AUTOMATIC SEGMENTATION OF LIVER USING A TOPOLOGY ADAPTIVE SNAKE

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Abstract

Most attempts at automatic segmentation of liver from computerised tomography images to date have relied on low-level segmentation techniques, such as thresholding and mathematical morphology, to obtain the basic liver structure. The derived boundary can then be smoothed or refined using more advanced methods. In this paper we present a method by which a topology adaptive active contour model, or snake, accurately segments liver tissue from CT images. The use of conventional snakes for liver segmentation is difficult due to the presence of other organs closely surrounding the liver. Our technique avoids this problem by adding an inflationary force to the basic snake equation, and initialising the snake inside the liver. Once the user has initialised the snake for one CT slice, the starting locations for other slices in a dataset are determined automatically from the center of gravity of the segmented area of previous slice. We present results from over 500 images, covering 4 different healthy datasets, and each liver slice is segmented in 2D before being compared to the equivalent segmentation performed by hand. Statistical analysis of the datasets shows that, in each case, there is no significant difference between the areas and the snake-segmented liver to the areas of hand segmented liver, here treated as the gold standard.

Key Words
T-snake, Snake, Liver, Segmentation, CT.

1. Introduction

The automatic detection of the liver from CT scans is considered one of the harder segmentation challenges in medical image processing. The difficulties arise due to large variations of liver geometry between patients, the limited contrast between the liver and the surrounding organs, and image noise. [1]

Early work on liver segmentation by Bae et al. [2] used simple thresholding and logic functions to obtain the outline of the liver before smoothing the boundary using B-splines. Gao et al. [1] extended this work by using mathematical morphology on the thresholded image to separate the liver from other organs, before refining the obtained contour with a fourier-based deformable contour model. The limitation of both of these methods is in the initial thresholding step - it is very difficult accurately to set upper and lower threshold limits that isolate the liver effectively, without including neighbouring tissues such as the kidneys and the spleen. As a result the initial starting point for the boundary refinement step is dependent on the inaccurate thresholding step. In an effort to counter this, Shimizu et al. [3] use the corresponding CT values from four different input images of the same liver (each at a different stage of contrast treatment) to obtain the rough contour. The main limitation of this technique is that four complete datasets are required for effective segmentation of one liver. Clinically this requires four different CT scans of the same patient in succession, and computationally it involves four times the memory and processing power that is used when analysing a single dataset.

Recent work by Qatarneh et al. [4] introduced snakes as a stand-alone liver segmentation tool as part of their work to construct a radiation therapy planning atlas. The limitation of this technique is again the initial placement of the contour, as it has to be defined so that it is close enough to the snake boundary so that it does not get trapped in local minima corresponding to boundaries of other tissues. In practice this is both time-consuming and awkward, especially if the ’standard’ organ outline predicted by the atlas needs to be modified, by hand, for each slice.

Therefore while snakes have been effectively used in liver segmentation as a boundary refinement tool, they are still heavily dependent on the problem of initial placement. Our solution to this problem is to add an inflationary force to the basic snake, similar to the one first proposed by Cohen [5], and expanded by McNerney and Terzopoulos [6] in the form of topology adaptive snakes (T-Snakes). As the snake expands from an initial seed point, the contour reparameterises at certain iterations so that the snake elements are completely reset and replaced. In our implementation, the resolution of the grid increases as the curvature of the snake increases, thus the snake is able to force its way into sharp corners. This paper presents preliminary results from 4 separate patient datasets.
2. Methods

The active contour model we have developed is a modified version of the T-Snake [6], where the internal energy forces act as a smoothness constraint while an inflation force is used to push the contour towards edges within the image. The key difference between a topology adaptive model and a conventional snake is that the set of snake nodes in a T-snake does not remain constant. As the contour moves under the internal and external forces, it is reparameterised, at regular intervals, to a grid superimposed upon the image. At each reparameterisation step, the previous set of nodes is removed and a new node added at each point where the contour intersects with the superimposed grid. This reparameterisation overcomes aliasing problems that naturally occur with inflationary contours, and allows the contour to ‘flow’ into the complex shape of the liver.

There are two major benefits of using an inflationary snake to segment the liver. The first is that the interior of a healthy liver is more uniform than the exterior, thus there are less noisy edges that can trap nodes as they move outwards towards the edge of the liver. The second is that the snake can be initialised at almost any point within the liver, without greatly affecting the final segmentation result. The importance of the these two points should not be underestimated as they completely avoid the major stumbling block of previous liver segmentation algorithms, that of correct contour intialisation, and thus provide a faster and more robust segmentation.

Our snake is defined in a similar way to the T-Snake [6], as a set of $N$ nodes, indexed by $0,...,N-1$. Associated with these nodes are time varying positions $x_i(t) = [x_i(t), y_i(t)]$. The movement of the snake is determined by the balance of internal forces versus external forces (generated by the image data) and inflationary forces [6,7]

$$a_i a_i + b_i b_i = \rho_i + f_i$$  \hspace{1cm} (1)

$a_i$ and $b_i$ represent the elastic and bending internal forces of the snake, the strength of which are controlled by $a$ and $b$. In our implementation the external energy function $f_i$ is the standard gaussian gradient function, which is greater at significant edges in the image, however we pre-process the image using a Kirsch edge-detection filter to maximise the impact of these edges.

A major modification to the basic snake equations is the addition of an inflationary force $\rho_i$ to push the contour towards image edges

$$\rho_i = qF(l(x_i(t)) n_i(t)$$  \hspace{1cm} (2)

where $n_i$ is the unit normal vector to the contour at node $I_i$ and $q$ is the amplitude of the force. The binary function $F(l(x, y))$ is based upon image intensity data and is slightly modified from the similar T-Snake function [6] in that it has two threshold levels, an upper and a lower threshold. If $I(x, y)$ is within the threshold levels, $F(l(x, y)) = 1$; otherwise it is set to -1 and the normal force is reversed. This prevents the snake from leaking into other organs in the abdomen at locations where the external image energy is not sufficient enough to stop the snake. To prevent the normal force from oscillating indefinitely between areas of intensity within/outside the threshold levels, as soon as a node begins oscillating the $q$ amplitude value is lowered progressively towards zero.

Here the reparameterisation of the snake is slightly different from that presented in [6]. The grid used for reparameterisation is set to a rectangular grid for simplicity, and a major modification is that the resolution of this grid changes depending on the curvature of the snake at each individual node. The data structure in fact consists of three separate grids of decreasing cell size (increasing resolution). Depending on the curvature of the snake (calculated simply by analysing the angles between the lines connecting the nodes), the contour is reparameterised on a specific grid. If the curvature is high, the contour is reparameterised on a smaller grid size; if the contour is relatively flat it is reparameterised to a larger grid size. The major advantage of this novel technique is that the resolution of the snake increases at complex and highly irregular areas of the shape to be segmented, thus enabling the inflating contour to push itself into sharp corners and avoid aliasing effects that might otherwise cause a false segmentation result. In areas where the contour is relatively straight a larger grid size is used for reparameterisation and less points are required to model the shape, reducing the number of unnecessary calculations and speeding up the performance of the snake. While there is still much potential to develop this concept further, the current implementation sees markedly better liver segmentation results compared to those obtained with a single, uniform grid, as the snake is able to push into sharp corners and wrap around complex structures that are common within the liver, particularly around the area where the portal vein leaves the organ.

We have also developed a different way of handling the problem of when the snake crosses itself. McInerney et al. [6] incorporate region information (based on the grid cells within/outside the snake) to determine whether the snake has merged with itself or another T-snake, and use this to split the contour into two separate snakes, the original and a separate new set of nodes. Our method detects crossing points for the snake by following the contour around in a clockwise direction, testing each pixel for a crossing point. We have abstracted the technique to a simple array implementation and as a result the method detects multiple crossing points and deals with them quickly and efficiently. While it is possible to use the detected crossing points to create new snakes, for the purposes of segmenting the liver as a whole we decided merely to merge the snake at each detected crossing point.
Accurate segmentation of the liver is highly dependent on the parameters used for the snake. In all there are six parameters to be set: the internal elasticity energy, the internal bending energy, the external (image) energy, the strength of the normal force, and the upper and lower thresholds. The levels of these parameters were determined empirically to obtain the best results and to prevent the snake from leaking into adjacent organs. We found that once the optimal levels for the first four parameters were discovered, they required little or no change for almost every liver slice, even for different livers. However, the upper and lower threshold values required a change for each patient, and in certain cases required different values for accurate segmentation of the upper and lower halves of the same dataset. Segmentation of a complete liver is initiated by the user selecting a seed point within the liver i.e. any slice in the volume. The snake then inflates from this seed point to segment the liver from that particular slice. From the resulting region enclosed by the snake contour, the co-ordinates representing the center of gravity are deduced and used as snake seed points for the slices above and below. In many scans, a lobe of the liver appears as a separate structure. In these cases the snake can be initialised on the lobe in much the same way as for the main body of the liver, and results added to the main segmentation.

2.1 Results

Complete scans from four different patients, giving a total of 501 separate liver slices, were used to test the proposed segmentation method. All the images used were 512x512 pixels and 256-level greyscale. Figure 1 shows two examples of the result of the segmentation, taken from two separate patients. The snake, represented by the thick white line, has inflated to mark the boundary of the liver with only one or two minor errors. Figure 2 is a graph showing data from one of the patient scans; it compares the areas of liver slices segmented using the snake against the areas of liver slices hand-segmented and verified by a health-care professional. The two graphs match very closely and this demonstrates the high quality of the snake segmentation. To test the accuracy of the data, a paired t-test was carried out on each dataset, comparing the areas of the snake segmented liver to those of the hand segmented liver. The null hypothesis for the t-test in each case was “There no difference in the areas of the snake segmented liver and the hand segmented liver.”, and the significant probability level (p) was set to 0.05. Table 1 shows the results of the t-tests: for each dataset, the t-value obtained is less than the t-statistic presented in the data tables. This means that we cannot reject the null hypothesis at the 0.05 level of significance, and must therefore assume that there is no detectable change, at this level of significance, in the values of the snake segmented and hand segmented data.

<table>
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<tr>
<th>Patient Number</th>
<th># Slices</th>
<th>T-value (experimental)</th>
<th>Critical T-value (p &lt; 0.05)</th>
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3. Conclusion

This paper presents a new method for the automatic segmentation of the liver from CT scans. It avoids the main problem affecting previous segmentation techniques, that of initialising the snake in an efficient manner, by employing an inflationary snake which reparameterises at certain iterations of the snake movement. The snake algorithm itself is a modified version of the T-Snake presented by McInerney and Terzopoulos [6] with the important added facility of increasing the resolution of the reparameterisation grid where the snake contour is highly curved. This addition contributes positively to the segmentation abilities of the snake, as it enables it to extend into corners that other ‘inflationary’ snakes would miss.

While our preliminary segmentation results are very encouraging, there is still much more to be done to improve the technique. An immediate and obvious improvement is to enable the software to set snake parameters automatically for each liver slice – at the moment the parameters must be set by hand for the entire liver volume. Another area to be improved is the technique used to estimate the curvature of the snake; at the moment ‘noisy’ areas (where the snake changes direction rapidly along a short stretch of the contour) cause an unnecessary increase in the grid resolution.

In addition, the external energy force for the snake could be improved by using the Gradient Vector Flow model [8], this would enable less emphasis to be placed upon the threshold values (used for reversing the normal force) as the gradient vector flow field would draw the snake to the image edges from both inside and outside the liver. A future goal is to develop a true 3D topology adaptive snake, incorporating our existing modifications and improvements, which would further improve the accuracy of the segmentation of the liver.

4. Acknowledgement

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References


