Liver Tumor segmentation in CT images using probabilistic methods

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July 9, 2008

Abstract

Liver tumors segmentation is an important prerequisite for planning of surgical interventions. For clinical applicability, the segmentation approach must be able to cope with the high variation in shape and gray-value appearance of the liver. We present a fully automatic 3D segmentation method for the liver tumors from contrast-enhanced CT data. The method consists of two main stages.

First an initial histogram and statistical distribution functions are created, and from them a new image is created where, in each voxel, a weighted function is attached in accordance with the probability of the voxel grey level. Next, we use the active contour method on the new image, where the active contour evolution is based upon the minimization of variances between the liver tumor and its closest neighborhood.

1 Introduction

Techniques of Image processing and data analysis are more and more used in medical practice. Mathematical algorithms of features extraction and measurements can exploit data to detect pathology in an individual, the evolution of the disease, or to compare a normal subject to an abnormal one.
We are using the assumption that the liver can be segmented ([MC],[FPFW],[LLS],[1], previous contest) and we will follow this assumption in the rest of the paper.

1.1 Description of the problem

Liver cancer is one of the most popular cancer diseases and causes a large amount of death every year [2]. In order to make decisions such as liver resections, doctors will need to know the tumor volume, and further, the functional liver volume. Thus, an important task in radiology is the determination of tumor volume. Accurate segmentation of liver tumor from an abdominal image is one of the most important steps in $3D$ representation for liver volume measurement, liver transplant, and treatment planning. Since manual segmentation is inconvenient, time consuming and depends on the individual operator to a large extent, automatic segmentation is much more preferred.

The main issue of automatic liver tumor segmentation from contrast-enhanced CT data is that the intensity values of the liver tumors are often similar to those of healthy parts of

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the liver. Approaches which are only based on local intensity or intensity gradient features are usually not sufficient to differentiate between liver tissue and other anatomical structures in those regions. In order to alleviate this problem prior knowledge about the typical shape and the intensity of a liver tumors may be incorporated into the process to constrain the segmentation process where the image information is not reliable.

1.2 Previous Work

A significant number of techniques has been proposed to deal with this and similar problems. The whole set of approaches can be roughly divided into three groups, variational geometric approach, texture analysis, machine learning.
Here we combine methods of prior analysis and energy based segmentation. Energy based segmentation we use here based on [TCLV],[CV]. Efficient numerical methods were developed for blood vessels segmentation [HKPG], and for liver segmentation []. A combination of Bayesian approaches and deformable surfaces for tumor segmentation was reported in [PHS], [PSDF].

In this paper we adopt the Chan-Vese method and develop a new model using the intensity likehood ratio test. Unlike the model in [LM], the energy based segmentation is preformed on a probability image which yields a better and less noise sensitive results.

2 Methodology

Our approach for evaluating models for automatic liver segmentation consists of the following stages: first, a probability image of the organ of interest is obtained by applying a binary classification model (liver/non-liver) obtained using pixelbased priors. Since the classifier model does not incorporate any spatial information, Chan-Vese segmentation algorithm is applied on the organ probability image to overcome this drawback and remove the noise introduced by misclassified pixels.

In this paper following([LM],[PHS]), we show how using the following two phases enables us to extract the tumor up to relatively small mistakes.

2.1 Modeling tumor appearance in CT by weighted non-parametric density estimate

Data obtained from manually segmented cases, was used as a reference to apply a learning procedure method. The manually segmented data consists of the VOI_{in} only. We then obtain another volume of interest , VOI_{out}, which is considered to contain only non-lesion tissue, by first dilating generously the original mask VOI_{in} using a $3D$ structuring element and then excluding VOI_{in} from the dilated mask. Morphological operations are restricted to respect other pre-segmented structures, including body outline, bone and other detected hotspots. A probabilistic model of tissue attenuation in CT in both the segmented tumor (i.e. lesion) as well as in the background (i.e. non-lesion) can be obtained in terms of CT intensity likelihood functions using weighted non-parametric density estimates. Let the CT value, $ICT(x)$, at a voxel, x, be $I(x)$, then we can approximate the likelihood of this intensity,

in a lesion, or outside a lesion by:

$$f(\alpha|in-tumor) = \frac{1}{|VOI_{in}|}\int_{\alpha-\gamma_1}^{\alpha+\gamma_1} dVOI_{in}$$
$$f(\alpha|out-tumor) = \frac{1}{|VOI_{out}|}\int_{\alpha-\gamma_2}^{\alpha+\gamma_2} dVOI_{out}$$

Where α is the intensity value, VOI_{in} is the measure of the region of the tumor and VOI_{out} is the measure of the region outside the tumor, and γ_1, γ_2 are parameters determined by $|VOI_{in}|, |VOI_{out}|$ respectively.

A joint-likelihood ratio $r(x)$ is calculated on a voxel-by-voxel basis in the CT domain to provide a measure of voxel being contained in tumor tissue as opposed to being in background,

$$r(x) = f(x|in\_tumor) - f(x|out\_tumor).$$

The choice of $r(x)$ is based on tests we made.

By this we can overcome problems of small variance, and also enhancing difference between the tumor and other parts (blood vessels) of the liver. This method prove its usefulness especially when when a variety of tissues surrounding the tumor.

2.2 $3D$ Image variational segmentation

Our method is based on geometric active surfaces that evolve according to geometric partial differential equations until they stop at the boundaries of the objects. We use a minimal variance term that measures the homogeneity inside and outside the object. The measure we use is the minimal variance term proposed by Chan and Vese [TCLV]. It penalizes lack of homogeneity inside and outside the evolving surface. In [TCLV], the image is divided into two segments, the interior and exterior of a closed surface. This model minimizes the variance in each segment. The model was generalized in [3][CV] to piecewise constant segmentation of more than two segments and higher dimensions. Given a $2D$ gray level image $I(x,y) : \Omega \to \mathbb{R}^2$, Chan and Vese proposed to use a minimal variance criterion given by the functional,

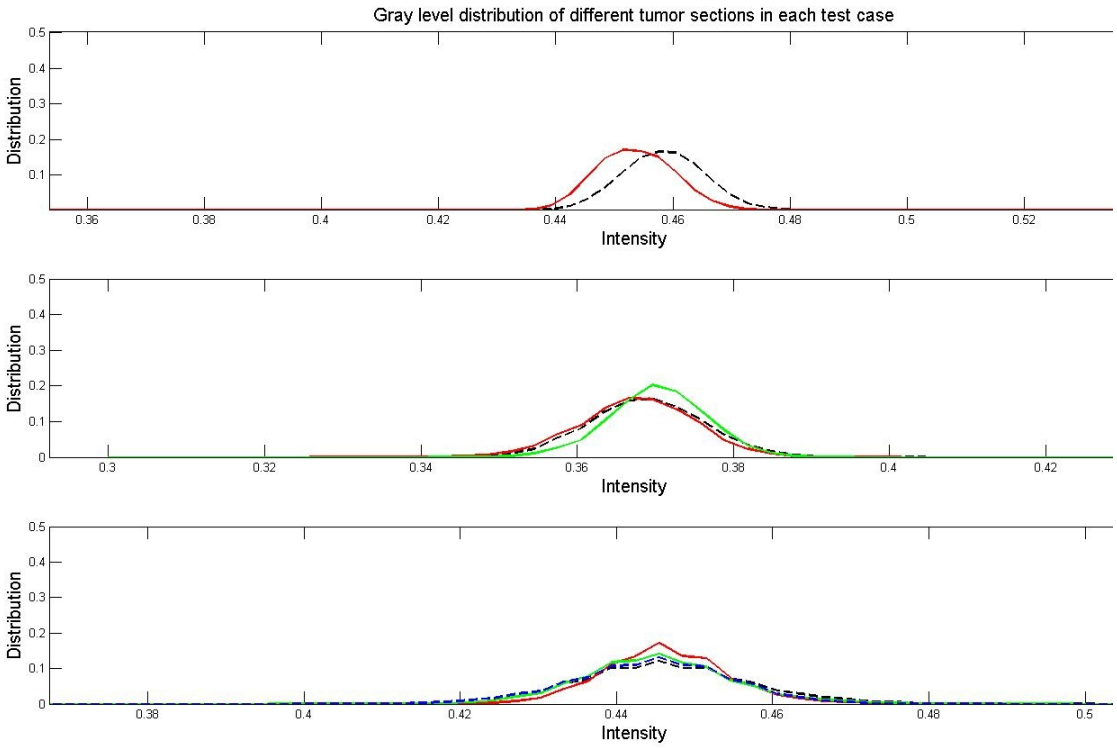
$$EMV(C, c_1, c_2) = \int\int_{\Omega_C} (I(x,y) - c1)^2 dxdy + \int\int_{\Omega\setminus\Omega_C} (I(x,y) - c2)^2 dxdy + v\int_C ds$$

(11) where C is the contour separating the two regions, Ω_C is the interior of the contour C, and $\int Cds$ measures the length of the separating contour, where v is a constant that determines the regularization level. While minimizing this functional, c_1 and c_2 obtain the mean intensity values of the image in the interior and the exterior of C, respectively. The optimal curve would separate the interior and the exterior with respect to their relative expected values.

Our method integrates two 'methods': a bayesian prior based tumor modelling, a homogeneity term based on the Chan-Vese functional. In the next section we discuss the experimental results.

3 Experimental Results

Our primary results are based on the CT images from the contest. In order to obtain priori knowledge we analyzed the intensity values of the liver tumors and of the healthy parts in the given test data.



The intensity values of the liver tumors are often similar to those of healthy parts of the liver, here we introduce some statistics (including the three relevant cases from the original data set) which demonstrate the problem of using variance minimization methods on the original picture: The intensity variance of 'tumor' pixels is:
Case 1: $5.1955 * 10^{-5}$
Case2: $5.1477 * 10^{-5}$
Case4: $1.0655 * 10^{-4}$

The intensity variance of the 'non-tumor' pixels is:
Case 1: $8.6659 * 10^{-4}$
Case2: $6.2 * 10^{-3}$
Case4: $1.2 * 10^{-3}$

One of the main problems is the small relative difference between the intensity of the tumor and the healthy part this cause that any energy based segmentation of the normalized intensity values will not work. We will demonstrate other problems which make methods as multiplication of all pixels by some large constant inefficient.

Therefore, with our method, given the assumptions approved by the provided data and figures, the result is that the distribution functions of the grey level of the tumors and the healthy parts are different. Just as well, the distribution functions of the the tumors are similar up to the expectation (by similar we mean that there is an isometry of the approximated functions s.t they are $\epsilon' < 10^{-4}$ close in the L_1 metric). This enables us segmenting the liver tumor, the accuracy of the segmentation depends on the accuracy of estimated the distribution function. In figure (3) we show graphically the advantage of our method.

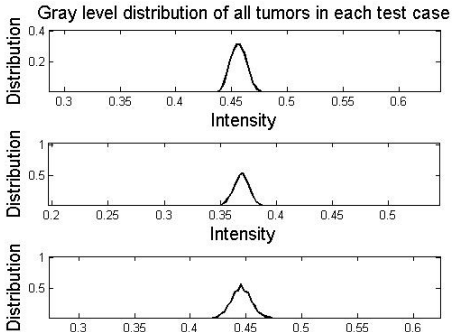


Figure 1: Grey level distribution of tumors 1,2,4

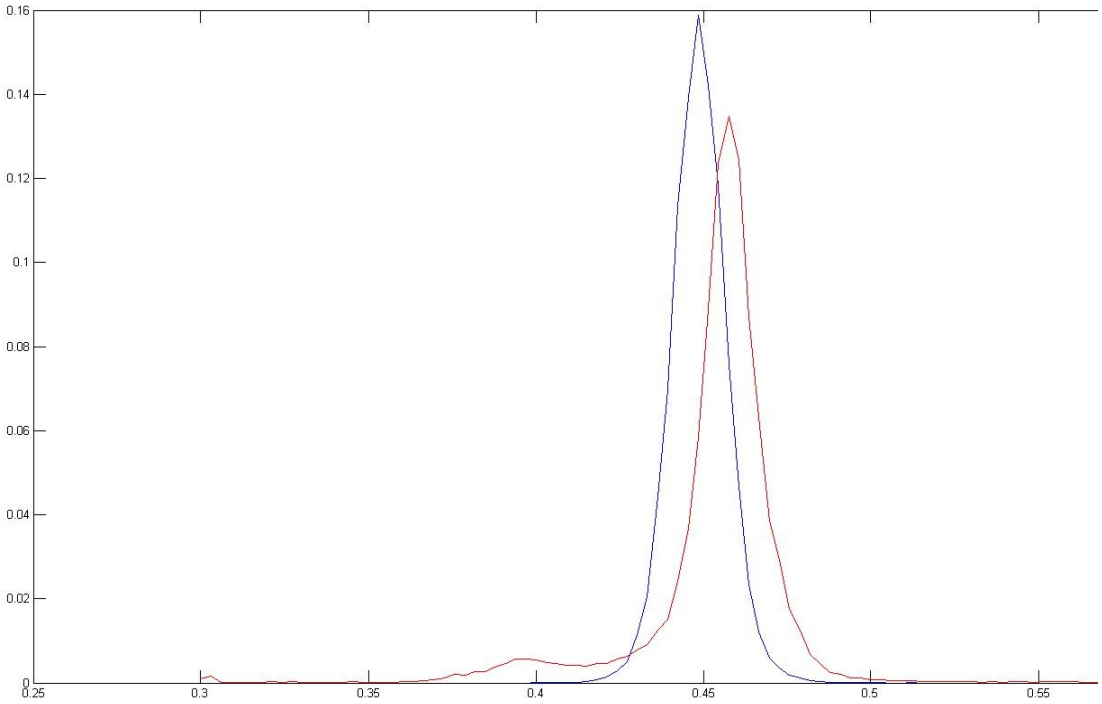


Figure 2: Grey level distribution of tumors is marked by the blue curve and the distribution of the healthy part is marked by the red curve

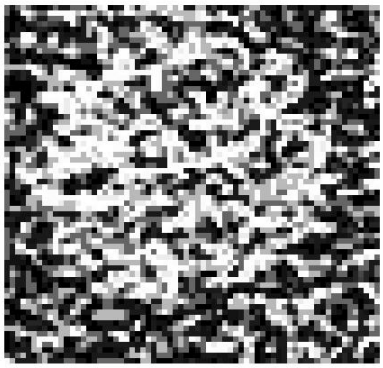


Figure 3: probability image of neighborhood of the liver tumor

An example for the segmentation is shown in figures **??**,5

An example of one advantage of our method of using the probability image can be seen in the following figures 6,**??** where the tumor is near the boundary of the liver and the tumor is surrounded by two different regions which both apply to the out tumor class.

The results comparison metrics and scores for all the ten test cases.

Tumor	Overlap Error (%)	Score	Volume Diff. (%)	Score	Ave. Surf. Dist. (mm)	Score	RMS Surf. Dist. (mm)	Score	Max. Surf. Dist. (mm)	Score	Total Score
IMG05_L1	30.66	76	17.37	82	2.36	40	3.24	55	12.08	70	65
IMG05_L2	40.77	68	35.78	63	1.53	61	1.92	73	5.80	85	70
IMG05_L3	52.48	59	51.06	47	2.33	41	3.00	58	7.77	81	57
IMG06_L1	86.91	33	86.90	10	3.25	18	3.51	51	6.88	83	39
IMG06_L2	41.85	68	2.80	97	1.11	72	1.79	75	8.94	78	78
IMG07_L1	39.18	70	36.54	62	5.27	0	6.34	12	23.50	41	37
IMG07_L2	30.21	77	0.53	99	1.45	63	2.02	72	8.81	78	78
IMG08_L1	24.96	81	23.36	76	2.87	28	3.55	50	12.77	68	60
IMG09_L1	97.49	25	94.59	2	7.37	0	8.46	0	17.28	57	17
IMG10_L1	46.66	64	46.28	52	2.81	29	3.42	52	9.94	75	54
Average	49.12	62	39.52	59	3.04	35	3.73	50	11.38	72	56

4 Conclusion and discussion

The benefits of this algorithm can be summarized as follows: Automatic detection of interior contours, robust with respect to noise, ability to detect and represent complex topologies (boundaries, segments) and extraction of geometric measurements such as length, diameter, area, volume intensity, of a detected tumor.

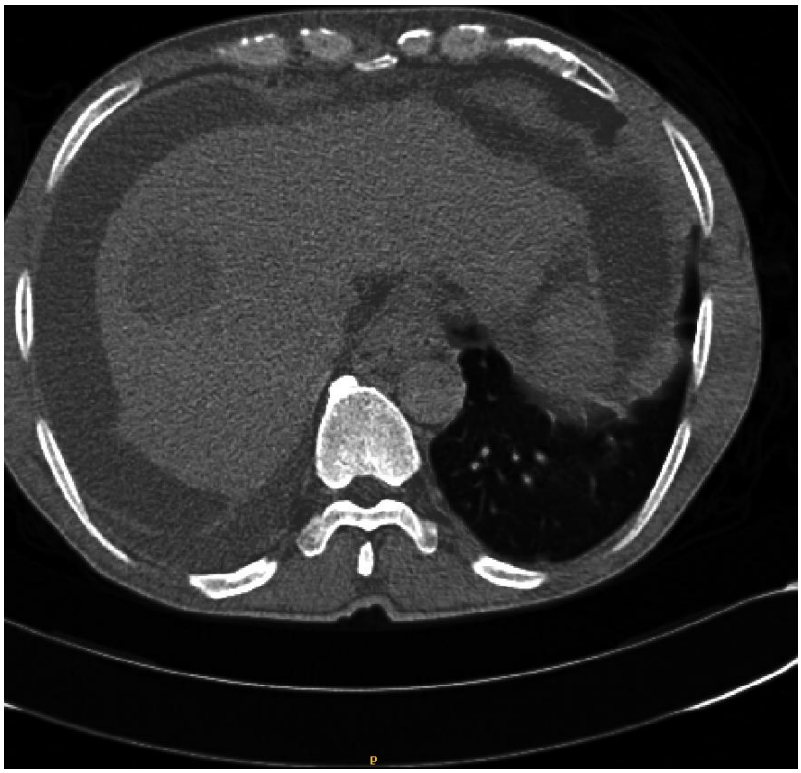
image.jpg 

Figure 4: Tumor in the Coronal Cut

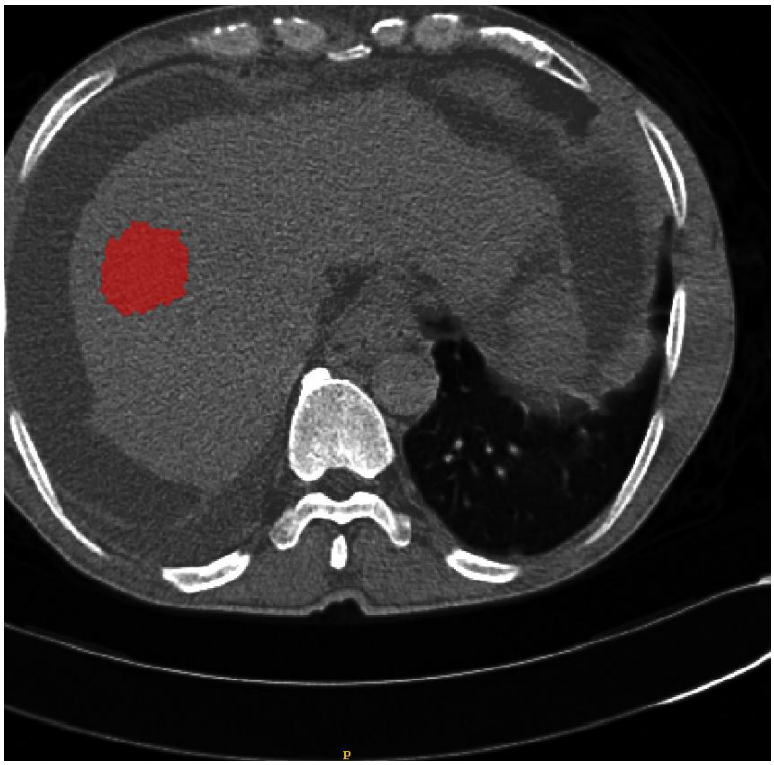
image segmented.jpg 

Figure 5: Tumor Segmentation Coronal Cut

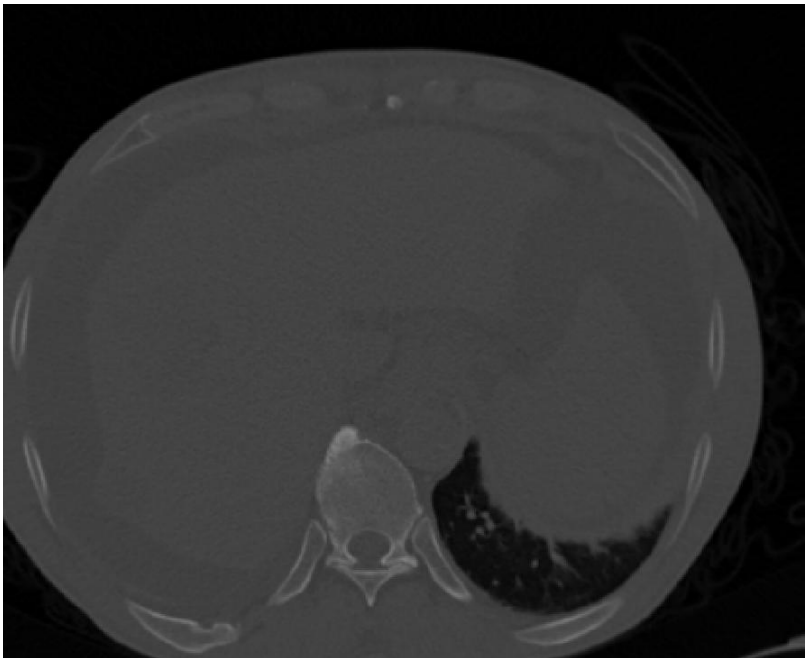
image edge.jpg 

Figure 6: tumor is in the image edge

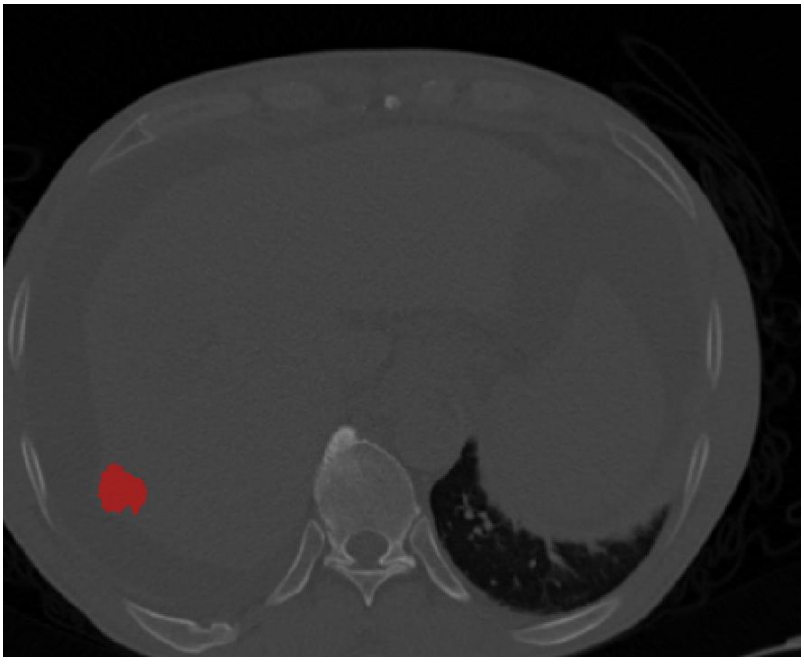
image segmented edge.jpg 

Figure 7: segmented tumor in the image edge

Further possible improvements could be in Validation of vessels segmentation, Liver partitioning to functional parts and Integration with pre-operative planning modules. And maybe Using the algorithm to segment other organs.

5 Acknowledgements

We would like to thank Dr. Moshe Lapidot at the Rambam Hospital, Haifa, Israel.

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