AUTOMATIC COUINAUD LIVER AND VEINS SEGMENTATION FROM CT IMAGES

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Abstract: This paper presents an algorithm to segment the liver structures on computed tomography (CT) images according to the Couinaud orientation. Our method firstly separates the liver from the rest of the image. Then it segments the vessels inside the liver area using a region growing technique combined with hysteresis thresholding. It separates the vessels in segments without any bifurcation, and using heuristics based on anatomy, it classifies all vessel segments as hepatic or portal vein. Finally, the method estimates the planes that best fit each of the three branches of the segmented hepatic veins and the plane that best fits the portal vein. These planes define the subdivision of the liver in the Couinaud segments. An experimental evaluation based on real CT images demonstrated that the outcome of the proposed method is generally consistent with a visual segmentation.

1 INTRODUCTION

By and large the CT data analysis is performed visually by a radiologist. This is a time consuming task, whose accuracy depends essentially on the experience of the analyst. Digital Image Processing techniques can be used to develop methods that automatically perform many of the tasks involved in the CT analysis, improving productivity and the overall accuracy.

The segmentation process is particularly arduous in abdominal CT images because different organs lie within overlaping intensity value ranges and are often near to each other anatomically. Many techniques have been proposed in the literature for the analysis of abdominal CT scans. They can be roughly divided in two main groups: model driven and data driven approaches (Masutani et al, 2005).

The blood vessel definition is an essential step in several medical imaging applications. They can be used as reference to segment different organs and structures in the human body. Kirbas et al (2004) presented a review of vessel extraction, in which many of the available techniques are described in details.

This paper presents a data driven method to segment the liver into the eight different regions proposed by Couinaud (1957), using the hepatic and portal veins position in the liver. It deals with the case of low contrast and erroneous connection between the hepatic and portal veins, as a improvement proposed in previous work (Oliveira et al., 2007).

The subsequent text is organised in the following way. Section 2 presents segmentation method in details, section 3 reports some results, and the main conclusions are presented in section 4.

2 THE 3D SEGMENTATION METHOD

The segmentation method consists of five main steps:

a) segmentation of organs and muscle tissues,
b) segmentation of the liver,
c) segmentation of the vessels within the liver,
d) classification of segmented vessels as hepatic and portal veins, and
e) determination of Couinaud sectors.

Details of each step are presented in the next subsections.

2.1 Segmentation of Organs and Muscle Tissue

Organs and muscles tissue are the main presence in abdominal images. Typical grey values of these tissues occur around the maximum (*CM*) of the grey value histogram for the whole CT sequence.
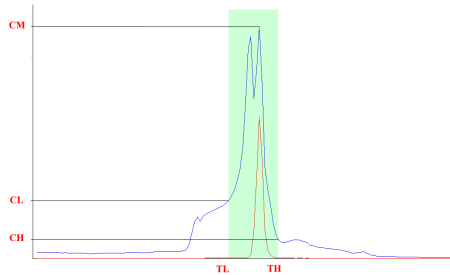

Figure 1: histogram for gray level range definition.

Figure 1 shows the histogram of a sample CT exam, the range of intensities corresponding to organs and muscles and the lower and upper limits *TL* and *TH* defining this range.

Let *CM* be the maximum CT histogram count, *TM* the corresponding intensity value, and *CL* and *CH* the counts corresponding respectively to *TL* and *TH*. It has been observed in our experiments that the ratios *RL=CL/CM* and *RH=CH/CM* do not significantly change from CT exam to CT exam. In fact these ratios lied around *RL*=0.6 and *RH*=0.2 through all our experiments.

This regularity suggests the following procedure to select the lower and higher threshold values:

a) Compute and smooth the histogram of the whole CT exam;
b) Detect the maximum histogram count *CM*;
c) Multiply *CM* by factors *RL* and *RH*, and obtain the count values *CL* and *CH*.
d) Search the smoothed histogram for the intensity values *TL* and *TH* closest to *TM* corresponding to *CL* and *CH*, such that *TL<TM* and *TH>TM*.

2.2 Liver Segmentation

The next step consists in segmenting the liver. Generally the liver appears as nearly homogeneous areas on CT slices, i.e. its intensities are restricted to a narrow grey value interval. This can be observed in Figure 1, where the histogram of pixels belonging to the liver is drawn in red over the histogram of the whole CT sequence shown in blue.

The extreme values of this interval are determined in the following way.

One image of the CT set where the liver is present is selected as the main sample and passed as an input parameter to the algorithm. Then, the largest connected component of this slice located on the upper-left side of the image (right side of the human body), is identified and its mean value on the original image is computed.

Using the pixels of organs and muscle tissue previously segmented, a new grey level range is determined following a procedure similar to the one described in subsection 2.1. The histogram count value corresponding to the liver mean value is used as the maximum count value and the range limits are calculated using as limiting ratios the value 0.8 for both cases. The threshold values obtained this way are applied to the regions selected in the previous step.

A simple procedure extracts the liver from the remaining objects. Starting on the main sample it is executed on the next adjacent slice upward and downward in the CT image set till all slices have been processed. It consists of three main steps:

a) Select the biggest object in the collection;
b) If its centroid is in the upper left quadrant of the CT image, go to step c, otherwise discard this object from the collection and go back to step a;
c) If the selected object is connected to another object of an adjacent slice previously classified as liver, classify it as liver, otherwise discard the object from the collection and go back to step a;

Clearly the first iteration does not pass through step c and the object selected in step b is set as liver directly.

2.3 Vessel Segmentation

Having segmented the liver, and considering only the region delimited by this organ, we select a threshold *VH*, such that the intensities above it identify unambiguously the vessels inside the liver. A second threshold *VL* (*VL<VH*) is further selected such that intensities below it clearly indicate liver parenchyma.

These two threshold values define three ranges of pixel intensities, namely:

- the strong vessel range, defined by intensities above *VH*,
- the weak vessel range, comprising intensities between VL and VH, and

- the liver tissue range, covering intensities below VL.

The construction of the vessel tree is performed by a region growing approach consisting of the following basic steps:

a) Build the weak vessel object set defined by the pixels with values above VL.

b) Build the strong vessel object set defined by the pixels with values above VH.

c) Take the strong vessel set computed in the preceding step as the initial vessel tree estimate, and add to it all objects of the weak vessel set connected to it.

d) Repeat the previous step using the current vessel tree estimated until it stops growing.

We searched appropriate values for *VL* and *VH* manually through many experiments using different CT sequences. We observed that the histogram counts for the manually selected values stayed at a roughly constant ratio to the intensity corresponding to the maximum count.

Considering *NM* the maximum liver histogram count, and *NL* and *NH* the counts corresponding respectively to *VL* and *VH*, the ratios $rl=NL/NM$ and $rh=NH/NM$ do not significantly change from CT exam to CT exam. These ratios were determined experimentally as rl=0.5 and rh=0.2.

Based on this regularity the following procedure is proposed to select the lower and higher threshold values:

a) Compute and smooth the histogram of the image region inside the liver;

b) Detect the maximum histogram count NM and the corresponding intensity VM.

c) Multiply NM by the ratios rl and rh, and obtain the count values NL and NH.

d) Search the smoothed histogram for the intensity values VL and VH corresponding to NL and NH, whereby both VL and VH are greater than VM.

2.4 Classification of Portal and Hepatic Veins

The hepatic and portal veins appear as separate three dimensional objects in most CT exams. However, sometimes these veins touch to each other on some CT slice, what may lead to identifying them as a single object. In such case the Couinaud segmentation becomes not possible.

This subsection describes a method to correctly segment the veins even when they touch in some CT slice.

Firstly, the method separates the vessel objects segmented previously in connected components, hereafter called objects, performing the following steps:

a) The first slice S1 containing any object is labelled.

b) The area projected by each object in S1 on the next adjacent slice S2 is verified. If it intersects only one object, the same label is set to the object in S2. If it intersects more than one object, new labels are created for each intersected object in S2.

c) Step b is repeated until all objects in the CT sequence are labelled.

As result vessels segments are obtained whose extremes are determined by bifurcations, as shown in Figure 2-b.

A second procedure is performed to classify these vessel segments as hepatic or portal vein. Based on knowledge of the anatomy, the following simple algorithm is proposed. It consists of six steps:

a) The first object identified on the top slice is selected.

b) If it is divided in three other objects in the next adjacent slice, it is classified as hepatic vessel, otherwise it is discarded and other object is selected on the top slice until this condition is reached.

c) For each of the three objects identified as hepatic branches, the next adjacent slice is analysed. The object with the largest intersection area is selected as continuation of the respective hepatic branch.

d) Step c is repeated recursively for each hepatic branch until no other segment can be merged to the hepatic vessel tree. At the end of this step, the major hepatic vessels have been identified.

e) The vessel segments not assigned to the hepatic vessel tree up to step d are examined and the largest 3D connected component is labelled as the portal vein.

f) Non classified segments which are connected to the hepatic vessel tree are merged to it.

In figure 2-a the hepatic and portal veins are shown as a single object because they touch on some CT slice. Figure 2-b shows in different colours several independent segments delimited by each bifurcation identified during the classification process. Figure 2-c shows the final result, where the hepatic and portal veins appear as separated vessel trees.
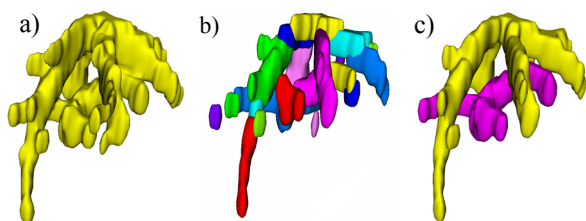
Figure 2: Vessel segmentation results – (a) the portal and hepatic veins (b) the independent vessel segments determined by bifurcations (c) the portal and hepatic veins as separated vessel trees.

2.5 Segmentation of Couinaud regions

The Couinaud paradigm divides the liver into eight independent segments each one having its own vascular inflow, outflow, and biliary drainage. Because of this division into self-contained units, each can be removed without damaging those remaining.

Our method estimates the subdivision of the liver in the eight Couinaud segments, by fitting planes to the portal vein, and to each of the hepatic vein branches. To separate the three main branches of the hepatic vein we apply the k-means algorithm on the 3 dimensional coordinates of the pixels identified in the preceding step as belonging to the hepatic vein. It is assumed that there are three clusters. A restriction for singleton value is imposed so as to guarantee that no cluster will be empty. This leads to three different objects corresponding to each branch of the hepatic vein.

Then, a least squares based procedure determines the four planes that best fit the points of each branch of the hepatic vein and the portal vein segmented before. These planes divide the liver in the Couinaud segments.

3 RESULTS

A software prototype implementing the proposed method has been built for validation purpose. It also implements both the surface and volumetric visualization of the internal liver structures. It receives as input the segmented structures of each image slice and the thickness of the CT slices available in the DICOM image file header.

Figure 3 shows an example of segmentation result produced by the proposed procedure as a 3D surface which can be visualized within our prototype. It is possible to observe the hepatic vein and the portal vein respectively in blue and red, and the Couinaud segments in different colours are also

present. It can be observed that the Couinaud segments are divided according to the veins orientation.
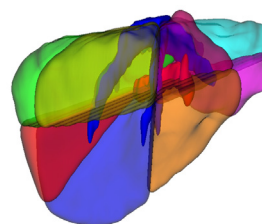

Figure 3: 3D models of segmented liver structures.

Experiments performed on seven different CT sequences have shown that the results produced by the proposed method are consistent with the visual perception of a specialist.

4 CONCLUSIONS

This work proposes an algorithm to segment the liver in computer tomography (CT) images according to the Couinaud classification.

Experiments conducted on a software prototype of the proposed algorithm upon 7 CT produced results consistent with the visual perception. The method has the potential of becoming a useful tool in various applications. It can be used to generate 3D liver representations to aid visual diagnostic and surgery planning. Shape attributes other than volume may also be measured from the 3D model and explored in Computer Aided Diagnostic environments.

The assessment of segmentation accuracy is a major concern in the continuation of this work.

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