



DETECTION OF RENAL TUMORS USING CT SCAN IMAGE PROCESSING BY ARTIFICIAL NEURAL NETWORK

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ABSTRACT

Renal tumour segmentation and analysis is a very important step for doctors in deciding the stage of cancer and determining the method of treatment. This paper examines a novel approach to develop an efficient algorithm to detect and further analyse the renal cancer tumours. The algorithm has been employed to pre-process and segment the image for better visualization and segmentation of the visible tumour. The pre-processing involves hybrid filter for noise removal and image enhancement. An artificial neural network has also been used by means of Hybrid Self Organizing Maps using which we have used for clustering of the image data and thereby highlighting the detected region. The correct output obtained by the medical team is then compared with the resultant image in order to improve algorithm to aptly understand the affected regions in human body and aid in better visualization of the tumor. We then apply a region growing method which looks for similar intensity regions in the images and thus segment out the tumour from the processed image.

Keyword: Image Processing, ANN, Renal Tumour, CT scan, SOM, Region Growing

1.INTRODUCTION

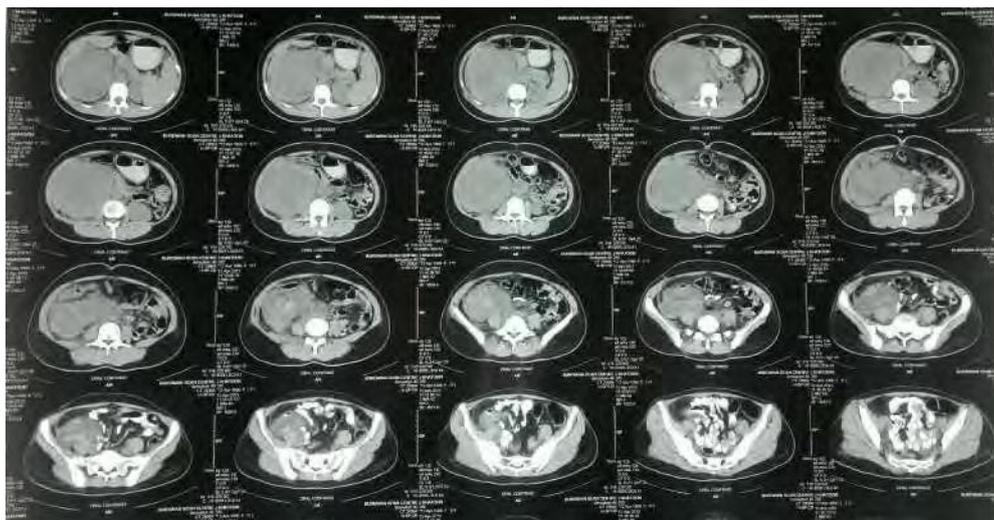
It is estimated that 65,150 men and women (40,430 men and 24,720 women) will be diagnosed with and 13,680 men and women will die of cancer of the kidney and renal pelvis in 2013. It is estimated that 72,570 men and women (54,610 men and 17,960 women) will be diagnosed with and 15,210 men and women will die of cancer of the urinary bladder in 2013. Digital Imaging and Communications in Medicine (DICOM) is a standard for handling, storing, printing, and transmitting information in medical imaging. The challenge is to employ computer aided detection (CAD) techniques for the purpose of assisting radiologists in the early detection of cancer, by processing and analysing images [1]. We have devised an algorithm and tested it using various real time data including RUB Computer Tomography Images [20][21] collected from different Hospitals in Bangalore. The pre-processing includes a noise removal technique employing by a hybrid filter and Contrast Limited adaptive histogram equalization technique. The segmentation technique proposed in this paper is based



on a region growing technique and is iterative, automatic and unsupervised process which works on the histogram of the image.

II. PRE-PROCESSING

Our first step involved conversion of the DICOM image to a JPEG image and automated cropping the image to our desired needs. Figure 1 shown below shows a typical CT scan outlining various slices of the renal, ureter and bladder region.



The pre-processing technique involves identifying the main source of noises and removing the noise with a proper filtering technique [4]. The common noises present in a Renal, Ureter, and Bladder CT Scan are salt & pepper noise, speckles, Gaussian and impulse noises [1], [4]. We have proposed a hybrid filter as a combination of adaptive median and wiener filter for noise removal and image enhancement. Image enhancement is also achieved using Contrast limited adaptive histogram equalization technique which is efficient in improving the contrast and making the medical image more informative [5]. We apply non-linear median filter to remove the salt and pepper noise. For Gaussian noise removal [7][9][10][11][19] each pixel in the image will be changed from its original value by a small amount. A histogram plot of the amount of distortion of a pixel value against the frequency, with which it occurs, shows a normal distribution of noise. While other distributions are possible, we use the Gaussian (normal) distribution model due to the central limit theorem that says that the sum of different noises tends to approach a Gaussian distribution. Figure 2 below shows our CT scan after various noise reduction techniques mentioned for better visualisation.

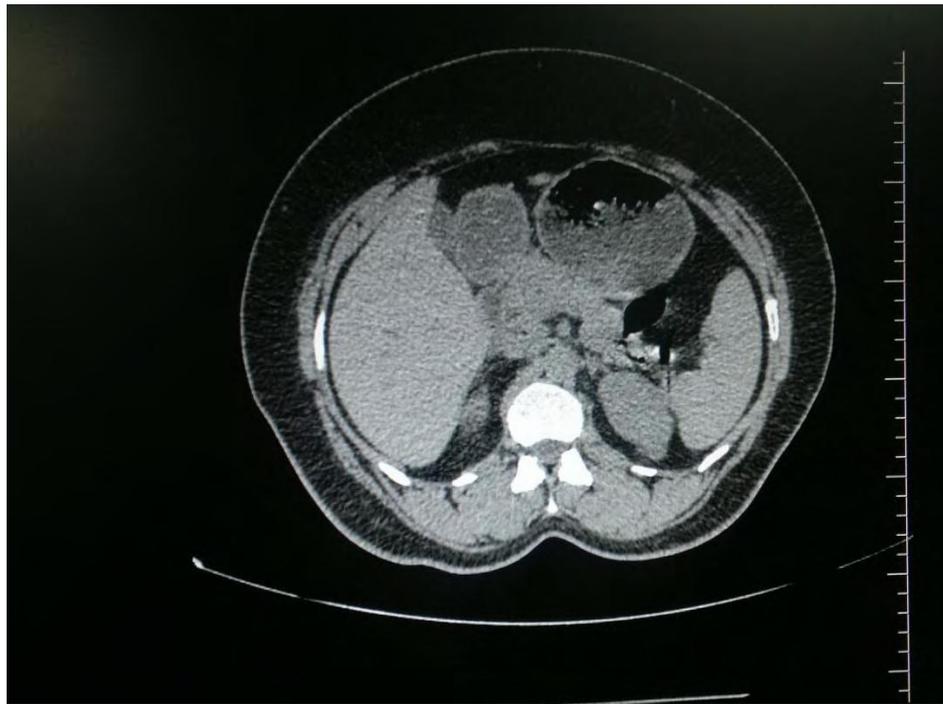


Figure 1: Image after converting to JPEG, cropping and filtering

We have also then performed closing operation on the image. Closing is, together with opening, the basic workhorse of morphological noise removal. Opening removes small objects, while closing removes small holes. The result is an evened out CT scan that is smoothen after all the noise removal in the previous step. The Contrast Limited AHE (CLAHE) differs from ordinary adaptive histogram equalization in its contrast limiting. This feature can also be applied to global histogram equalization, giving rise to contrast limited histogram equalization (CLHE), which is rarely used in practice. In the case of CLAHE[2][3][12], the contrast limiting procedure has to be applied for each neighbourhood from which a transformation function is derived. CLAHE was developed to prevent the over amplification of noise that adaptive histogram equalization can give rise to. This is achieved by limiting the contrast enhancement of AHE. The contrast amplification in the vicinity of a given pixel value is given by the slope of the transformation function. This is proportional to the slope of the neighbourhood cumulative distribution function (CDF) and therefore to the value of the histogram at that pixel value. CLAHE limits the amplification by clipping the histogram at a predefined value before computing the CDF. This limits the slope of the CDF[14][15] and therefore of the transformation function. The value at which the histogram is clipped, the so-called clip limit, depends on the normalization of the histogram and thereby on the size of the neighborhood region. Common values limit the resulting amplification to between 3 and 4 times the histogram mean value. In either case, the noise at different pixels can be either correlated or uncorrelated; in many cases, noise values at different pixels are modeled as being independent and identically distributed, and hence uncorrelated. We finally compliment the output image to make the tumor toward the dark region and less intensity values for better segmentation results. Figure 3 shoes the result we typically achieve after this step.

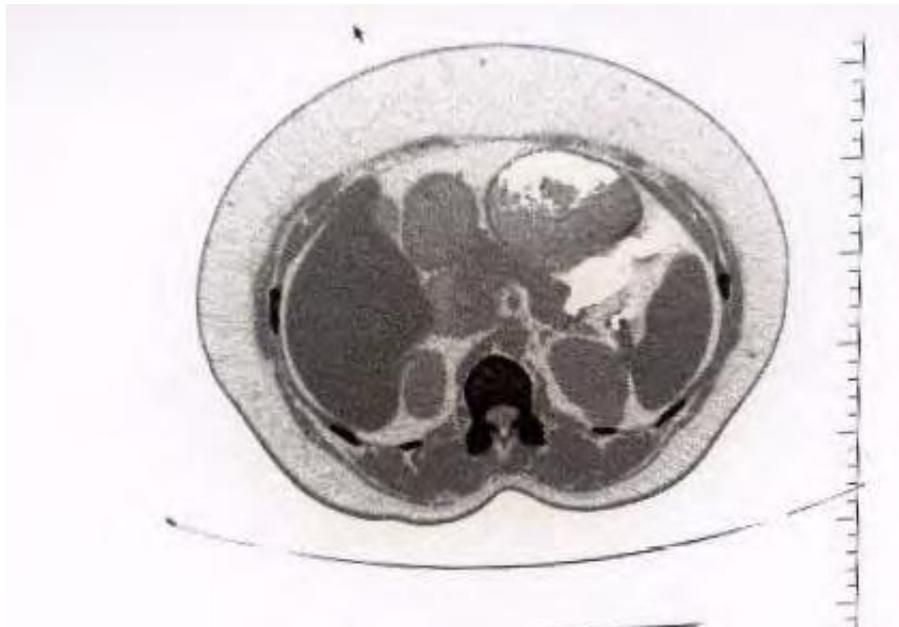


Figure. 3. Resultant image of complementing the CT scan image and noise reduction

III. SEGMENTATION

The segmentation of the pre-processed image essentially affects the overall performance of any automated image analysis system. Image regions, homogeneous with respect to some usually textural or colour measure, which result from a segmentation algorithm are analysed in subsequent steps. Watershed segmentation on the other hand leads to over segmentation and hence the output does not appear meaningful. Figure 4 below shows the tumor after implementing our segmentation algorithm.



Figure 4: Segmented Tumour

Steps No.	Step Description
1	Conversion from DICOM to JPEG
2	Crop to Scale size
3	Applying complementing
4	Applying filters
5	Applying Denoising technique
6	Applying clustering technique
7	Applying segmenting technique
8	Applying Hybrid/Growing SOM
9	Applying thresholding technique
10	Image grown to scale using region growing
	Benign/ Malignant Testing using ANN

TABLE 1: Proposed Algorithm

With the segmented tumor available it is not easier for us to analyse the tumor using various measures that could help decide the course of further treatment. The figure 5 below shows the tumor with edge detection technique implemented to calculate the visual appearance of patterns in terms of size, speculation, contrast, location, surface area, volume, colour, density and risk.



Figure 5: Tumour after edge detection for analysis

The following table will show the overview of the operations performed on the slicing

IV. CLUSTERING AND REGION GROWING

We have used several methods of clustering to compare and contrast the different effects of clustering algorithms on our renal CT scan image. Firstly, in centroid-based clustering, clusters are represented by a central vector, which may not necessarily be a member of the data set. When the number of clusters is fixed to k , k means clustering gives a formal definition as an optimization problem: find the cluster centers and assign the objects to the nearest cluster center, such that the squared distances from the cluster are minimized.

The optimization problem itself is known to be NP-hard [16][22], and thus the common approach is to search only for approximate solutions. A particularly well known approximate method is Lloyd's algorithm, often



actually referred to as "k-means algorithm". It does however only find a local optimum, and is commonly run multiple times with different random initializations. We also tried a variation of the above choosing the best of multiple runs, but also restricting the centroids to members of the data set choosing medians or choosing the initial centers less randomly (K-means++) or allowing a fuzzy cluster assignment (Fuzzy c-means)[18]. Most k-means type algorithms require the number of clusters to be specified in advance, which is considered to be one of the biggest drawbacks of these algorithms. Furthermore, the algorithms prefer clusters of approximately similar size, as they will always assign an object to the nearest centroid. This often leads to incorrectly cut borders in between of clusters.

Secondly we used Self-Organizing maps technique for clustering. Three variations of SOM were used- Simple Self-Organizing maps, Hybrid SOM and Growing SOM. The SOM was implemented in a dynamic technique and took approx. 2500 to 3000 iterations to reach convergence. The hybrid SOM technique also was implemented in a dynamic fashion and took approximately 2000 to 2500 iterations to converge. However the main disadvantage we faced in the method was in identifying the suitable map size in the SOM.

A growing self-organizing map (GSOM)[2][3] is a growing variant of the popular self-organizing map (SOM). The GSOM was developed to address the issue of identifying a suitable map size in the SOM. It starts with a minimal number of nodes and grows new nodes on the boundary based on a heuristic. By using the value called Spread Factor the data analyst has the ability to control the growth of the GSOM.

All the starting nodes of the GSOM are boundary nodes, i.e. each node has the freedom to grow in its own direction at the beginning. New Nodes are grown from the boundary nodes. Once a node is selected for growing all its free neighboring positions will be grown new nodes. The GSOM process we employed first initialized the weight vectors of the starting nodes with random numbers between 0 and 1 and then calculated the growth threshold for the given data set of dimension according to the spread factor (SF). Then input was presented input to the network. The weight vector was determined and mapped to current feature map. An adaptation rule was applied where we decreased the value of SF in the GSOM depending on the number of nodes existing in the map at time and increased the error value of the winner (error value is the difference between the input vector and the weight vectors). We then grow nodes distributing weights to neighbors if the winner is a non-boundary node. We then initialize a learning rate and update at every epoch. We repeat the procedure until all inputs have been presented; node growth is reduced to a minimum level and convergence is achieved. Afterwards, we enter the smoothening phase wherein we reduce learning rate and fix a small starting neighborhood; find winner and adapt the weights of the winner and neighbors in the same way as in growing phase.



Figure 6: After Region Growing

We have used a simple region growing algorithm. This includes a simple region-based image segmentation method that is also known as a pixel-based image segmentation method since it involves the selection of initial seed points. We have used around 500 seed point and grown the image from those basic points to provide a 3 D image of the tumor for better visualization. This approach to segmentation examines neighboring pixels of initial “seed points” and determines whether the pixel neighbors should be added to the region. The process is iterated on, in the same manner as general data clustering algorithm. Figure 6 above shows the same.

V. NEURAL NETWORK TRAINING

Literature review suggested [11][13][17][18][20] helps in our scheme for distinction of the malignant tumors from the benign ones. For selecting the training malignant nodules, we classified malignant nodules into several groups based on the visual appearance of patterns in terms of size, speculation, contrast, location, surface area, volume, colour, density and risk. We used the method for a training set to determine systematically based on the ranking in the scores obtained from the trained set. We then selected several benign nodules from each of the groups in such a manner that benign nodules in each group cause different degrees of difficulty in classification.

VI.RESULTS AND DISCUSSION

The proposed algorithm is evaluated on the basis of comparisons done with different approaches for segmentation and from the values obtained from feature extraction, applied on the region of interest in the renal, ureter and bladder area as shown in fig 8. Features extracted for various images of breast consisting cancer. The results of features of different methods of segmentation are given along with the comparison of the different clustering algorithms used. The features we have extracted and compared are [given in fig 7]:

- Mean: The mean of the pixel values in the defined window, estimates the value in the image in which central clustering occurs.
- Standard Deviation: The Standard Deviation (σ) is the estimate of the mean square deviation of grey pixel value $p(i, j)$ from its mean value. Standard deviation describes the dispersion within a local region. (Image size $M*N$).
- Moment: It gives the measure of homogeneity of the image.



- Skewness: It is characterizes the degree of asymmetry of a pixel distribution in the specified window around its mean. Skewness is a pure number that characterizes only the shape of the distribution.
- Kurtosis: Kurtosis, measures the peak or flatness of a distribution relative to a normal distribution.

VII. CONCLUSION

In this paper we have proposed divide and conquer algorithm for Growing SOM to cluster and ANN to check if the tumor is benign or malignant. The average execution time=0.85 sec as our method iterates dynamically until convergence is reached for our data sets. To improve the complexity of the algorithm we increased the probable error value less gradually and got a faster and more efficient algorithm. However we found that doing that compromised the accuracy of the clustering. Since medical procedures rely on accuracy we have maintained a low level of probable error values. In case of Renal, ureter bladder CT scans, the features extracted will be useful in recognizing the class of the image (normal/abnormal) by training and testing using classifiers. The values obtained by different methods of segmentation shows variations in the feature values for same image. The feature extracted using segmentation based on our proposed method has an added advantage of reducing false positive result and is efficient for detecting infiltration areas from CT scans.

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