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Segmentation of liver tumor on CT images by using Modified DRLS and FLICM

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ABSTRACT

For view the internal structures of human body such as liver, brain, kidney etc have wide range of different modalities for medical images are provided now a days. Computer Tomography is one of the most significant scanning method used for studying various techniques and also used to calculate the performance analysis of the liver tumor. Segmentation method is used for the detection of tumor from the CT scan is proposed. Gaussian convolution is used for smooth the CT image and level set *al*gorithm is used for liver segmentation automatically. In this, Distance Regularized Level Set Method is used. Fuzzy Local Information C-Means Clustering Algorithm (FLICM) is used to extract liver tumor region automatically from the liver segmentation image. Morphological operations are used as post-processing. Finally, the experiment result shows that the method can achieve high Accuracy, Sensitivity, and Specificity based on Ground truth image.

KEYWORDS: Computer tomography image, fuzzy local information c means clustering, level set, tumor, morphological operator.

INTRODUCTION

Imaging techniques such as Computed Tomography (CT), Magnetic Resonance Imaging (MRI), or Positron Emission Tomography (PET) are nowadays standard instruments for the diagnosis of liver pathologies such as cirrhosis, liver cancer, and fulminant hepatic failure. Among these techniques, CT images are often preferred by diagnosticians since they provide more accurate anatomical information about the visualized structures, thanks to their higher signal- to- noise ratio and better spatial resolution. CT scans indeed offer exceptional resolution and good accuracy for the liver metastases. For example, sensitivities of respectively 69-70% and 73% have been shown for metastases and colorectal ones, as well as specificities of 86-91% and 96.5%. These image characteristics, and the advances in the digital image processing techniques, motivate the great deal of research work aimed at the development of computerized methods for the automatic liver analysis.

This is usually done by expert radiologists, by manually tracing the liver contour on each CT slice. [1] proposes that the liver is one of the most important organs in the human body. It carries out a variety of functions including filtering the blood, making bile and proteins, processing sugar, breaking down medications, and storing iron, minerals and vitamins. The liver is prone to many diseases such as hepatitis C, cirrhosis, and liver cancer.Liver cancers are deadly diseases with an important frequency in the world.However, the detection of liver tumors is challenging due to the small observable changes between healthy tissues and tumoral ones. Then, the whole segmentation process should take no more than a few minutes in order to satisfy the speed standards of physicians. Figure below shows an example of CT slices of patients suffering from liver cancer.
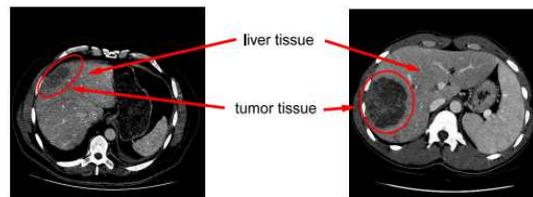
Fig. 1: Examples of CT slices of patients suffering from liver cancer.

II Related Work:

Luo *et al* [7]. presented an automatic liver segmentation that is categorized into three main classes including gray level based method, structure based method and texture based method. Li *et al* [8]. presented a segmentation of liver CT scans using fuzzy c-mean clustering and level set was present. First, the contrast of original image is enhanced to make boundaries clearer. Second, a spatial fuzzy c-mean clustering combining with anatomical prior knowledge is employed to extract liver region automatically. Thirdly, a distance regularized level set is used for refinement. Finally, morphological operations are used as post-processing. Kumar *et al* [9]. presented automatic and effective segmentation using connected region growing facilitated by pre-processing and post processing functions for automatic segmentation of liver and Alternative Fuzzy C-Means clusters for lesion segmentation. Danciu *et al* [10]. presented a 3D liver segmentation, based on the 3D Discrete Cosine Transform applied on volume blocks for feature extraction. The segmentation is refined in a post-processing step through a 3D median filtering, 3D morphological operations, and 3D connected components analysis was presented. Yang *et al* [1]. presented a liver segmentation method based on the fast marching and graph cuts methods was introduced. The algorithm is composed of three main steps: first, rough edge of the liver is extracted from the CT image by fast marching method. Second, hard constrain of the foreground and background which is used for initial calculation of graph cut. Third, the graph cuts are utilized to refine the segmentation boundary of the liver. Chen *et al* [12]. Presented a segmentation method consists of two steps. In the first step, we use K-means clustering and a priori knowledge to find and identify liver and non-liver index pixels, which are used as "object" and "background" seeds, respectively, for graph-cut. In the second step, a graph-cut based method is used to segment the liver from the low-contrast Open MR images.

IIIMethodology:

There is different segmentation techniques used for images segmentation but in this thesis level set segmentation method is used. Gaussian convolution is used to smooth the images and distance regularized level set method is used for image segmentation. Clustering method and morphological operations is mainly used in these liver segmented images and to identify the tumor from the segmented liver image.

The input CT image is converted into the Gray scale image. The gray scale image is smoothed by Gaussian convolution. Secondly, the DRLS method is used to segment the liver.Figure below shows the flow chart of the proposed system.
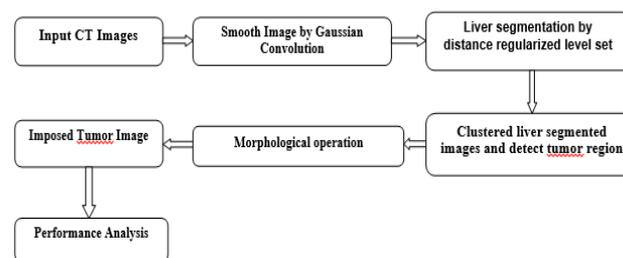

Fig. 2: Methodology

Distance Regularized Level Set Method:

A level set method termed as DRLS model. The DRLS model uses an edge-based active contour method to drive the Level Set Function (LSF) to the desired boundary, and provides a simple and efficient narrowband implementation without reinitialization. [2] proposes the problem with the DRLS model in the case of liver segmentation is that the curve will evolve and deviate from the liver boundary in the region with weak or without edges. In this contribution, we will modify the DRLS model by adding a new balloon force to guide the evolution process and discourage the evolving contour from leaking at a region with a weak or without an edges and from going far from the liver boundary.

IV Modified DRLS Model:

Since the liver boundary to be segmented is not far from the contour propagated from the previous slice, a shape and intensity prior information will discourage the evolving contour from leaking at a region with a weak edge or without an edge. We have modified the DRLS method by adding the probability density energy term to the evolution equation and use it as a balloon forces to control the direction and the speed of the evolution process. [3] proposed that the DRLS model, evolving the contour in the direction of the object boundary, speeding up the evolution process when the evolving contour is far from the object boundary and slowing down the evolution process when the evolving contour is close to the object boundary. The second stage concerns with the refinement of the segmentation.

$$E(\phi) = \rho.R_p(\phi) + \lambda.L_g(\phi) + \alpha.B(\phi)$$

Where ρ, λ and α are the coefficients of the regularization term, the length term, and the probability term, respectively. This energy functional can be minimized by solving the following gradient flow:

$$\frac{\partial \phi}{\partial t} = \rho.div(d_p(|\nabla\phi|)\nabla\phi)\lambda.div\left[g\frac{\nabla\phi}{|\nabla\phi|}\right] + \delta_g(\phi).\alpha.B(\phi)$$

The above procedure is repeated until the contours in all 2D slices of the 3D image are segmented. A 3D liver surface is reconstructed from the contours segmented from all 2D slices. The figure (1) shows the input image. Figure (2) shows the applied DRLS level set. Figure (3) shows the segmented liver region by DRLS method.
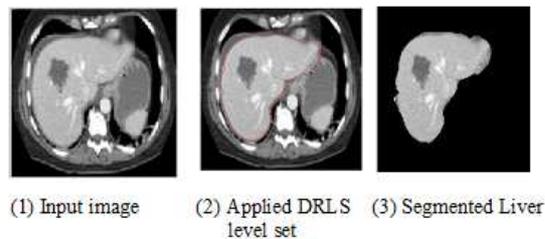

(1) Input image   (2) Applied DRLS   (3) Segmented Liver
level set

Fig. 2: Applied DRLS Level Set.

V Clustering:

FLICM clustering is applied to segmented liver image.The FCM algorithm is one of the most widely used fuzzy clustering algorithms. However, one disadvantage of standard FCM is not to take into account any spatial information in image context, which causes it to be very sensitive to noise and other imaging artifacts. FCM algorithm functions well on segmenting most noise-free images but it fails to segment images corrupted by noise, outliers, and other imaging artifacts, such as the intensity in homogeneity induced by the radio-frequency coil in MRI. In this paper, a novel and robust FCM framework for image clustering called FLICM clustering algorithm. In order to overcome the above mentioned disadvantages a new fuzzy factor G in FCM objective function is needed. [4] The new factor should have some special characteristics:

➢ To incorporate local spatial and local gray level information in a fuzzy way in order to preserve robustness and noise insensitiveness.

➢ To control the influence of the neighbourhood pixels depending on their distance from the central pixel.

➢ To use the original image avoiding pre-processing steps that could cause detail missing.

➢ To be free of any parameterselection.

[5] The novel fuzzy factor G_{ki} defined as:

$$G_{ki} = \sum_{\substack{j=N_i \\ i\neq j}} \frac{1}{d_{ij}+1}(1-u_{kj})^m\|x_j - v_k\|^2$$

From Stelios and Vassilios [4] the $i-th$ pixel is the centre of the local window, k is the reference cluster and the $j-th$ pixel belongs in the set of the neighbours falling into a window around the $i-th$ pixel $(N_i).d_{i,j}$ is the spatial Euclidean distance between pixels i and j, u_{kj} is the degree of membership of the $j-th$ pixel in

the $k-th$ cluster, m is the weighting exponent on each fuzzy membership, and v_k is the prototype of the centre of cluster k. It is easy to see that the factor G_{ki} is completely free of using any parameter that controls the balance between the image noise and the image details. The control of this balance is automatically achieved by the definition of the fuzziness of each image pixel (both spatial and gray level). Also, by using d_{ij}, the factor G_{ki} makes the influence of the pixels within the local window, to change flexibly according to their distance from the central pixel. Thus more local spatial information can be used. It is worth indicating that the shape of the local window used in our experiments is square, but also, windows with other shapes such as diamond or circle can easily be adapted to the algorithm.

By using the definition of G_{ki}, we now propose a robust FCM framework for image clustering, named FLICM clustering algorithm. It incorporates local spatial and gray level information into its objective function, defined in terms of:

$$J_m = \sum_{i=1}^{N} \sum_{k=1}^{c} \left[u_{ki}^m \| x_i - v_k \|^2 + G_{ki} \right]$$

The two necessary conditions for J_m to be at its local minimal extreme, with respect to u_{ki} and v_k is obtained as follows:

$$u_{ki} \equiv \frac{1}{\sum_{j=1}^{c} \left(\frac{\| x_i - v_k \|^2 + G_{ki}}{\| x_i - v_j \|^2 + G_{ji}} \right)^{\frac{1}{m-1}}}$$

$$v_k = \frac{\sum_{i=1}^{N} u_{k_i x_i}^m}{\sum_{i=1}^{N} u_{ki}^m}$$

Thus, the FLICM algorithm is given as follows:
Step 1: Set the number c of the cluster prototypes, fuzzification parameter m and the stopping condition ε.
Step 2: Initialize randomly the fuzzy partition matrix.
Step 3: Set the loop counter b = 0.
Step 4: Calculate the cluster prototypes.
Step 5: Compute membership values.
Step 6: If max $\left\{ U^{(b)} - U^{(b+1)} \right\} < \varepsilon$ then stop, otherwise set b=b+1 and go to step 4.

When the algorithm has converged, a defuzzification process takes place in order to convert the fuzzy partition matrix U to a crisp partition. The maximum membership procedure is the most important method that has been developed to defuzzify the partition matrix U. This procedure assigns the pixel i to the class C with the highest membership:

$$C_i = \arg\{\max\{u_{ki}\}\}, \qquad k = 1,2,..........\varepsilon.$$

It is used to convert the fuzzy image achieved by the proposed algorithm to the liver segmented image.The major characteristics of the FLICM are summarized below:
➢ It provides noise-immunity.
➢ It preserves image details.
➢ It is free of any parameter selection.

Figure (4) shows FLICM cluster image. This image is obtained from segmented image (3). Figure (5) shows the Binary image. Figure (6) shows the Tumor segmented from binary image. Figure (7) shows the imposed tumor image. Figure (8) shows the Ground truth image. This image is used to obtain the sensitivity, specificity and accuracy in the results. Figure (4),(5),(6),(7),(8) are the resultsobtained from CT Images.
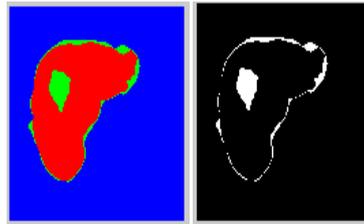
(4) FLICM cluster image(5) Binary image
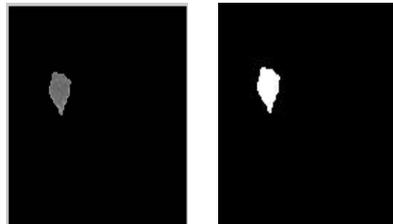
(6) Tumor segmented (7) Imposed Tumor image image

(8) Ground Truth

VI Simulation and Results:

In this work fifteen cancer affected images are used to test the proposed method. All the images are of 8-bit gray scale images and are of size 512x512pixels. In all the images, areas of the ground truth (or gold standard) regions (T) for cancer affected area is marked manually to assess the accuracy of proposed method. Then the boundaries of affected cancer area are detected.

[6] A simple and effective overlap measure of the match between the ground truth region and detected region(R) by the proposed method is used to measure the accuracy (M) as follows:

$$M = \frac{AREA(T \cap R)}{AREA(T \cup R)} \tag{9}$$

The other 2 accuracy measures used are

$$\text{Sensitivity (S)} = \frac{TP}{TP+FN} \tag{10}$$

$$\text{Specificity} = \frac{TN}{TN+FP} \tag{11}$$

Where,True positive TP= R n T;
False Positive FP=R - (R n T);
False Negative FN=T - (R n T).

The number of true negatives, i.e. the number of pixels that are not classified as tumor pixels, neither by the grader nor by the algorithm is very high. So the specificity is always near100%. This is not very meaningful. Therefore, alternative is to calculate the Predictive Value as

$$\text{PV} = \frac{TP}{TP+FP} \tag{12}$$

PV is the probability that a pixel which has been classified as tumor is really a tumor.

Table 1: shows the performance of the proposed method on detecting the area in Pixels for cancer affected image.

S.NO	Sensitivity	Specificity	Accuracy
1	79%	100%	99%
2	76%	100%	98%

Conclusion:

The main objective of this research was to study an accurate liver segmentation method using a DRLS algorithm. In order to segment the liver tissue automatically in computed tomography has proved. A FLICM clustering algorithm has been developed to find the tumor tissue from the segmented liver was presented.The FLICM introduces a new factor as a local similarity measure which aims to guarantee robustness both to noise and outliers. Also, the algorithm is relatively independent of the type of the added noise, and as a consequence, in the absence of prior knowledge of the noise, FLICM is the best choice for clustering.Experimental results have shown that our method produces satisfactory Performance analysis, especially when dealing with over-segmentation problems comparing with the other Level set model. Image Fusion may be used for future work, in order to fuse the PET images by using various techniques. Finally, CT and PET images will get fused.

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