Accuracy of a semi-automated liver segmentation method using CT scan

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**Purpose**

Determining liver volume is clinically relevant in a variety of medical and surgical contexts. Liver volume has been shown to be an important biomarker for disease progression in cirrhosis [1] and fulminant hepatic failure [2]. In liver surgery, assessment of volume is a key issue in two major settings: major hepatectomy and living donor transplantation [3, 4]. Pre-operatively, it is important to establish the total liver volume as a first step in determining the future liver remnant (FLR) volume. The FLR is a direct indicator of residual liver function and post-operative outcome [3]. In transplantation, determining liver volume during surgical planning is essential to establish size compatibility between donor and recipient [4].

Given the wide variability in liver morphology there is an important need for accurate and reproducible liver volumetry using CT. Dynamic CT is the most appropriate for image analysis due to the short acquisition time required and high spatial resolution [5]. The current gold-standard method to estimate liver volume involves manually delineating the liver outline, a process called manual "segmentation", on consecutive CT axial images [6]. This method is time-consuming and impractical for clinical use. Thus, there is a clear clinical need to develop automated segmentation methods for volumetry that are fast, reliable, and specifically adapted to the liver.

The purpose of this study was to evaluate the accuracy of a semi-automated liver segmentation method developed at our institution using a publicly available database as the reference standard. The semi-automated method was compared with manual segmentation for liver volume determination on CT images. The interaction time for semi-automated segmentation was recorded.

**Methods and Materials**

**Patients**

This retrospective, institutional review board approved study was conducted on the publicly available 3D Image Reconstruction for Comparison of Algorithms Database (3D-IRCADb). This database contains anonymized medical images with manual segmentation of organs completed by experts. The 3D-IRCADb-01 database contains 3D abdominal CT scans from 20 patients; 10 men, 10 women, with an average age of 57.6 years. These scans contain a spectrum of liver morphologies (5 normal, 15 tumors, 18 with ambiguous borders) amongst other segmentation pitfalls.
Reference method

The IRCAD website provided axial images with manually segmented livers in the form of structural masks. The DICOM files were loaded and processed using MATLAB® computational software. The number of pixels within each structural mask provided the liver area on a section-by-section basis. This cross-sectional area was multiplied by the slice thickness and the summation of each section volume gave the total liver volume for each patient. Figure 1 shows examples of CT axial slices from the same patient with corresponding structural masks.

**Fig. 1**: 56 year old healthy male. (A, B, C): Axial CT slices with manual segmentation performed on the liver (liver contouring in red), (D, E, F): Corresponding segmentation masks. DICOM images were obtained from the publicly available 3D Image Reconstruction for Comparison of Algorithms Database (3D-IRCAD-01)

References: IRCAD

Semi-automated method (3 phases)

The semi-automated method used in this study was developed at the Laboratoire de recherche en Imagerie et Orthopédie (LIO) with collaboration from the clinical and engineering teams. The method uses minimal path surface segmentation with a novel approach to deformable models. An experienced image analyst performed the segmentation using MATLAB® computational software and recorded the interaction time required.

Initialization:
The average intensity of the organ is determined with a cursor by placing a control point inside the liver. A thresholding based on the estimated liver intensity is applied to the images such that only the connected region containing the control point in the axial, coronal and sagittal planes is maintained, a concept called "connected thresholding". The same thresholding is applied to subsequent slices where the most overlapping connected region is conserved, allowing the volume to dissipate in the axial, coronal and sagittal directions. The 3D connected region with the best coherence is used as the initial mask. (Figure 2)

**Fig. 2:** Initialization. The first step in semi-automated segmentation performed on axial (A, B), coronal (C, D) and sagittal (E, F) slices with different windowing leads to an initial segmentation solution using a "control point" and "connected thresholding".  

**References:** Radiology, Université de Montreal - Montreal/CA

**Deformation:**

The mask obtained during the initialization phase is smoothed and converted to a mesh composed of vertices and quadrangular faces. This quadrangular mesh can be deformed in an elastic manner by the user (Figure 3). The surface is thus displaced in 3D until it approximately outlines the liver contours.
Fig. 3: Deformation. The mesh can be deformed in an elastic manner by the user. The surface is thus displaced in 3D until it adequately outlines the liver contours.  

References: Radiology, Université de Montreal - Montreal/CA

Fine segmentation:

The surface model is then subject to a "snapping" algorithm where the model snaps around the organ to represent the fine details (Figure 4). This model can also be converted to volumetric masks to exclude vessel insertion points and hepatic fissures, areas that are often difficult to segment using this approach.
**Fig. 4:** Fine Segmentation. (A, C, E): Images after initialization step of semi-automated segmentation, (B, D, F): corresponding images after fine segmentation using a "snapping" algorithm.

**References:** Radiology, Université de Montreal - Montreal/CA

**Inter-method agreement**

Agreement between the semi-automated segmentation method and IRCAD reference was determined by Bland-Altman analysis.

**Segmentation accuracy**

Segmentation accuracy was further established using 3 error measures described in the imaging literature [6]:

1) **Volumetric overlap error**: The overlap error between two sets of segmentations A and B (Figure 5) is given as a percentage and calculated as:
Fig. 5: Volumetric overlap error (VOE). VOE is calculated using the ratio between intersection and union between two sets of segmentations (A and B). Reference: Heimann, T., et al. (2009), Comparison and evaluation of methods for liver segmentation from CT datasets. IEEE Trans Med Imaging. 28(8): p. 1251-65. References: Radiology, Université de Montreal - Montreal/CA

The volumetric overlap error is 0 for a perfect segmentation and 100 for segmentations with no overlap.

2) Relative volume difference: The relative volume difference (Figure 6) between two sets of voxels A and B is given as a percentage and calculated as:

\[ RVD(A, B) = \left( \frac{|A| - |B|}{|B|} \right) \times 100\% \]


A value of 0 means that the volumes of the two sets of voxels A and B are identical.

3) Average symmetric surface distance (ASSD): The ASSD of surface voxels from two segmentations A and B is given in millimeters. For each surface voxel of segmentation A, the Euclidean distance to the closest surface voxel of B can be calculated (Figure 7). The ASSD is the average of all the calculated distances from A to B and B to A, with a perfect segmentation giving an ASSD of 0 mm [6].
**Fig. 7**: Average symmetric surface distance (ASSD). ASSD is calculated using surface voxels from two segmentations A and B. For each surface voxel from segmentation A, the Euclidean distance to the closest surface voxel of B is calculated (Dn). The ASSD is the average of all distances calculated from A to B and B to A. Reference: Heimann,
Interaction time

Interaction time was recorded for the semi-automated segmentation method.

Images for this section:

Fig. 1: 56 year old healthy male. (A, B, C): Axial CT slices with manual segmentation performed on the liver (liver contouring in red), (D, E, F): Corresponding segmentation masks. DICOM images were obtained from the publicly available 3D Image Reconstruction for Comparison of Algorithms Database (3D-IRCAD-01)
**Fig. 2:** Initialization. The first step in semi-automated segmentation performed on axial (A, B), coronal (C, D) and sagittal (E, F) slices with different windowing leads to an initial segmentation solution using a "control point" and "connected thresholding".

**Fig. 3:** Deformation. The mesh can be deformed in an elastic manner by the user. The surface is thus displaced in 3D until it adequately outlines the liver contours.
Fig. 4: Fine Segmentation. (A, C, E): Images after initialization step of semi-automated segmentation, (B, D, F): corresponding images after fine segmentation using a "snapping" algorithm.

\[
|A \cap B| = \text{Intersection} \\
|A \cup B| = \text{Union} \\
VOE(A, B) = (1 - \frac{|A \cap B|}{|A \cup B|}) \times 100\% 
\]

Fig. 5: Volumetric overlap error (VOE). VOE is calculated using the ratio between intersection and union between two sets of segmentations (A and B). Reference: Heimann, T., et al. (2009), Comparison and evaluation of methods for liver segmentation from CT datasets. IEEE Trans Med Imaging. 28(8): p. 1251-65.

\[
RVD(A, B) = \left(\frac{|A| - |B|}{|B|}\right) \times 100\%
\]
Fig. 7: Average symmetric surface distance (ASSD). ASSD is calculated using surface voxels from two segmentations A and B. For each surface voxel from segmentation A, the Euclidean distance to the closest surface voxel of B is calculated (Dn). The ASSD is the average of all distances calculated from A to B and B to A. Reference: Heimann, T., et al. (2009), Comparison and evaluation of methods for liver segmentation from CT datasets. IEEE Trans Med Imaging. 28(8): p. 1251-65.
Results

Illustrative Case

Figure 8 illustrates the superposition of liver outlines obtained from the semi-automated and IRCAD methods of liver segmentation. This allows for visual inspection of the meshes obtained from both methods to document any gross differences.

Fig. 8: Video example comparing the contour meshes obtained from semi-automated segmentation (red) with the IRCAD reference standard (green).

References: Radiology, Université de Montreal - Montreal/CA

Inter-method agreement
The mean volume difference between the semi-automated segmentation method and the IRCAD reference was 3.3 +/- 78.9 ml (bias +/- repeatability coefficient). The 95% limits of agreement were found to be -75.6 and 82.2ml using the Bland Altman analysis (Figure 9).

**Fig. 9**: Bland-Altman analysis to verify agreement between the semi-automated and IRCAD reference for accurate liver volumetry.

**References**: Radiology, Université de Montreal - Montreal/CA

**Segmentation accuracy**

As described in the methods and materials section, liver segmentation accuracy was proven using 3 error measures.

**Table 1. Results of error measures for 20 study patients**

<table>
<thead>
<tr>
<th>Error Measure</th>
<th>Mean</th>
<th>Standard Deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>1) Volumetric Overlap Error</td>
<td>5.5%</td>
<td>1.0%</td>
</tr>
</tbody>
</table>
2) Relative Volume Difference
-0.1% 2.4%

3) Average Symmetric Surface Distance
2.0mm 0.3mm

**Interaction time**

Mean interaction time for the semi-automated segmentation method was found to be 7:43 +/- 1:09 min:s per case.

**Images for this section:**

**Fig. 8:** Video example comparing the contour meshes obtained from semi-automated segmentation (red) with the IRCAD reference standard (green).
**Fig. 9:** Bland-Altman analysis to verify agreement between the semi-automated and IRCAD reference for accurate liver volumetry.
Conclusion

In this study we introduce a novel semi-automated liver segmentation method for CT imaging based on a combination of minimal path surface segmentation and deformable models. We have validated the accuracy of this method by using manual segmentations from a publicly available imaging database as the reference standard.

As summarized by Campadelli et al. [7], there are a variety of segmentation approaches that have been developed including live-wire approaches, grey-level based methods, model-fitting methods, and level-set methods. Our novel approach combines minimal path surface segmentation with elastic and rigid model deformation. Udupa et al. [8] described reasons limiting the performance of segmentation algorithms. Amongst others these included: small data sets, inappropriate ground truths and poorly defined performance metrics. Our validation process utilized an independently validated imaging database that contained a variety of liver morphologies. We also measured accuracy using appropriate performance metrics described by Heimann et al [6]. Thus, our segmentation method is promising for future clinical use.

The mean volume difference between the semi-automated segmentation method and the IRCAD reference was found to be 3.3 +/- 78.9mL with limits of agreement of -75.6 and 82.2mL. In a similar study examining hepatic volumetry prior to liver transplantation, the mean volume difference between automated and manual segmentation methods was 48.8mL with limits of agreement of -230.3 and 327.9mL [5]. The same study described a mean measurement time of 4.4 +/- 1.9 minutes for automated segmentation, similar to the interaction time required for our method.

In terms of segmentation accuracy, our segmentation method obtained a mean volumetric overlap error of 5.5 +/- 1.0%, a mean relative volume difference of -0.1 +/- 2.4% and a mean average symmetric surface distance of 2.0 +/- 0.3mm. Heimann et al. [6] describe similar results in a liver volumetry competition where 16 teams evaluated their liver segmentation algorithms on a database of 20 patients. The highest-scoring interactive segmentation algorithm obtained a mean volumetric overlap error of 5.2 +/- 0.9%, a mean relative volume difference of 1.0 +/- 1.7% and a mean average symmetric surface distance of 0.8 +/- 0.2mm. These results highlight the accurate performance of our segmentation method when judged by these error measures.

Our proof-of-concept study had certain limitations. First, our reference database only contained 20 patients and thus limited the number of cases we could utilize for segmentation. While the database cases contained a variety of segmentation difficulties, they were not necessarily reflective of what may be seen in common clinical practice.
Finally, given the potential benefit of MR-based quantification of liver biomarkers, this study was limited to validation of our method on CT.

Manual segmentation is a time-consuming process used clinically to extract liver volumes from available CT imaging. Semi-automated volumetry represents a faster means to obtain this important information with satisfactory accuracy.

References


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