

Detection of Renal Tumours using Artificial Neural Network and Image Processing of CT Scan

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Abstract— Renal tumour segmentation and investigation is an imperative advance for specialists in understanding the phase of the disease and deciding the technique for treatment. This paper inspects a novel way to recognize and additionally examine the renal disease tumours using an efficient algorithm. The algorithm has been utilized to pre-process and segment the image for better perception and division of a visible tumour. The pre-processing includes a hybrid channel for noise removal and picture upgrade. An artificial neural system has likewise been utilized by methods of Hybrid Self Organizing Maps which we have used for the clustering of the image information and accordingly featuring the distinguished region. The right output obtained by the medical group is then compared with the resultant image with the end goal to make a better calculation and for the algorithm to aptly understand the influenced regions in the human body and help in better perception of the tumour. We then apply a region growing technique which searches for regions with similar intensity and sections out the tumour from the prepared image.

Index Terms— Image Processing, Renal Tumour, ANN, CT filter, Region Growing, SOM

I. INTRODUCTION

Kidney cancer is the ninth most commonly occurring cancer in men and the fourteenth most commonly occurring cancer in women. There were over 400,000 new cases in 2018. Digital Imaging and Communications in Medicine (DICOM) is a standard for taking care of, storing, printing, and transmitting data in medical imaging. The challenge is to utilize Computer Aided Detection (CAD) systems to assist radiologists in the early identification of the disease, by processing and analysing images [1]. We have devised an algorithm and tried it utilizing different real-time information including RUB Computer Tomography Images gathered from various hospitals in Bangalore. The pre-processing incorporates a noise removal strategy utilizing a hybrid filter and Contrast Limited adaptive histogram equalization technique. The segmentation strategy proposed in this paper is based on a region growing procedure and is an iterative, automatic and unsupervised process which works on the image's histogram.

II. PRE-PROCESSING

Our initial step included converting the DICOM image to a JPEG image and computerized cropping the image to our coveted needs. Figure 1 shown below demonstrates a common CT scan laying out different slices of the renal, ureter, and bladder area.

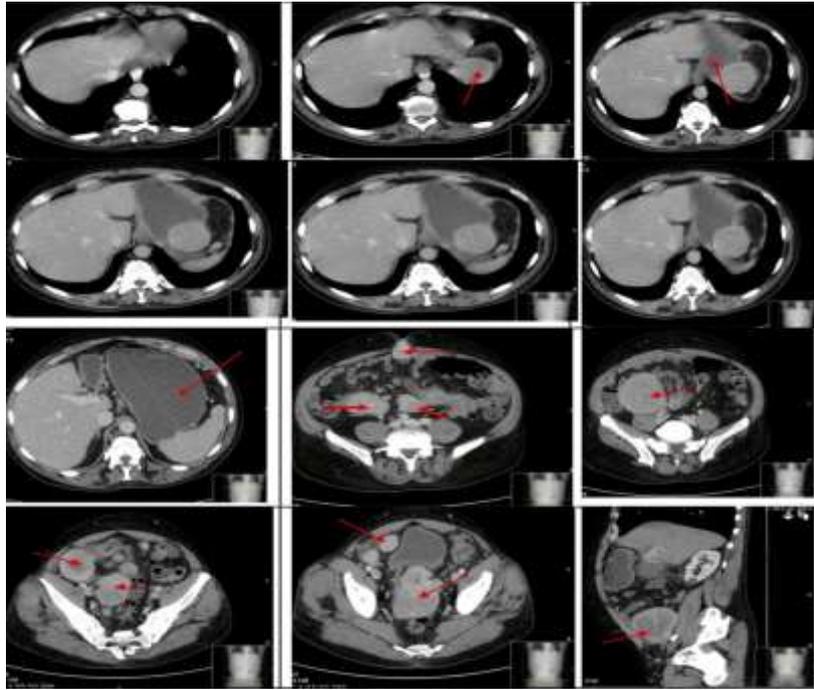


Figure 1: Example of a typical CT scan

The pre-processing technique includes identifying the fundamental sources of noise and expelling the noise with an appropriate filtering technique [4]. The basic noises present in a Renal, Ureter, and Bladder CT Scan are salt and pepper noise, speckles, Gaussian and impulse noises [1], [4]. We have proposed a hybrid filter as a mix of adaptive middle and Wiener filter for noise removal and image upgrade. Image enhancement is also accomplished utilizing Contrast limited adaptive histogram equalizing method which is effective in enhancing the contrast and making the medical image more useful [5]. We apply a non-straight median filter to remove the salt and pepper noise. For Gaussian noise removal [7] [9] [10] [11] every pixel in the image will be changed from its original value by a small amount. A histogram plot of the measure of distortion of a pixel value against the frequency, with which it occurs, demonstrates a normal distribution of noise. While different distributions are conceivable, we utilize the Gaussian (normal) distribution model because of the central limit technique states that the aggregate of different noises tends to approach a Gaussian distribution. Figure 2 below demonstrates our CT scan after different noise reduction procedures mentioned for better visualization.



Figure 2: Image after converting to JPEG, cropping, and filtering

We have likewise then performed a closing operation on the image. Closing is, as one with the Opening, the fundamental workhorse of morphological noise removal. Opening removes small objects, while closing removes little holes. The outcome is an evened out CT scan that is smoothened after all the noise removal in the previous step. The Contrast Limited AHE (CLAHE) varies from ordinary adaptive histogram equalization in its complexity constraining. This feature can likewise be applied to global histogram equalization, giving rise to contrast limited histogram equalization (CLHE), which is rarely used in practice. On account of CLAHE [2] [3] [12], the contrast limiting technique must be applied to each neighbourhood from which a transformation function is determined. CLAHE was developed to reduce the over-amplification of noise that adaptive histogram equalization can give rise to. This is accomplished by restricting the contrast enhancement of AHE. The contrast amplification in the region of a given pixel value is given by the slope of the transformation function. This is corresponding to the slope of the neighbourhood cumulative distribution function (CDF) and in this way to the value of the histogram at that pixel

value. CLAHE limits the amplification by clipping the histogram at a predefined value before processing the CDF. This restricts the slope of the CDF [14] [15] and along these lines of the transformation function. The value at which the histogram is cut, the so-called clip limit, relies upon the normalization of the histogram and accordingly on the neighbourhood region. Common values restrict the subsequent amplification to somewhere in the range of 3 and 4 times the histogram mean value. In either case, the noise at different pixels can be either correlated or uncorrelated; in numerous cases, noise values at various pixels are modelled as being independent and identically distributed, and henceforth uncorrelated. We at last compliment the output image to make the tumour toward the dark region and fewer intensity values for better segmentation results. Figure 3 shows the outcome we commonly accomplish after this step.

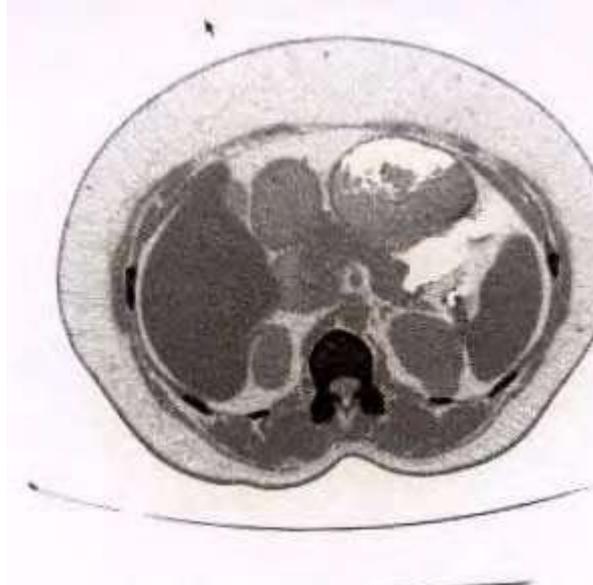


Figure. 3. Resultant image of complementing the CT scan image and noise reduction

III. Segmentation

The segmentation of the pre-processed image basically influences the overall performance of any automated image analysis system. Image regions, homogeneous with respect to some usually textural or colouring measure, which result from a segmentation algorithm are examined in consequent steps. Watershed segmentation, on the other hand, leads to over-segmentation and henceforth the output does not seem important. Figure 4 beneath shows the tumour after executing our segmentation algorithm.



Figure 4: Segmented Tumour

With the segmented tumour accessible it isn't less demanding for us to analyse the tumour utilizing different estimates that could help choose the course of further treatment. The figure 5 beneath demonstrates the tumour with edge detection

technique executed to compute the visual appearance of patterns in terms of size, contrast, speculation, area, location, volume, colour, density, and risk.

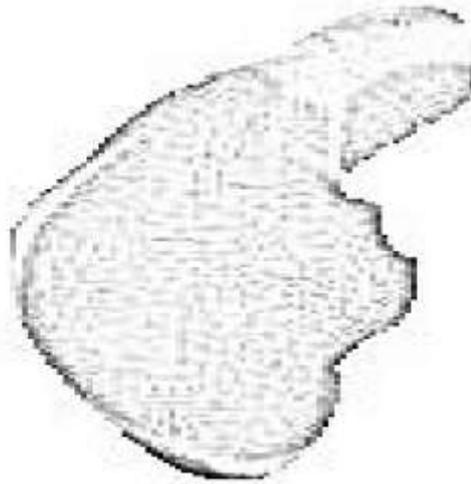


Figure 5: Tumour after edge detection for examination

The following table will demonstrate the outline of the activities performed on the slicing

TABLE 1: Proposed Algorithm

Step Number	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 the thresholding technique
10	Image developed to scale utilizing region growing
11	Benign/Malignant Testing utilizing ANN

IV. CLUSTERING AND REGION GROWING

We have utilized several techniques of clustering to compare and contrast the different effects of clustering algorithm on our renal CT scan image. Firstly, in a centroid-based grouping, clusters are represented by a central vector, which may not really be a member of the data set. At the point when the number of clusters is fixed at k , k -means clustering gives a formal definition as an optimization problem: find the cluster centres and allocate the objects to the closest cluster centres, with the end goal that the squared distances from the cluster are minimized.

The optimization issue itself is known to be NP-hard [16], and along these lines, the basic methodology is to search for approximate solutions. An especially well known approximate method is Lloyd's algorithm, often actually referred to as "k-means algorithm". It does anyway just locate a local optimum and is regularly run on numerous occasions with random utilizations. We additionally attempted a variety of the above picking the best of different runs, yet in addition, limiting the centroids to individuals from the data set picking medians or picking the initial centres less arbitrarily (K-means++) or permitting a fuzzy cluster assignment (Fuzzy c-means). Generally kmeans- type calculations require the number of clusters to be indicated in advance, which is taken into account to be among the most important drawbacks of these algorithms. Furthermore, the algorithms prefer clusters of roughly similar size, and they'll continuously assign objects to the closest centroid. This usually leads to incorrectly cut borders in between of clusters.

Secondly, we made use of Self-Organizing maps technique for clustering. Three variants 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 succeed in convergence. The hybrid SOM technique conjointly was implemented in a dynamic fashion and took close to 2000 to 2500 iterations to converge. But, the most 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 favoured self-organizing map (SOM). The GSOM was developed to deal with the problem of identifying an appropriate map size within the SOM. It starts with a minimal

number of nodes and grows new nodes on the boundary supported by a heuristic. By using the value referred to as Spread Factor the data analyst has the ability to manage the growth of the GSOM.

All the beginning nodes of the GSOM are boundary nodes, i.e. each node has the liberty to grow in its own direction at the beginning. New Nodes are fully grown from the boundary nodes. Once a node is chosen for growing, all its free neighbour positions will be grown new nodes. The GSOM method we employed first initialized the weight vectors of the starting nodes with random numbers between zero and one and so calculated the growth threshold for the given dimensional data set according to the Spread Factor (SF). Then input was presented to the network. The weight vector was determined and mapped to the current feature map. An adaptation rule was applied to decrease the value of SF within the GSOM depending on the number of nodes existing within the map at a time and increased the winners error value (error value is the difference between the input vector and the weight vectors). We then grow nodes distributing weights to neighbours if the winner is a non-boundary node. We then initialize a learning rate and update at each epoch. We then repeat the procedure till all inputs are presented; node growth is reduced to a minimum level and convergence is achieved. Afterward, we enter the smoothening phase whereby we reduce the learning rate and fix a small starting neighbourhood; find the winner and adapt the weights of the winner and neighbours in the same manner as in the growing phase.

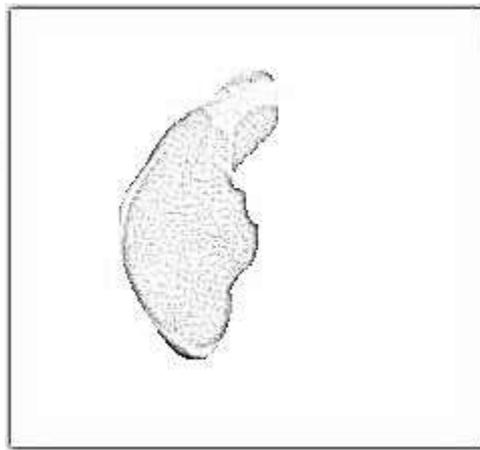


Figure 6: After Region Growing

We have used a straightforward region growing algorithm. This includes a simple region-based image segmentation technique that's conjointly called a pixel-based image segmentation technique since it involves the selection of initial seed points. We've used around 500 seed points and fully grown the image from those basic points to produce a 3D image of the tumour for better visualization. This approach to segmentation examines neighbour pixels of initial "seed points" and determines whether or not the pixel neighbours ought to be added to the region. The method is iterated on, within the same manner as general data clustering algorithm. Figure 6 above shows the same.

V. NEURAL NETWORK TRAINING

The literature review suggested [11] [13] helps in our scheme for the distinction of the malignant tumours from the benign ones. For choosing the training malignant nodules, we have a tendency to classify malignant nodules into many groups based on the visual appearance of patterns in terms of size, speculation, surface area, volume, contrast, location, colour, density, and risk. We used the strategy for a training set to determine systematically based on the ranking within the scores obtained from the trained set. We then selected many benign nodules from each group in such a fashion that benign nodules in every group cause completely different degrees of a problem in classification.

VI. RESULTS AND DISCUSSION

The proposed algorithm is evaluated on the premise of comparisons done with completely different approaches for segmentation and from the values obtained from feature extraction, applied on the region of interest within the renal, canal and bladder space as shown in figure 8. Features extracted for varied images of breast consisting cancer. The results of features of various methods of segmentation are given alongside the comparison of the various clustering algorithms used. The features we've extracted and compared are [given in fig 7]:

- i. **Mean:** The mean of the pixel values within the defined window estimates the value within the image during which central clustering occurs.
- ii. **Standard Deviation:** The Standard Deviation (σ) is the estimate of the mean square deviation of the grey pixel value $p(i, j)$ from its mean value. Standard deviation describes the dispersion among a local region. (Image size $M*N$).
- iii. **Moment:** It provides the measure of homogeneity of the image.
- iv. **Skewness:** It characterizes the degree asymmetry of a pixel distribution within the specified window around its mean. Skewness may be a pure number that characterizes solely the form of the distribution.
- v. **Kurtosis:** Kurtosis, measures the peak or flatness of a distribution relative to a normal distribution.

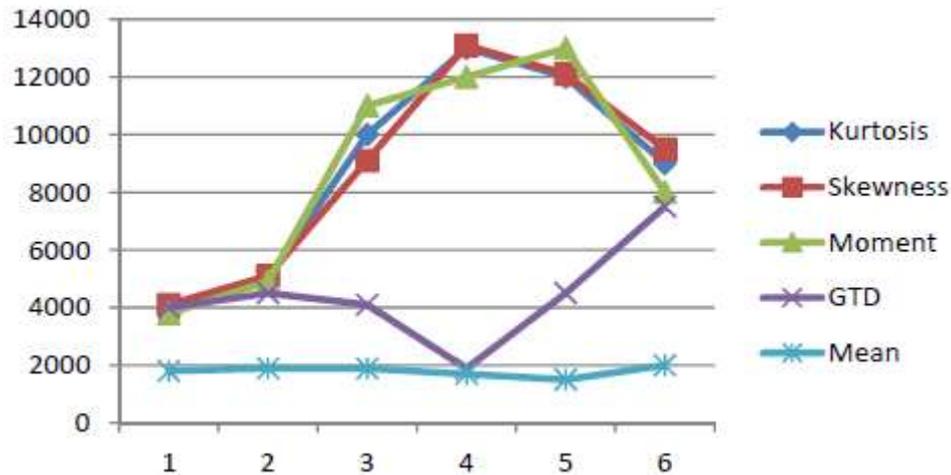


Figure 7: Comparative Line plot of all parameters

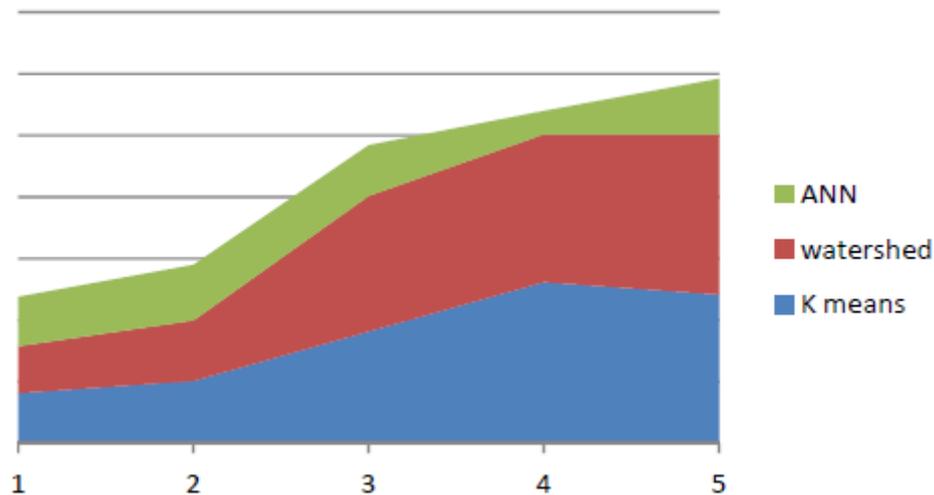


Figure 8: Comparative Time Complexity of all segmentation techniques

VII. CONCLUSION

In this paper, we've proposed a divide and conquer rule for Growing SOM to cluster and ANN to visualize if the growth is benign or malignant. The typical execution time is 0.85 sec as our technique iterates dynamically till convergence is reached for our data sets. To improve the complexity of the algorithm we increased the probable error value gradually and got a quicker and more efficient algorithm. But we found that doing this compromised the accuracy of the clustering. Since medical procedures rely on accuracy we've maintained an occasional level of probable error values. In case of the Renal, ureter bladder CT scans, the features extracted are helpful in recognizing the category of the image (normal/abnormal) by training and testing using the same image. The values obtained by different ways of segmentation shows variations within

the feature values for the same image. The feature extracted using segmentation supported by our proposed method has a new advantage of reducing false positive result and is economical for detection infiltration areas from CT scans.

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