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Diagnosis of Rectal Cancer through Images

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----------ABSTRACT----------

Human health is the real wealth for a society. Consequently prevention of health from complex diseases like cancer needs the diagnosis of these entire viruses at an early stage. Colon cancer, the most common one, reached the highest rate among all the other types recently. Colorectal cancer gets developed either in colon or in the rectum inside the large intestine, due to the abnormal growth of the cells. Computer-aided decision support system has become one of the major research topics in medical imaging field during the past two decades to detect cancers. Detecting and screening of colorectal cancers are done by a Computed Tomography. The implemented algorithm determines the locations and features of glands which are affected by cancer tissues and save this information for the subsequent diagnosis. The proposed algorithm carries out the diagnosis with two modules: One known as the gland detection and the other one referred as the nuclei detection. Gland detection is performed in the proposed algorithm using color segmentation either through HSV or LAB transformation. Noise removal and erosion of the input image is performed for enhancing the selection of the affected tissues. The boundary detection and connection is established through Markov Chain model to identify the affected tissues with proper threshold. The first module detects the glands where the possibly of miss detection is more. Hence to remove the miss detected glands the algorithm proceed for the second module referred as nuclei detection. The most well known region growing methodology is slightly modified to increase the speed and reduce the memory size To provide the execution in low-end clients, the whole image is cracked into smaller tiles and after the processing of each individual tiles , the results are to be merged to get back the original size. After nuclei detection if the number of nucleus is more that glands are miss detected glands and they are removed

Keywords - Gland detection, colon cancer, nuclei detection

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1. INTRODUCTION

In the modern age, cancer is one of the most spreading complex diseases. Identifying such cancer without biopsy at an early stage is further imperative since often taking biopsy is not good for health also. Cancer has been caused primarily by genetic instability and accumulation of multiple molecular alterations. Cancer is also caused by abnormal activation of cellular genes that control cell growth or cell mitosis. In addition cancer is diagnosed and treated too late. Due to this problem, cancer has overtaken heart disease as the leading cause death for any age on, all over the world. As per the latest research, a great percentage of the patients suffer with breast, lungs, prostate and colon cancer. Large intestine performs wide variety of functions as ranging from breakage of large molecules to nutrients and water absorption. Colon is one major constituent of large intestine. It mainly affects the lowest part of the digestive system

Traditionally colon cancer is diagnosed by means of microscopic analysis of colon samples. Researchers have been working since decade to get rid of manual inspection [1-3] and to develop trustworthy technique to diagnose the difficult colon cancer at an early stage through image processing. Given the fact that colorectal cancer is a largely preventable disease through routine detection and removal of adenomatous polyps, colon cancer prevention has now moved to the forefront. The infections and the tumor mostly evolve from the mucosal layer, the most important layer of the colon structure. Levels of colon can be explained as**:** Colorectal cancers begin as polyps. As polyps enlarge, they are more likely to develop into a cancer which has the ability to disseminate through the body. The most important colorectal polyp is the adenoma, a small begin tumor growing to about 2 cm in size. Colonic adenomas are common and in the majority of patients there is no side effect on health. They are more common with increasing age.

Retinal cancer detection from side to side is carried out by by Waheed eta al, exercising Bayesian classifier, and k means algorithm [4]. The processing of microscopic tissue images and the segmentation of tissue components are done by S. D. Olabarriaga and others, through digital imagery and special immunodiagnostic software products [5].. An improved gradient vector flow

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(IGVF) is considered as an essential method to segment an image appropriately for colon cancer detection. This new algorithm, IGVF can improve [6] GVF snake model's ability to capture thin boundary indentation like the boundary of cancer image. Yoshida and Nappi [7], firstly computed the geometric features to characterize polyps, folds and colonic walls at each voxel in the extracted colon .An adaptive level set method for segmenting colon filled with air and pacified fluid in CT colonography is implemented in [8] .Semantic segmentation in microscopic images seems to yield good result in extracting the cellular, nuclear or tissue component [9], for the cancer detection in rectal.

Signal processing plays an important role in the work of pathologists; it is especially true for image processing software products. High-resolution digital images have taken over the role of traditional tissue slides on a glass plate. In addition to the direct effects of this advancement (sharing images, remote access, etc.), a new option appeared: the possibility of using image processing software for automatic (or semi-automatic) diagnostics. One of the most important tasks in this procedure is the segmentation of the tissue images; to identify the main components. In the case of colon tissue samples, these are the cell nuclei, glands and surface epithelium. The aim of our work is to design and implement a software solution, which supports quantitative histological analysis of hematoxilin eosin (HE) stained colon tissue samples, identify tissue structures – nuclei, glands and epithelium, using image processing methods. Furthermore, based on the result of the histological segmentation, a opinion for the negative or malignant status of the samples can be obtained automatically

2. METHODOLOGY.

The proposed a method using HSV color to remove element outside the area of nucleus. In order to extract the gland shape, we proposed a gland tracking boundary and segmentation. By using the result of gland tracking, nucleus size that forms the glands are measured. Multilayer perceptron is being used to detect the shape of glands. By combining result of gland shape and nucleus size, the classification is carried out.

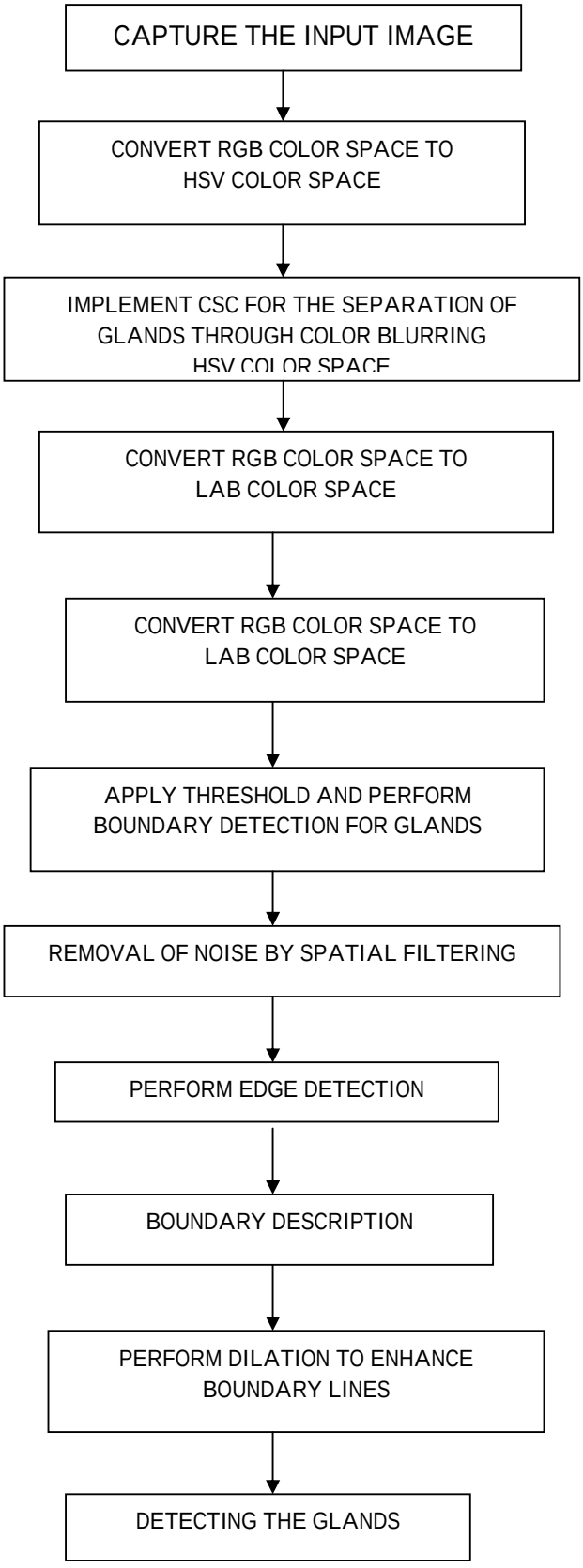
For the gland and nuclei detection the colon segmentation is done through the following processes

- Thresholding
- Boundary generation end matching
- Removal of miss detected gland
- Nucleus positions

The above algorithms determine the nucleus region with bigger precision and also the possibility of non-detected and miss detected glands are found to be less than 20%.

2.1. Gland detection

The images acquired from digital microscopy suffer with lot of noises and homogeneous area which in turn trouble and hinders the glands detection. Hence there comes the need of using a processing stage referred as color



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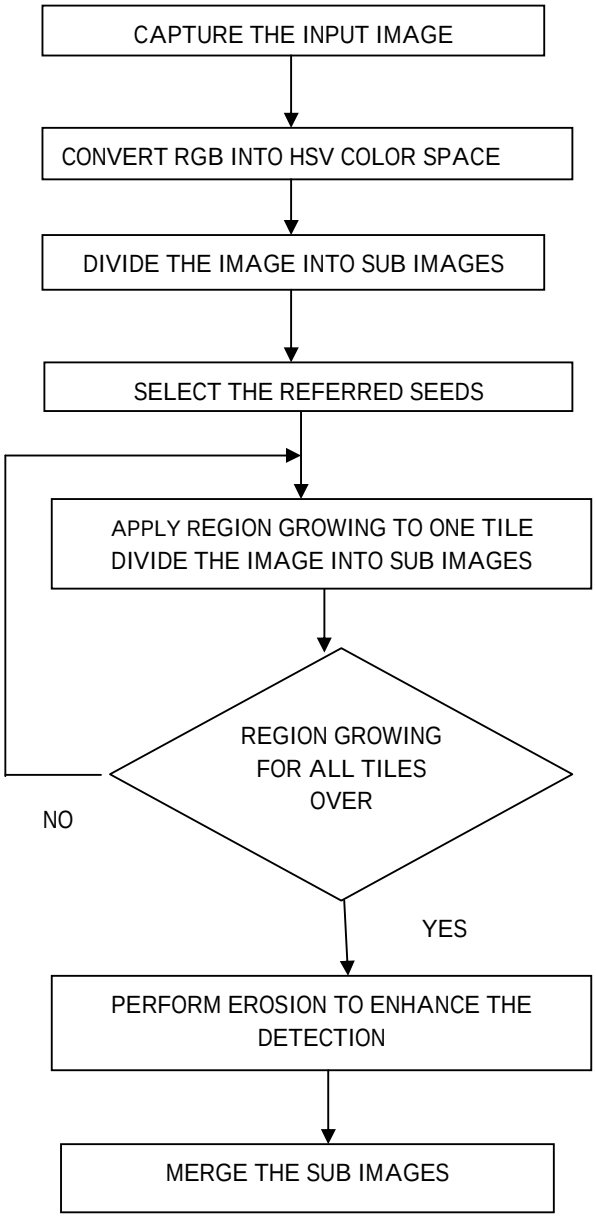
Structure code (CSC) , whereby the similar color shades in HSV space are blurred with the same value. The boundaries of the glands are well separated from the other part of mucosal layer and the different colors are separated into different bands. Thus the white interiors of the gland are clearly identified.

A threshold value is determined considering the ratio of the average intensity of homogeneous regions and the inhomogeneous regions in LAB space for the "A", component. The result is an image which contains the contour curves of glands. In our tests nearly fifty tissue images were used to determine the appropriate threshold value..



Consequently edge detection is to be executed and connected component analysis is to be applied. After skipping the small regions the boundary lines of glands are detected. As the last step dilation is used to enhance the boundary lines to detect the glands on the border of the tissue as it can be seen in.Figure1.offer the flow diagram for gland detection

2.2 Nuclei Detection

Nuclei detection can be done by way of different routines as K means, Fuzzy logic or edge detection techniques. Nevertheless the region growing approach, a classical image segmentation method is the most promising algorithm. The proposed algorithm is slightly modified from the conventional algorithm to reduce the usage of memory and also to increase the speed. Conventional seeded region growing performs the segmentation of an image with respect to a set of points, called seed points. Initially, these points are referred as the region candidates. An iteration of the main loop felicitates the addition of few similarity pixels to the already existing region. Generating the contour of each region candidate and also selecting the most promising point to extend each region within the contour plays a vital role in this segmentation. The iterations are to be repeated until the above said conditions are met out. Flow diagram of this process is depicted in Figure 2.However this most well known region growing methodology is quite memory intensive and time consuming. The size of high-resolution tissue images can easily reach the order of a hundred megabytes therefore the memory requirement for the region growing is more than one gigabyte. To provide the execution in low-end clients, the whole image is cracked into smaller tiles and after the processing of each individual tiles, the results are to be merged to get back the original size.

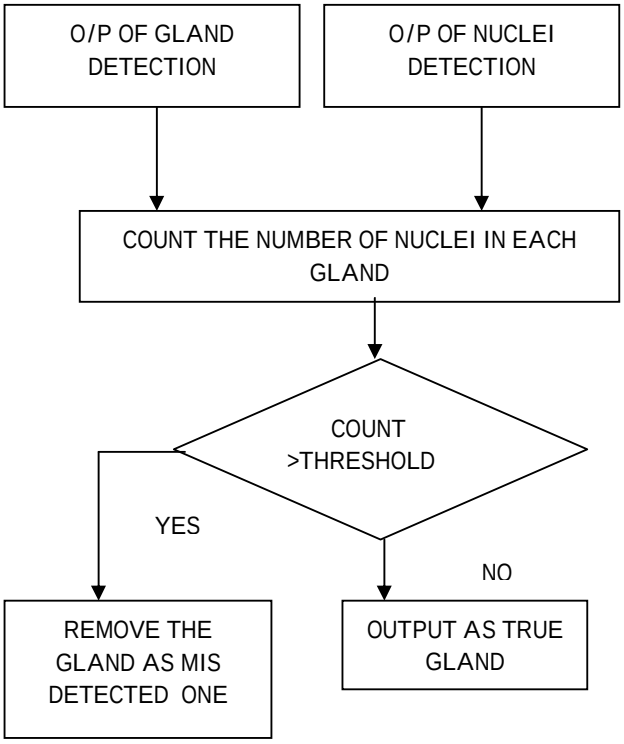


Figure 3 Removal of miss detected glands

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2.3 Removal of miss detected glands

Process explained till now should detect the true glands. But honestly saying the algorithm produces the output in such a manner certain non glands will be detected as glands. This may be avoided by counting the number of nuclei in the gland region. If the fraction of the nuclei in a gland candidate region is too high then these glands are to be considered as non gland and to be removed as miss detected glands. Schematic diagram of this third step is given in Figure 3

3. EXPERIMENTAL RESULTS

Proposed algorithm is tested with various images and the rate at which the glands are detected positively and the respective percentage are estimated with few parameters as, 'true positive', 'false positive', 'true negative' and 'false negative'. These in turn are used to determine the precision, accuracy and sensitivity. The input and the output images are bestowed in Figure 4

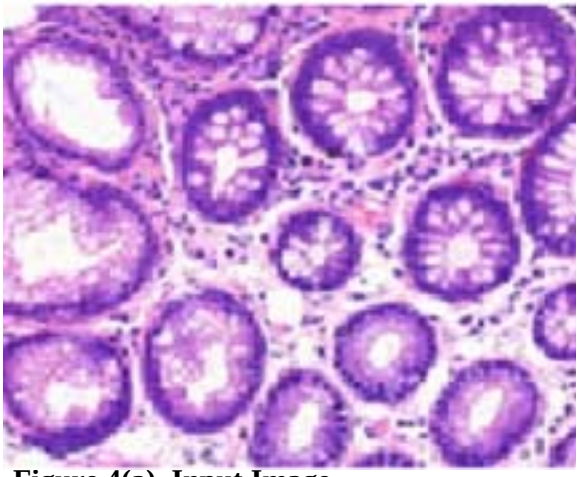

Figure 4(a) .Input Image

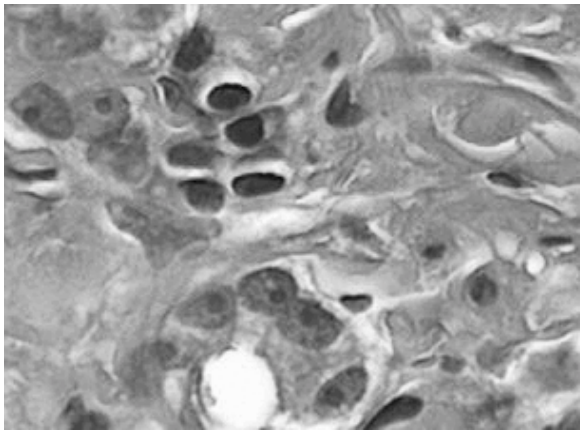

Figure 4(b). L component in lab image

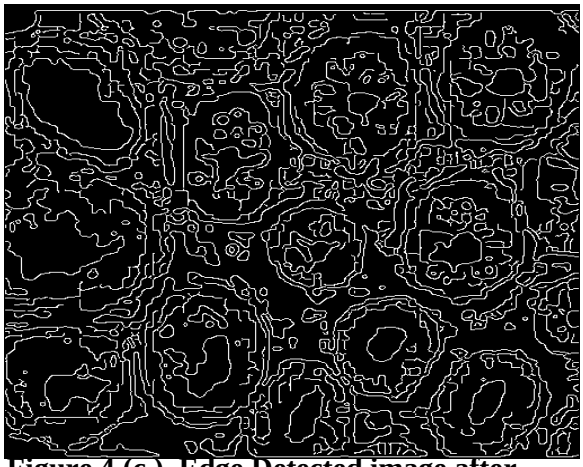

Figure 4 (c) Edge Detected image after thresholding

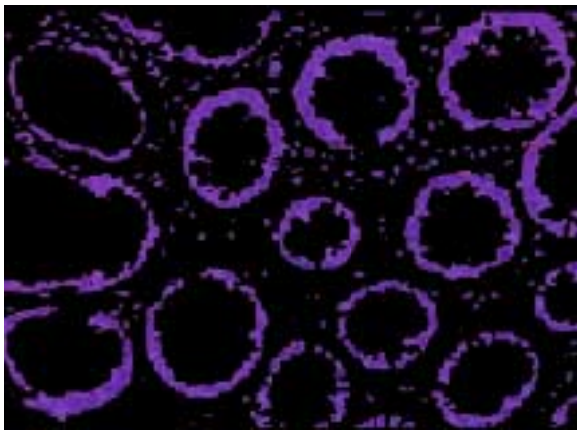

Figure 4(d) Gland detected image

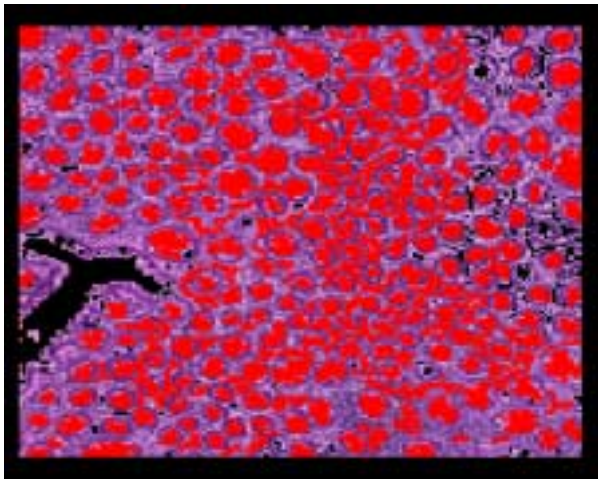

Figure 4 (e) Nuclei detected image

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