admission followed by an acute prolonged deceleration (n = 37). The first and highest nucleated red blood cell value and the time of nucleated red blood cell disappearance were assessed. Significant differences were obtained between each of the three groups of neurologically impaired neonates and the normal group, with respect to initial nucleated red blood cells (group I, 48.6 +/- 106.9; group II, 11.4 +/- 9.8; group III, 12.6 +/- 13.4; p < or = 0.000002). Maximum nucleated
red blood cell values were higher in group I (mean 51.5 +/- 108.9) than in groups II and III combined (mean 12.7 +/- 11.9) (p = 0.0005). Group I also had a longer clearance time (119 +/- 123 hours) than groups II and III combined (mean 59 +/- 64 hours) (p < 0.001). In general, the closer the birth was to the asphyxial event, the lower was the number of nucleated red blood cells. There data suggest that cord blood nucleated red blood cells could assist in the timing of fetal neurologic injury.

In a study Boskabadi et al. [27], levels of nucleated red blood cell per 100 white blood cells and absolute nucleated red blood cell counts in venous blood were compared for 42 asphyxiated (case group) and 49 normal neonates (control group). These parameters were also related to the severity of asphyxia and clinical outcome. A statistically significant negative correlation existed between nucleated red blood cell level and indicators of the severity of perinatal asphyxia, first minute Apgar score and blood pH (P<0.001), respectively. A positive correlation was demonstrated between these parameters and severity of asphyxia, acidosis, and poor outcome (P<0.05). The authors concluded that NRBC/100 WBC and/or absolute nucleated red blood cell are simple markers for assessment of severity and early outcomes of perinatal asphyxia.

V. CONCLUSION
Platelets and blood cell counting is a mandatory and efficient approach in determination of various blood related disease. The cell count provides optimal information of the fitness of an individual as the blood is carrier of various essential elements. The approaches of cell count are autonomic in nature and accuracy depends on algorithmic capability of various methods. This paper gives knowledge about preprocessing, feature extraction, and statistical pattern recognition techniques.

REFERENCE
International Journal of Computer Science and Network Security, 8(12), 211-8