VOLUME BASED SEGMENTATION AND CLASSIFICATION OF LIVER TUMOR USING MARKER CONTROLLED WATERSHED TRANSFORM

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ABSTRACT

Tumors in liver have become a disease of major concern in recent times. Detection of the tumor and finding whether it is cancerous or non-cancerous is a crucial task for diagnosis of liver tumor as there is no established framework for evalution of medical imaging segmentation till now. Segmentation techniques can help in detecting these and also separating the region of interest from the rest of the neighbouring tissues of same intensity. This paper presents a method for detecting tumors in liver and separating the liver organ from its neighboring organs using Marker Controlled watershed segmentation. It also presents a classification model to categorize the tissues into tumored and untumored cells. This technique could correctly detect and classify the tumor tissues in liver in the patients' computed tomography images. The accuracy of the classification model is satisfactory and the estimated sensitivity and specificity correctly validates the segmentation and the classification model used for this research.

Keywords: ROI, Marker Controlled watershed segmentation, Edge detection, tumor, CT image, median filter, SVM

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INTRODUCTION

Hepatocellular carcinoma (HCC) is a primary liver cancer disease in recent times. It has been found that most of the liver tumors gets transformed to secondary tumors in due course of time. Hence clinical applications like detection of the tumor tissues, separating the tumor tissues from the healthy tissues, planning for its treatment and its frequent monitoring requires accurate segmentation of liver and liver tumors. Hence, a computer-aided detection (CAD) system with high accuracy level in segmentation methods for tumors would be an effective approach to treatment of liver cancer. The main goal of this paper is to propose an effective segmentation technique for tumor detection.

It has been found that Computed Tomography (CT) images provide high resolutions with proper anatomical information. But a normal CT image has the possibility of high level of noise in it. The noise in CT images can be discarded with the help of preprocessing step. Preprocessing discards the unwanted noise elements from the input image.

Liver tumors normally have a high variability in their appearance as the size and the structure of the tumors vary largely and these tumors may appear practically anywhere within the liver with ill-defined edges. Therefore, their localization also varies a lot. Moreover, the liver and tumor tissues need to be separated from the neighboring organ tissues like spleen, stomach and heart which have similar intensities and fuzzy boundaries.

The tumors in liver sometimes appear darker as compared to the neighboring healthy liver tissues. This is termed as hypodense tumors. While in case of hyperdense tumors, the tumor appears brighter. The images captured vary from one patient to another and also vary on the type of the lesions, the state of the tumor tissues and the equipment, timing of capturing, settings of the camera and the contrast method used for performing the scan.

Segmentation identifies and separates the liver tissues from the tumor tissues in the liver. It also provides details of the exact localization of the tumors in the organ and extracts the region of interest by removing the portions which are not required to be analyzed for treatment planning and monitoring. Some treatment planning procedures for liver tumors are mentioned in papers [23],[24], [25] and [26]. In Selective Internal Radiation Therapy (SIRT) treatment, the medicinal dosage to be given to a patient is found by analyzing the volumetric capacity of the tumor tissues. The volume of cancerous tissues inside the organ can be calculated by segmentation technique as it segments the tumor tissues from the neighboring healthy tissues and computes its volume. Tumors with small size are difficult to detect using segmentation method. The tumor size in a liver organ is measured by calculating the maximum axis of the tumor in the computed tomography images. According to RECIST standard [3], first the maximum axis of the tumors needs to be calculated. Thereafter only those tumors that have an axis of greater than 10 mm should be considered as the tumors, while the rest of the tumors should be ignored. When treatment starts for a particular patient, the maximum axis is computed for the tumors at regular intervals to check for an increase or decrease in the length. If the axis length of the tumor in the liver is decreased by 30% or more, it is considered that the patient has partially responded to the treatment. However, if there is an increase of 20 % or more in the tumor axis length, it is considered that the patient has a progressive tumor. Segmentation of the tumor tissues is an efficient way to detect the tumors and extract important information about it. Segmentation techniques are many and not a single technique alone would effectively segment the tumor tissues. Moreover, the segmentation technique should be suitable for the medical CT images. This method should recognize or identify the object of interest from its neighboring organs with similar intensity and then segment the image to extract meaningful information.

LITERATURE REVIEW

Many semi-automatic and automatic techniques have been proposed by researchers since many years to improve the effectiveness of liver tumor segmentation. These techniques are based on techniques mentioned in research papers [6–19]. Techniques based on region growing, thresholding and clustering are easy to implement and has low computational cost but considers only the intensity of the liver tumor thus resulting in blurred tumor boundaries. However, this can be overcome by implementing algorithms to preserve the edges. Another important thing to focus is the intensity of spleen, stomach and heart and their boundaries with the liver which is fuzzy. Hence, we need to focus more separating these from the liver during the segmentation process. The watershed transform segmentation can the nearby organs and locate the region of interest. But in doing so the low contrast boundaries are not properly detected and also oversegmentation is an issue. This technique is also sensitive to noise.

Here comes the utility of marker controlled watershed technique which uses a marker function. This marker function helps to determine the possible number of ROI and its possible localization previously.[31] Thus the pitfall of watershed transform is overcome. Few of the comparative analysis of marker controlled watershed transform with other segmentation techniques is described below in table 1.

Table 1: Analysis of Marker Controlled Watershed Technique with other segmentation approaches

References	Segmenation technique	Performance
Stawiaski et al. [32]	Watershed and graph cut	Segmentation time of watershed transform is negligible. Graph cut technique consumed lot of time
Ng H et al. [33]	Watershed transform algorithm	Accuracy-92.2% is achieved with region merging based on texture.
Prasad et al. [34]	Marker Controlled Watershed Segmentation and Thresholding approach	Accuracy of Marker Controlled Watershed-(85.165%), Accuracy of Thresholding-(81.835%). Segmented image quality was found to be much better.
Rahman et al. [35]	Marker controlled watershed transform and K-Means clustering technique	Marker controlled watershed detected tumor cells in lungs with better segmentation results.
Kanitkar et al. [36]	Thresholding and Marker controlled watershed transform	Accuracy of Marker controlled watershed transform-100%. Detection of cancerous and non-cancerous tumors in lungs was done and also the tumor stage was detected accurately.
V. Grau et al. [37]	Watershed Transform	Computation cost is less.Reduces the post processing effort.
C Wei-bin and W Zhejiang [38]	Watershed Transform	Accuracy level is satisfactory.
A kaur and A Verma [39]	Marker Controlled Watershed	Accuracy level is better than watershed transform.

Many of the techniques described in table 1 cited the problem of marking region optimization in case of marker controlled watershed technique. The solution to this problem is mentioned in this paper by preprocessing the input image using median filter and then applying the segmentation algorithm on the filtered image.

MATERIALS AND METHODS

Image processing techniques are used in this research and implemented in MATLAB R2019a and python. Median filter is applied as a preprocessing step to remove unwanted noise from the image and marker controlled watershed transform is used for segmentation. It has been found that the performance is enhanced by this combination. The dataset used for this research is publicly available liver tumor clinical dataset 3Dircadb from Research Institute against Digestive Cancer (Ircad 2016) so that real time data would be used to evaluate the proposed model. The patient tumor image is captured at different enhancement phases.

PROPOSED METHODOLOGY

In the first phase of preprocessing, Median filter is applied on CT images. Filtering the image using median filter will reduce distortion and noisy elements present in the image and will also preserve the edges of the image.

Thereafter segmentation algorithm is implemented to the preprocessed image to detect and segment the region of tumor from the liver organ as explained below.

I. Marker Controlled Watershed Transform:
The simulated flow of Marker controlled watershed transform algorithm for liver tumor detection is as follows.

1. Determine the marker function for localizing the ROI using gradient magnitude.

2. Calculate the foreground marker function.

3. Calculate the background marker function.

4. The marker function is then formulated.

5. Calculate the watershed transform by applying it on modified marker function.

II. **Support Vector Machine Classifier**:
The Support Vector Machine (SVM) uses a multi class learning technique to categorize the tumor tissues into different classes. SVM is considered most suitable and efficient classifier with high dimensionality feature spaces. It is a two-class classifier.

To start with the SVM classifier, the training and testing datasets is formed in order to train the model. Thereafter, classification of the dataset using SVM for untumored and tumored tissues in liver is computed.

For this research work, datasets of five different patients are considered. Contrast enhanced computed tomography images are captured for all the patients at different time intervals and then SVM is used to classify the patient liver into tumored and untumored liver cells. The predictive analysis of the model is presented in this paper on the basis of the confusion matrix or error matrix evaluated in the results.

The following parameters are calculated for the above procedure and the results obtained are described in the results section:

1. **Accuracy:** It is calculated as follows:

Accuracy=$\frac{\mathrm{TP+TN}}{\mathrm{TP+TN+FP+FN}}$* 100

2. **Sensitivity:** It is an evaluation measure borrowed from statistical decision theory measures [45].

Sensitivity= $\frac{\mathrm{TP}}{\mathrm{TP+FN}}$ * 100

3. **Specificity:** It is an evaluation measure borrowed from statistical decision theory measures [45].

Specificity = $\frac{\mathrm{TN}}{\mathrm{TN+FP}}$ * 100

4. **Dice Similarity Coefficient (Dice):** Many researches [41,42,43,44] have used Dice as the main parameter for evaluation of segmentation model accuracy. It is a spatial overlap metric and ranges from 0 to 1,where 0 would mean no spatial overlap between two segmentation outcomes whereas 1 would specify complete overlap.

Dice=$\frac{2*\mathrm{TP}}{2*\mathrm{TP+FP+FN}}$

5. **Volumetric Overlap error (VOE):** The value of VOE if 0 would mean perfect segmentation model.

VOE=$1-\frac{\mathrm{TP}}{\mathrm{TP+FP+FN}}$

Where,

True positive (TP) refers to a test result that correctly indicates the presence of tumor tissues

True negative (TN) refers to a test result that correctly indicates the absence of tumor tissues

False positive (FP) refers to a test result which wrongly indicates that a tumor tissue is present

False negative (FN) refers to a test result which wrongly indicates that a tumor tissue is absent

The confusion matrix is formulated for calculation of parameters which has been described in the above explanation.

EXPERIMENTAL RESULTS
The original CT image goes through the preprocessing stage in order to remove the existing noise. Thereafter, the segmentation function is calculated using gradient magnitude. The output of segmentation algorithm is illustrated in series of diagrams as shown in figure 1(a)-(j).

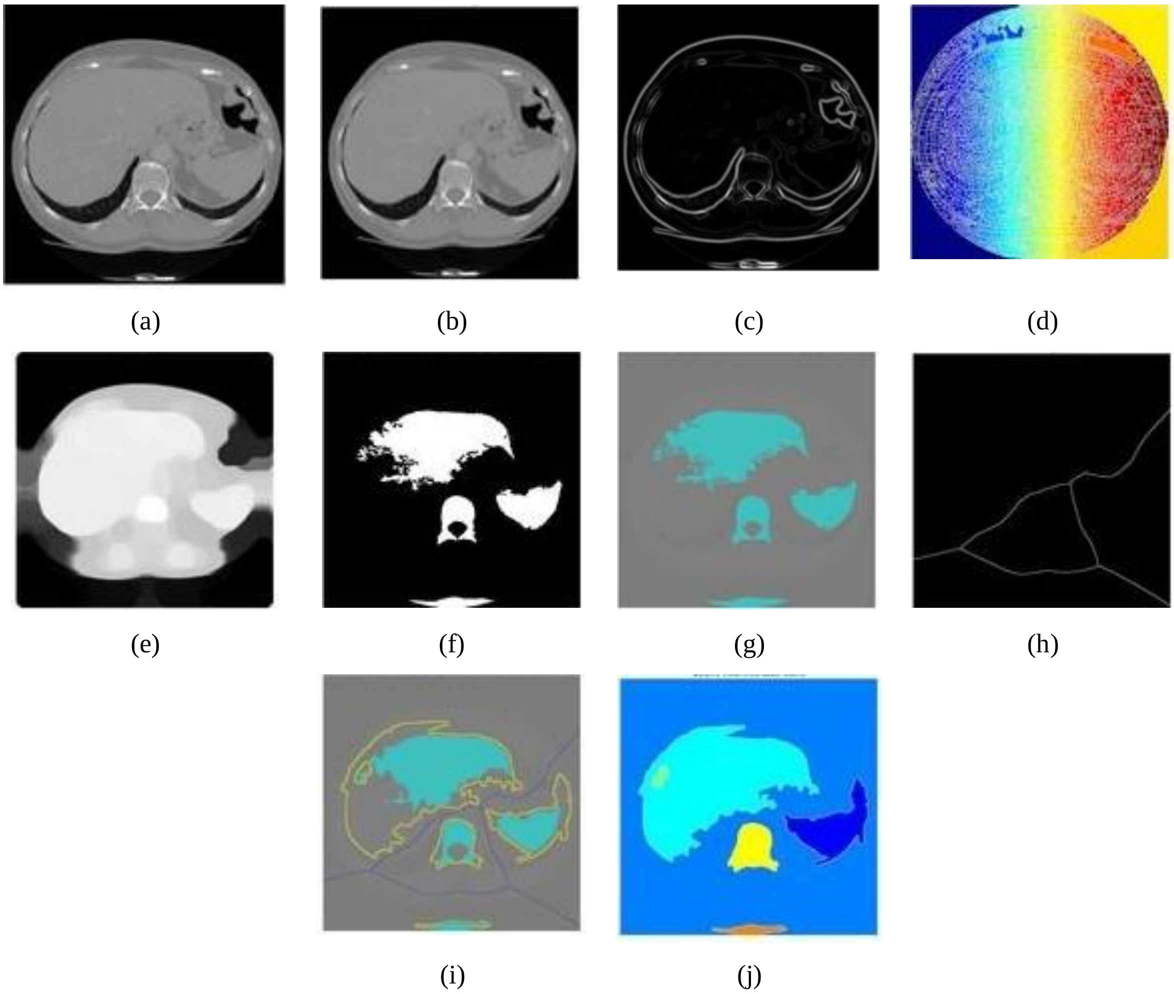

Figure 1. (a)original image, (b) filtered image, (c) gradient magnitude, (d)watershed transform, (e) opening and closing, (f)Regional maxima of opening-closing by reconstruction, (g)Regional maxima superimposed on original image, (h)Watershed Ridge lines, (i)Markers and object boundaries, (j)Coloured Watershed Label Matrix

The confusion matrix is then evaluated in order to determine the effective performance of the classification model using a given set of CT images of patients' data. This matrix helps in finding the errors present in the classification model. Using the parameters of the confusion matrix, the accuracy of tumored tissues is found to be 92%. The sensitivity comes out to be 99% and the specificity of the model is formulated to be 96%. The DICE is calculated to be 95.71% and VOE is 8.21%.

The figure 2 is the confusion matrix for our segmentation and classification model.

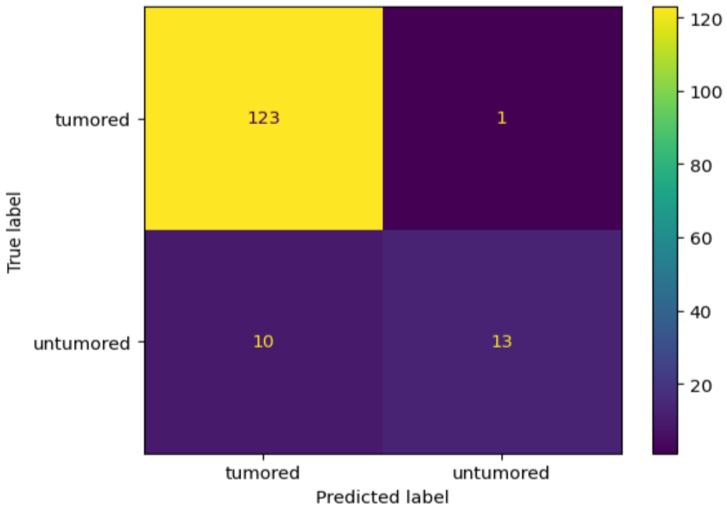

Figure 2: Confusion Matrix

CONCLUSION

The proposed algorithm of marker controlled watershed identifies the different objects:organs in this case, and separates them with significant watershed ridge lines. Tumors in the liver are identified well using this approach. The drawback of optimization problem has been sorted by combining the median filter preprocessing step with that of marker-controlled watershed segmentation technique. The results of segmentation found are satisfactory with the algorithm identifying the different neighbouring organs and detecting the region of interest in the said organ. Thereafter SVM is used to classify the patients CT images into untumored and tumored tissues. SVM is a powerful tool to help improve the decision-making process during tumor diagnosis. The confusion matrix is a powerful tool which helps in evaluating the performance of the classification model, i.e, SVM in this case. It helps in determining the number of correct and incorrect predictions made by a classification model. The accuracy achieved is highly satisfactory and outperforms many models used by researchers.

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