# Liver Segmentation from CT Scans

Paola Campadelli, Elena Casiraghi, Stella Pratissoli
Università degli Studi di Milano
Dipartimento di Scienze dell'Informazione
Via Comelico 39/41, Milan, Italy
{campadelli, casiraghi, pratissoli} @dsi.unimi.it

Automatic and semi-automatic liver segmentation is a challenging task in the field of medical image processing. In this paper we briefly describe our automatic gray level based liver segmentation method that employs a fast marching technique. We will provide a short description of our system, since a detailed paper has been submitted for publication and it cannot become publicly available until any decision has been made.

## 1 Materials and Methods

We have developed and tested our method on a private dataset containing 40 abdominal contrast enhanced CT scans of the third phase, and their ground truth manually traced by three experts. These volumes start from the mid height of the heart, and finish below the kidneys.
To obtain a further assessment of our method we have tested it on the CT images provided by the organizers of the Liver Segmentation Gran Challenge [1]. These volumes might start from the top of the lung; in this case the user is requested to sign the slice at the mid height of the heart. This slice is then used as the starting slice for the following processing.

## 2 Preprocessing

Before processing, all the DICOM images have been scaled to the range $[0, 255]$. To this aim, we compute the HU (gray level) histogram of the image in the range $[-500, +500]$[1], find the range, $[H_{min}, H_{max}]$, around the unique peak, and scale it to the gray level range $[0, 255]$. Next, to speed up computation, we reduce the axial slices' size to be $256 \times 256$ pixel, and extract a 3D body box, $BB$, by discarding the black background with thresholding (see figure 1). Inside $BB$ the lung volumes are extracted by finding the darkest and biggest connected volumes. The lung volumes are used, if needed, to rotate the scan around the vertical axis, so that the patient is in supine position. To this aim, we compute their orientation along the vertical axis and, if this is greater than 5 degrees, we rotate the patient scan.
Next, to reduce noise and make regions as piecewise constant as possible, without blurring the organs' edges, we use a 3D diffusion filter [4, 6, 3].
The filtered $BB$ is used as input of the following processing steps. The employed schema can be easily adapted to segment different abdominal organs by exploiting the same processing steps, opportunely adapted to cope with the different organ characteristics. In this pages we will describe the details of the procedure aimed at liver segmentation only.

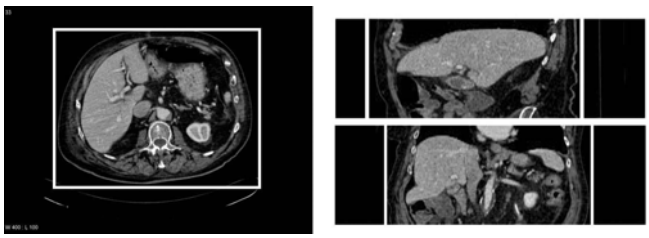

**Figure 1.** Body box perimeter in an axial, coronal, and sagittal slice.

## 3 Liver Segmentation

***I. Liver gray level estimation and extraction of the under-segmented liver volume***
To segment the liver we automatically extract a 'liver 3D box', $BB_{Liv}$ (see figure 2), based on established and not

[1]The range $[-500, +500]$ HU surely includes soft tissue voxels, that is voxels belonging to abdominal organs [2].

critical anatomical knowledge, mainly containing liver voxels; therefore, its gray level histogram always shows a unique peak corresponding to the liver gray level range $[g_{min}, g_{max}]$.

An initial under-segmented liver volume is then obtained by thresholding $BB_{Liv}$ with $[g_{min}, g_{max}]$; this is followed by a morphological processing to discard small regions. Finally, the biggest 3D volume is selected as the under-segmented liver volume, $V_{Liv}$.

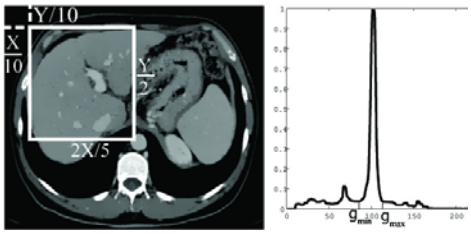


**Figure 2.** Left: the axial section of the liver box, and its proportions to the body box axial size. Right: the gray level histogram of the liver box, and the estimated liver gray level range $[g_{min}, g_{max}]$.

***II. Volume segmentation through multi-planar 2D fast marching***

The liver volume thus obtained, $V_{Liv}$, is used to initialize a modified fast marching algorithm [5]; the algorithm processes each axial, coronal, and sagittal slice separately, starting by the initial front, $f_0$, that is the 2D contour of $V_{Liv}$ in the processed slice. $f_0$ is evolved outward, according to a speed function, $F$, that accounts of both gray levels and gradient information.

The 2D fast marching algorithm assigns to each pixel a distance value $T_{ij}$; since we apply the algorithm in three directions (axial, coronal and sagittal), we obtain 3 values of $T_{ij}$ for each voxel ($T_{ij}^k$ , $k = 1, 2, 3$). To select voxels belonging to the liver, we use the $T_{ij}^k$ histogram to automatically define a threshold $T_{th}^k$ (see Fig. 3). A voxel is then added to the liver volume, $V_{Liv}$, if $T_{ij}^k \leq T_{th}^k$ in at least one direction.

Although the first run of the fast marching algorithm expands the liver volume outside $BB_{Liv}$, it does not always reach the real liver boundaries, for it is initialized by the under-segmented volume, and the thresholds $T_{th}^k$ are set purposedly high. Therefore, a further fast marching expansion is applied starting from the obtained liver volume; moreover, in this second run we set a less restrictive criterion to select the value of $T_{th}^k$.

***IV. Post-processing***

To smooth the contour and remove any over segmentation error, we at first apply a morphological opening operation.

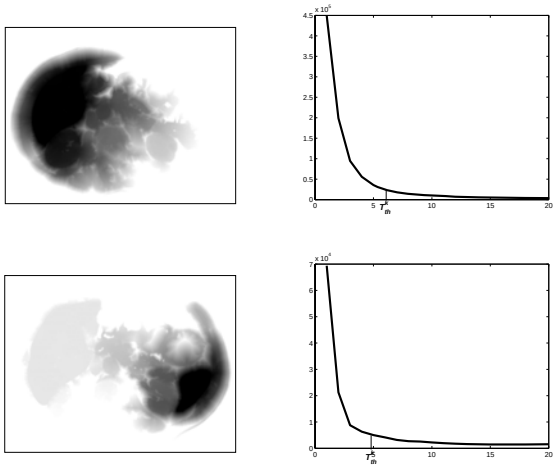

**Figure 3.** Left: a visualization of the distance values $T_{ij}^1$, assigned to each pixel $(i, j)$ by the fast marching algorithm, when is starts from the undersegmented liver (top), and the undersegmented spleen (bottom). Right: the $T_{ij}^1$ histograms of the whole 3D image.

Next, we remove vessels by deleting from each axial slice small regions near the center. The biggest connected volume in the resulting 3D image is the final liver volume.

## References


[1] B. Ginneken, T. Heimann, and M. Stiner. 3d segmentation in the clinic: A grand challenge. *T. Heimann, M. Styner, B. van Ginneken (Eds.): 3D Segmentation in The Clinic: A Grand Challenge*, pages 7–15, 2007.

[2] S. Jackson and R. Thomas. *CROSS-SECTIONAL IMAGING MADE EASY, Elsevier Health Sciences*. 2004.

[3] H. Lamecker, T. Lange, and M. Seebass. Segmentation of the liver using a 3D statistical shape model. *ZIB-Report 04-09*, 04–09:1–25, 2004, April.

[4] P. Perona and Jitendra Malik. Scale-space and Edge Detection Using Anisotropic Diffusion. *IEEE Transactions on Pattern Analalisys and Machine Intelligence.*, 12(7):629–639, 1990.

[5] J.A. Sethian R. Malladi and B.C. Vemuri. Shape modeling with front propagation: a level set approach. *IEEE Trans. Pattern Anal. Mach. Int.*, 17:158–174, 1995.

[6] J. Weickert. A review of nonlinear diffusion filtering. *Scale-Space Theories in Computer Vision*, pages 3–28, 1997.