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RESEARCH ARTICLE

RECONIZING TUMOR CELLS IN LIVER IMAGES USING PROBABILITISTIC NEURAL NETWORK

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ABSTRACT

Image processing has become an essential component in many fields of biomedical research such as tumor detection, automatically determining the volume of a heart chamber, screening lung scans for possible diseases. Different techniques for automatic detection of liver tumor involve various steps: image acquisition, segmentation, classification using neural network and optimization, and identification of tumor type. This paper presents a new approach to detect and segment liver tumors. The detection and segmentation of liver tumors can be formulized as novelty detection by pre-processing, segmentation feature extraction. The main objective of the proposed method is to precisely identify the presence of tumor cells in liver images as an early indication of malignant cells that may cause to the demise of patients. The proposed hybrid kernel classifier is compare with existing techniques which shows it have better accuracy, sensitivity and specificity.

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INTRODUCTION

Liver cancer is one of the major death factors in the world. Early identification and accurate staging of liver cancer is a critical issue in practical radiology. A liver lesion indicates to those abnormal tissues that are creating in the liver. Liver cancer is malignant TUMORs that develop on the surface or inside the liver. It is caused by chronic hepatitis B or C infections, obesity, alcohol, diabetes and hemochromatosis. Various types of liver tumors are identified by abdomen CT scan. It can provide precise information about the size, shape and position of any type of tumors in the liver. CT scan is more preferred than MRI as it allows for evaluating extra-hepatic abdomen, comfortable, patient-friendly protocols, less cost and shorter examination time. To diminish the demise rate due to liver cancer efficient treatment should be given to the patient [Geetha, 2013]. There are two types of liver cancer namely Primary Liver Cancer and Secondary Liver Cancer. Primary livercancer is the cancer that originates from the liver itself. Secondary liver cancer is the cancer which originates other organs but then spreads to liver Secondary liver cancer is also known as Metastatic liver cancer [Neha Bangar and Akash Deep, 2014]. An accurate liver segmentation method is critical for avoiding donor recipient volume mismatches in case of living donor liver transplantation (LDLT) surgeries and in defining the precise course of action for tumor resection procedures [Neha Bangar and Akash Deep, 2014].

Liver segmentation is a challenging task because of two main reasons. First, the liver's appearance and shape has a large inter-patient variability; it is one of the largest organ of the human body, after the skin, and imaged patients may suffer from heavy diseases such as cancer. Second, the neighboring structures have similar appearance in abdominal computed tomography (CT) or magnetic resonance (MR) images, there is little difference in the gray-value intensities of adjacent tissues [Neha Bangar and Akash Deep, 2014; Vimal Singh, 2012]. This promptslossof boundary for liver in regions close to organs such as: diaphragm, kidney, pancreas, stomach, and heart. At such boundary-less regions, segmentation using simple intensity based heuristic approaches, seed-initiatedregion growing techniques and edge-detection based evolution algorithms leak into the surrounding organs and need to be corrected manually. Due to the limitations of established techniques for liver segmentation, commonly used systems in clinical practice rely either on manual segmentations or on tools requiring an expert to segment the organ correctly. This process is monotonous, tedious and generally not-reproducible [Vimal Singh, 2012]. Segmentation of liver tumors is an essential task before any surgical intervention. An exact and precise examination of the lesions/tumors allows for accurate staging and evaluation of the available therapies that can be provided to the patient. It can help in deciding the best treatment approach as well as track the progress of the therapy over an interval of time. Also, tumor segmentation plays a vital role in the development of 3D surgical tools that can help and

guide the surgeon for the complete removal of the tumor rendering the patient free of the underlying disease [Rui Lu, 2005]. Figure 2displays tumor segmented from the liver region using threshold algorithm. The tumor regions are accurately identified from the CT image [Geetha, 2013]. Atumor contour of the initial slice is extracted by learning a SVM using randomly selected samples from a 2D CT slice. With the morphological operations (dilation and erosion), the contours after dilation and erosion are projected to its neighboring slices [Akanksha Sharma and Parminder Kaur, 2013]. The region within the dilation contour gives the suspicious tumor region and the region within the erosion region serves as the positive tumor samples to train the SVM classifier. After the tumor region of the neighboring slices is detected, the semi automatic approach is applied recursively on the next neighboringslice [Weimin Huang, 2013]. Segmentation is a technique that subdivides a digital image into multiple segments. Segmentation is based on one of two basic properties of intensity: similarity and discontinuity [Weimin Huang, 2013]. Detecting Similarities means to partition an image into regions that are similar according to a set of predefined criterion this includes image segmentation algorithms like thresholding, region growing, region splitting and merging. Detecting Discontinuities means to partition an image based on abrupt changes in intensity, this includes image segmentation algorithms like edge detection. Different Approaches for Medical Image Segmentation [Rajagopal, 2015]:

- Level set
- Edge Detection
- Threshold Based
- Clustering Based
- Region Based

Generally, tumor segmentation methods for a multi-stage segmentation technique comprise of five main stages and are explained below:

- Liver extraction: first step in the segmentation is to extract the liver region.
- Image de-noising: performed using a median filter to improve the contrast of the tumors in the liver and to reduce specular noise.
- Intensity based region growing: a semi-automatic step requiring a single point per tumor as a seed. The region growing aims at encompassing regions of similar intensity to segment the tumor.
- Localized contouring: coarse tumor segmentation obtained in step 3 is improved upon using a localized contouring algorithm to improve the detection of the tumor region.
- Rendering and volume calculations: tumor/tumors are rendered in 3-D space to display location, size and extent of the tumor within the liver. Volume calculations are carried out based on the number of voxels comprised within the tumor.

In the pre-processed image, the contrast is improved for well differentiation of the liver from its surrounding tissues with similar intensity levels. The noise removal and enhancement of contrast are done using filter and the fine details of the image are further improved. Then, morphological operations are applied to further improve the tumor region segmentation accuracy by extracting the image components from the binary image to extract the region shape. Liver tumor segmentation has several applications, such as treatment planning and evaluation, and computer-assisted surgery. Manual delineation of tumors is time-consuming and laborious, and the results depend on the observer [Akanksha Sharma and ParminderKaur, 2013]. For these reasons, there has been increasing research interest directed at segmentation methods that take advantage of existing computing capabilities.

Literature survey: Researchers in the past have investigated about this topic. Hong *et al.* [2013] proposed an automatic system to perform the liver tumor reorganization. Shape information is used to distinguish and perceive a lesion adjacent to the border of the liver and the lesion is extracted by means of Fuzzy C-means clustering technique. The proposed system performs a 3D consistency check based on three dimensional diagnoses to increase the recognition rate .This work is significant as it can help medical practitioner in focusing to the area of tumor and making it easy for classifying tumor as benign or malignant. As a result the accuracy of the C-means method and is very less, near to the actual image [Neha Bangar and Akash Deep, 2014]. Choudhary *et al.,* employed fixed threshold methodology for allpixels in the image and therefore works only if theintensity histogram of the input image contains neatlyseparated peaks corresponding to the desired object andbackground. Whereas, this technique cannot deal with images containing, a strong illumination gradient [Rajagopal, 2015]. Huang *et al.* Proposed Extreme Learning Machine, it was is a single-hidden-layer feed-forward neural network (SLFN). It had been shown that the learning speed was much faster than those of other learning algorithms such as SVM and other learning algorithms An advantage of ELM was the randomly generated hidden layer parameters {*wi, bi*} were independent of the training data. The ELM algorithm maps took input data from the input space to the L-dimensional hidden layer feature space. Later Kernel based ELM is introduced to enhance the robustness with a regularization coefficient**.** In RamanjotKaur*et al.*, an enhanced k-means clustering algorithm is implemented for liver segmentation in which the given dataset is classified into certain number of clusters and each cluster is provided with a centroid. Then, morphological opening was applied on the output of k-means clustering algorithm for better segmentation of cyst area in liver the image. This technique was not very effective with noisy or outlying points and with clusters of unequal sample sizes and different volume. The SSM (Statistical Shape Model) based segmentation framework was first proposed by Cootes *et al.* [1995]. The techniques involved in the SSM include shape correspondence, shape representation, and search algorithms. As the SSM-based approaches were sensitive to initialization an initial position of the model should be estimated in contrast with manual or the time consuming evolutionary algorithm [Heimann *et al.,* 2007] proposed earlier. Zhang *et al.,* [2010], proposed automatic liver segmentation included average liver shape model localization in CT via 3Dgeneralized Hough Transform, subspace initialization of Statistical Shape Model through intensity and gradientprofile and then deforming the model to liver contour through optimal surface detection method based on graph theory [Cootes, 1995]. Mika Pollari *et al.,* [2012] proposed Segmentation technique by semi automation that require only minimal initial user interaction They have proved that it could be to provide reliable results with accuracy similar to interactive methods [Deng, 2008].

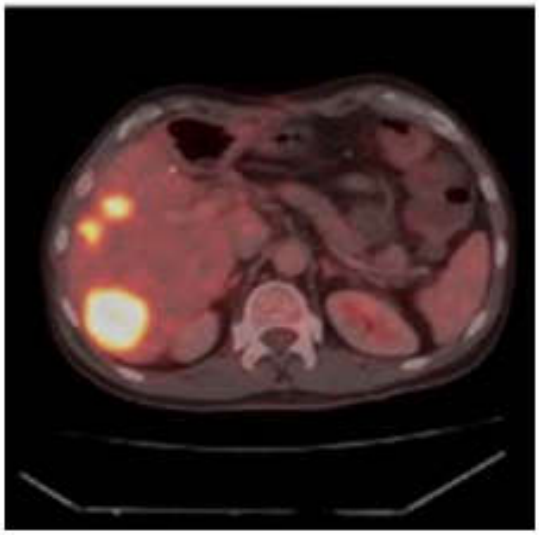


Figure 1. Original CT scan image of liver

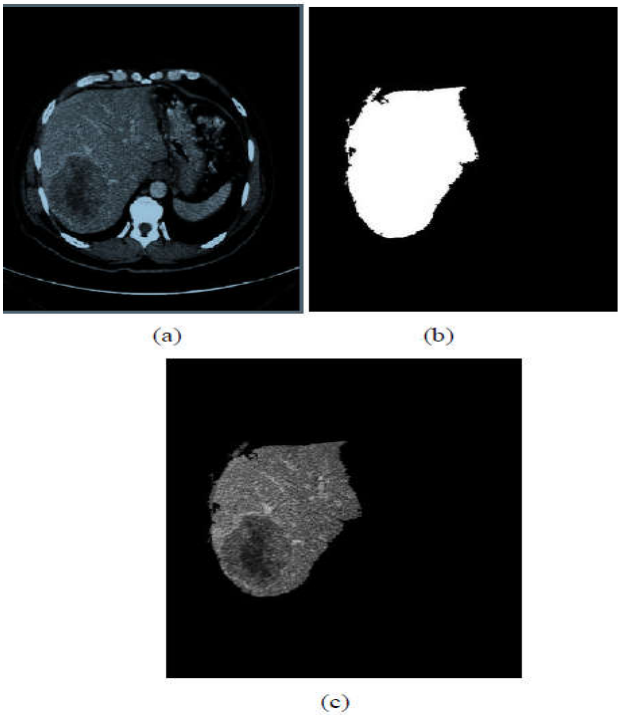


Figure 2. Segmented liver region (a) Original image (b) Morphological Image, (c) Liver Region

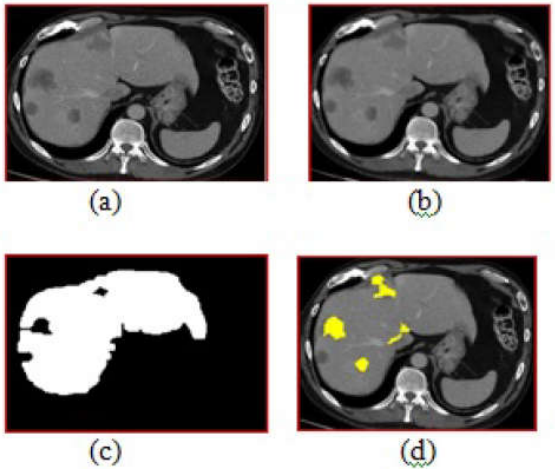


Figure 3. (a) Liver CT image; (b) Preprocessed image; (c) Feature Extracted image; (d) Tumor regions segmented image

Fully automatic methods generally suffer from lower accuracy and robustness, as well as a significantly higher computational cost.

RESEARCH METHODOLOGY

The main objective of the proposed method is to precisely identify the presence of TUMOR cells in liver images as an early indication of malignant cells that may cause to the demise of patients. Fig. 5 demonstrates the general architecture for the proposed framework. The proposed framework is sub divided into three stages: pre-processing, segmentation feature extraction, and detection of diseases. The primary stage executes the background estimation and enhance the image and reduce the speckle without destroying the features of liver images for diagnosis. The second stage the image is divided into non-overlapping regions and separates the lesions from the background. The boundaries of the lesions are delineated for feature extraction. To segment liver cancer from the images technique will be carried out. In the third stage the Gabor filter bank isutilize to extract the all conceivable area of malignant cells and presents each area by the feature extraction methods. Thus the final stage of this proposed method, it is use to categorize the TUMOR cells and detect the disease by using the hybrid classifier.

Pre-processing: In the proposed pre-processing algorithm the features of the voxels from the images on these three planes are generated and a training dataset is constructed using these features for classification process. With a proper selection of threshold for the outcome of the classification results, each voxel is labeled as either TUMOR and or non-TUMOR class. The proposed algorithm is tested based on the classifier on the region of suspicious TUMOR of each slice. different contrast and CT images also contain procedure noise. The contrast adjustment is done simply by normalizing the window level and range around liver intensity histogram. Moreover, in order to reduce the noise level gabor filter is adopted. The filtered blocks are then returned to their original positions. Because these blocksoverlap with each other, many different estimates were obtained for each pixel. For each TUMOR cells, we first generate an edge image and then superimpose it with two circles Lin and Lout having radius rin and rout, respectively, and centres corresponding to the centre of the TUMOR candidate's 2D ROI. Their parameters are defined in Eq. 1 and 2

$$rout = 4 + \frac{L}{2}, rin = rout/2, if(L \geq 10) \quad (1)$$

And

$$rout = 2 + \frac{L}{2}, rin = \frac{rout}{2} - 1, if(L < 10) \quad (2)$$

Where,

L is the length of the longer side of the filtered image. If the shape of a TUMOR candidate is approximately spherical, then a major portion of the TUMOR region is bounded by the circle Lin and the edge of the TUMOR is between the circles Lin and Lout.

Segmentation: Hybrid region-based segmentation schemes attempt to group pixels with similar characteristics into regions. Conventionally, these are global hypothesis testing techniques. The process can start at the pixel level or at an intermediate level. The region-growing based approaches can provide good results on contrast enhanced images.

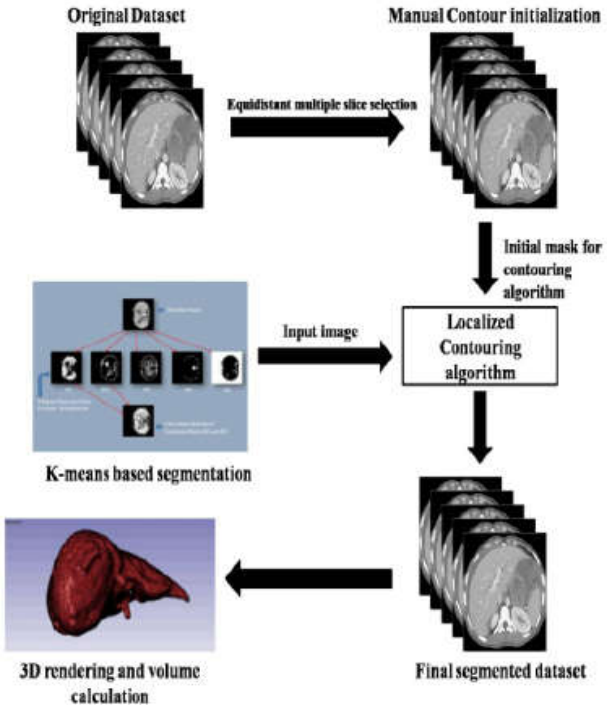


Figure 4. K-means based algorithm for 3D liver segmentation

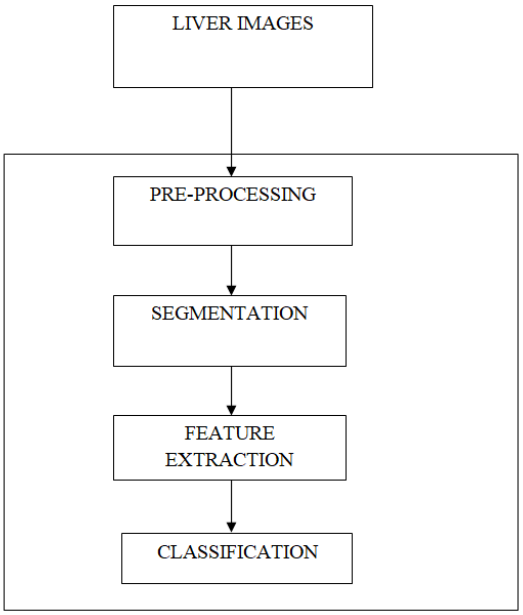


Figure 5. System Architecture diagram of the proposed system

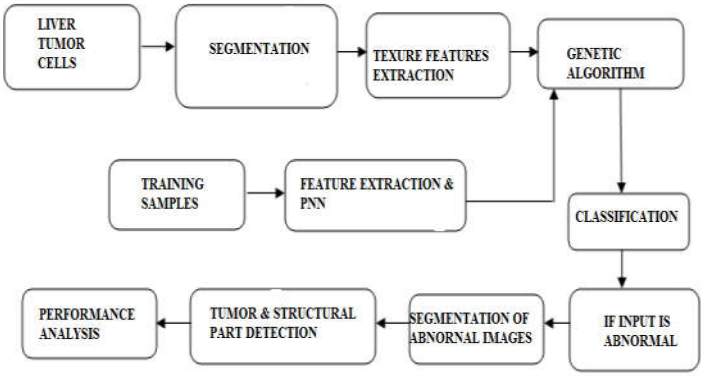
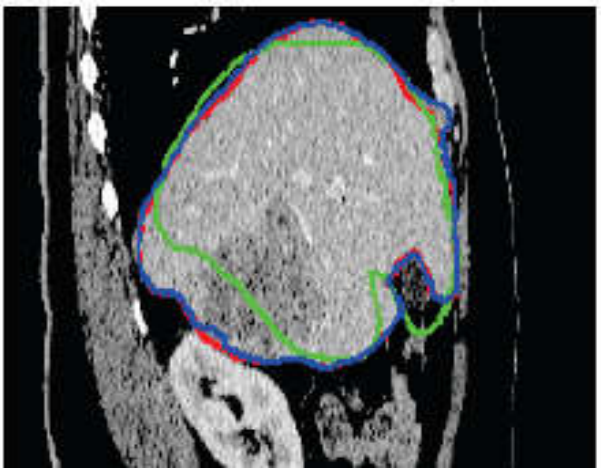
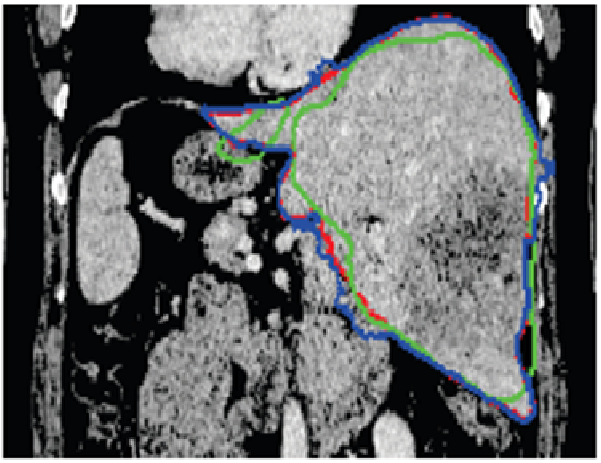


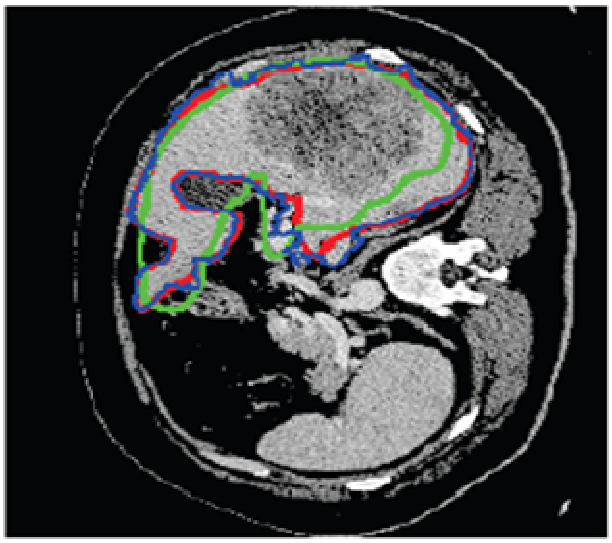
Figure 6. Block diagram for the feature extraction and classification process



(a)A sagittal slice of a liver after segmentation



(b) A coronal slice of a liver after segmentation



(c) A transversal slice of a liver after segmentation

These methods generally starts with the provision of a small region as seed point and proceeds with the addition of the neighbouring voxels, which are of homogeneous intensities, iteratively to the grown region. This continues until the segmented region is accurately obtained. There are two approaches in region-based methods: region growing and region splitting. In the region growing methods, the evaluated sets are very small at the start of the segmentation process.

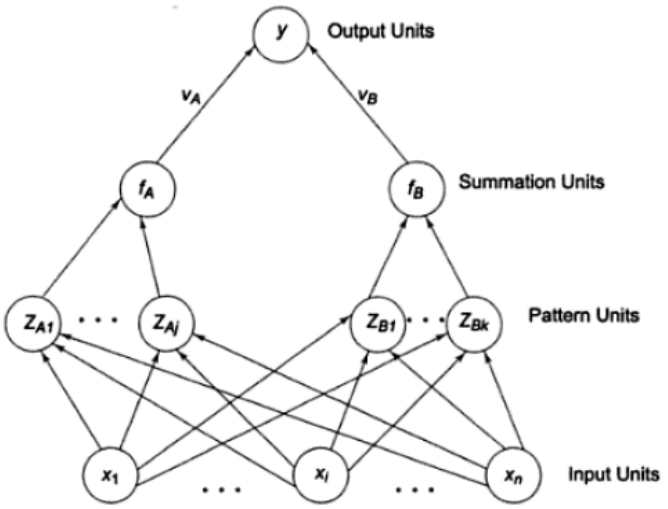


Figure 8. Architecture of PNN

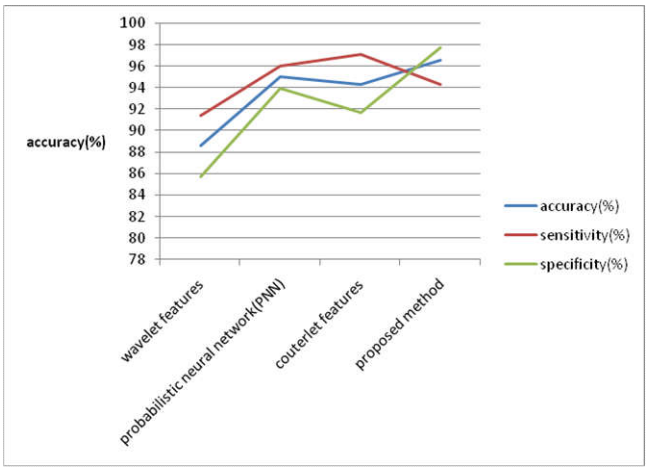


Figure 9. Performance analysis of extraction features

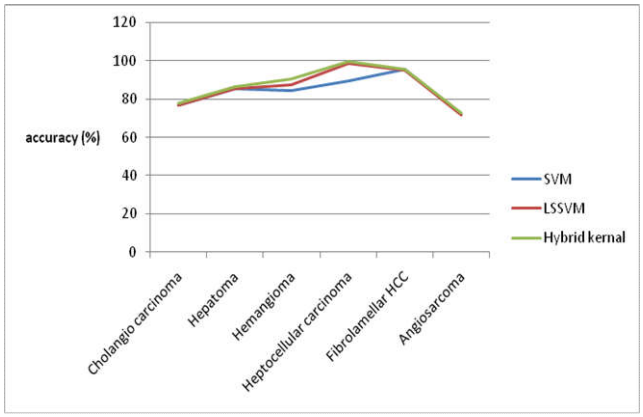


Figure 10. Performance analysis of classifiers

Table 1. Comparison of extraction features

Method	Accuracy (%)	Sensitivity (%)	Specificity (%)
Proposed method	96.56	94.33	97.78
Probabilistic Neural Network(PNN)	95	96	94
Counterlet features	94.3	97.1	91.4
Wavelet features	88.6	91.4	85.7

The iterative process of region growing must then be applied in order to recover The surfaces of interest in the region growing process, the seed region are expanded to include all homogeneous neigh bours and the process is repeated.

Table 2. Performance comparison of classifiers (accuracy in %)

Types of tumors	SVM	Lssvm	Hybrid kernal
Cholangio Carcinoma	76.97	77.18	77.52
Hepatoma	85.79	85.91	86.29
Hemangioma	84.38	87.50	90.63
Heptocollular carcinoma	89.88	98.91	99.91
Fibrolamellar HCC	95.85	95.19	95.89
Angiosarcoma	72.14	72.00	72.61

Fig. 7 shows the segmentations achieved in liver using the proposed hybrid method. The green contours show the initial shape obtained at each plane in the first step of the segmentation stage. It can be observed that the estimates obtained are very close to the reference segmentation contours, which are shown in red colour. The blue contours show the final shape to which our liver estimate evolves using the level-set formulation.

Feature extraction: For each segmented image its texture features are generatedin terms of its neighborhood mean and variance, intensity, intensity power, entropy, intensity co-occurrence, Law'st exture . The sefeatures are generated in 3D volume that makes them more representative.

$$Entrophy = \sum_{i=1}^{N} \sum_{i=1}^{N=} \mathrm{p(l,f)log2p(l,f)} \quad (3)$$

$$mean = \frac{1}{M*N} \sum_{i=1}^{M} \mathrm{x(i,j)} \quad (4)$$

The thickness of the pixels in the fundus image described as matrix quantized as numbers from 0 to 255 for every primary colour (Red, Green, Blue), yields about a $M \times N \times 3$ lattice of whole numbers. Based upon either ordinary or TUMORcondition, the image has different granular structures which are self comparable form at distinctive scale termed "texture". It denoted to the properties in admiration to the smoothness, roughness and consistency of any structure

Color feature extraction: In the color feature extraction normalized Histogram and Discrete Cosine Transform are used. In the Histogram methods, thereference image is compared with each image block in terms of its histograms. The difference between the individual peaks is taken and the mean squared difference is determined. Each block with relatively smaller difference matches the template and hence can be extracted as part of that texture. If the difference between the template and the current block is smaller than a particular threshold, then that feature is marked YES for that particular block. As in the case of color, we also evaluated the performance of these methods and found that for the training image the Histogram with bins method was the most accurate.

Wavelet feature extraction: Edge features are particularly important for some of the darker images. Fortunately, the training image was of normal quality and hence we did not use the edge feature. However, we do use it for some of the darker images in the set for testing. The Canny edge detection method with default threshold was used. Edge feature alone has very little efficiency; hence we need to combine it with a stronger feature, like color. It is combined with the color feature to describe the boundaries and inner regions of tumors in liver.

Counterlet feature extraction:' Multiscale and time-frequency localization of an image is offered by wavelets. But, wavelets are not effective in representing the images with smooth contours in different directions. Contour let Transform (CT) addresses this problem by providing two additional properties viz., directionality and anisotropy. Contour let transform can be divided into two main steps,

- Laplacian pyramid (LP) decomposing
- directional filter banks (DFB).

Probabilistic neural network (pnn): PNN is generally used in classification problems. When an input is present, the first layer computes the distance from the input vector to the training input vectors. This produces a vector whose elements indicate how close the input is to the training input.

The second layer sums the contribution for each class of inputs and produces its total output as a vector of probabilities. Finally, a whole transfer function on the output of the second layer picks the maximum of these probabilities, and produces a 1 (positive identification) for that class and a 0 (negative identification) for non-targeted classes. In figure 8,

- ***Input units:*** Hear input unit x(p), p=1,2,…..P are connected to all pattern units.
- ***Pattern units:*** Create pattern unit ZP .Weight vector for unit ZP is computed as WP=x(p). Unit ZP is either ZA or ZB unit.
- ***Summation units:*** Connect the pattern unit to summation unit. If x(p) belongs to class A, connect pattern unit ZP to summation unit SA. Else connect pattern unit ZP to summation unit SB.
- ***Output units:*** It sums the signals from fA and fB. Input vector is classified as class A if the total input to decision unit is positive. y is the final output.

Classifier: A neural network classifier is trained by using specially designed feature descriptor to distinguish normal liver and two types of tumor: hepatoma and hemageoma. In our work, we propose to use the hybrid kernel based Extreme Learning Machine to detect and segment liver tumor voxels in CT scans. This hybrid kernel based ELM achieves a better performance compared to traditional ELM, and it is faster than SVM classifier. There are certain steps involved in classification:

- The tumor samples (positive samples) and/or the non-tumor samples (negative samples) can be selected.
- From those samples, an ELM classifier is learned for voxel classification,
- Morphological smoothing (erosion and dilation) is done in order to remove the detected suspicious region of TUMOR and then segment it using this classifier.

To ease the selection of TUMOR training samples, one class ELM is proposed for detecting the tumor cells where the user only needs to select healthy liver samples. The two-class ELM classifier for automatic liver TUMOR detection assuming some training tumor samples are available.

Hybrid kernal elm: In the proposed hybrid kernel ELM,a positive regularization coefficient is introduced in order to make the learning system more stable. Assume H'H is nonsingular, the coefficient $1/\lambda$ is added to the diagonal of H'H in the more stable and with better generalization performance. We then can have,

$$\beta = H'\left(\frac{1}{\lambda} + HH'\right)e - 1$$

$$f(x) = h(x)\beta = h(x)H'\left(\frac{I}{\lambda} + HH'\right)e - 1\ (T)$$

The output function can be written as,

$$f(x) = h(x)H'\left(\frac{I}{\lambda} + HH'\right)e - 1\ (T)$$

The hidden layer feature mapping **h**(**x**) need not to be known to users, instead its corresponding kernel *K* (**u**, **v**) can be computed. Here the Gaussian kernel is used, *k* (**u**, **v**) = exp(-γ||**u**-**v**||2). The enhanced kernel ELM was designed for two class classification and regression. However when only one class data is used for ELM training, it is showed one class classifier.

- Let's assume tj=1, which means only one class data is used for training. The result β becomes a linear approximation mapping g(·) to T.
- In geometry, it is a hyper plane approximation. Then it can be shown that the difference |f(x)-1| is the distance of any point (a sample, in either class) to the hyper plane constructed by the ELM.
- Thus if the hyper plane can be used to represent one class, any point away from the plane will indicate that it is not in the same class, which means we can use it to detect novelty.
- In the original ELM, as it is only a linear transformation, the one-class mapping is not represented accurately using the hyper plane. The detection result is thus not satisfying. With the hybrid kernel transform the data is mapped to a higher dimension space, similar to many other kernel methods

Genetic Algorithm: It utilizes three fundamental administrators, selection/generation, cross over and mutation. It considers an approximate of variable and the matching solution as initial resolutions. Any estimation of sigma has been selected as the initial variable and the matching fitness function which is the normal exactness over the three folds of NN classifier is processed. In the generation function, different cases (runs) of the variable sigma are produced and a matching bit string is produced. A cross over points is selected and the bit function is partitioned into two sections. Two parts of bit strings really belonged to various strings are employed to finish cross over operation. A certain rate of strings is connected with cross over operation only and rest are left unaltered. Small amount of function in mutation probability are characterized and also given subsets of strings which was selected from the cross over function. A given bit position is selected for cross over function and the matching bit is flipped. Again all new strings are examined with the matching fitness function capacity. The strings with grater fitness function capacity are held and strings with less fitness function capacity are rejected. This completes single generation. The procedure is continued for so many generations until it achieves the very higher fitness function value of the strings and hence it enhances the system.

Performance analysis: The performance of the algorithm is evaluated using the measures like accuracy, sensitivity, specificity, positive predictive value or precision and negative predictive value defined as follows:

$$Accuracy = \frac{TP + TN}{TP + TN + FN + FP}$$

$$Sensitivity = \frac{TP}{TP + FN}$$

$$Specificity = \frac{TN}{FP + TN}$$

Where,

TN=True negative
TP=True positive (carcinoma cases are correctly classified as hepatoma (TP))
FN=False positive (hemangioma (FN))
FP=False positive

Conclusion

In this paper, the proposed framework for identifying tumor cells in the various phases have been presented. In this System, it is consists of three stages such as preprocessing, segmentation, feature extraction and classification, have been proposed. The preprocessing stage extracts backgrounds pixels to empower the working on further stages on the foreground pixels only. In the segmentation process the ROI method is carried out whereas region growing is adopted here. In the region growing methods, the evaluated sets are very small at the start of the segmentation process.

After segmentation, the feature extraction had done it shows that the proposed method have high accuracy than counter let, wavelet, PNN methods. The extracted images are then classified by using the best classifier, however the hybrid kernel classifier is used here. Thus the stimulation results had displayed that proposed system results am average accuracy of 96.56%, sensitivity of 94.33% and Specificity of 97.78% respectively. Thus the proposed modal had enhanced the overall performance and increases the efficiency of the system. Hence the proposed methods is significant than the previous methods and it can be utilized as an efficient diagnostic tool by the clinicians during the detection of tumor cells.

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