Accuracy of a semi-automated liver segmentation method using MR imaging

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Purpose

Determining liver volume is clinically relevant in a variety of medical and surgical contexts. 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 anticipated future liver remnant (FLR) volume. The FLR is a direct indicator of residual liver function and post-operative outcome [3].

The current reference standard method to estimate liver volume involves manually delineating the liver outline, a process called manual "segmentation", on consecutive CT axial images to calculate volume. 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. Most segmentation algorithms have been developed for CT images because of better accessibility and superior spatial resolution. However, MRI offers the advantage of simultaneous assessment of vascular anatomy, biliary anatomy, and liver fat content [5]. In light of recent concerns about CT radiation dose [6] and contrast-induced nephropathy [7], there is a clear need to develop liver segmentation methods based on MRI, an imaging modality that does not use ionizing radiation and does not require contrast agents for liver segmentation.

The purpose of this study was to evaluate the accuracy of a semi-automated liver segmentation method for MRI developed at our institution, compared with manual segmentation as the reference standard. A secondary aim was to compare the interaction time required for volume determination between methods.
Methods and Materials

Patients

This retrospective, transversal, institutional review board approved study was conducted on 21 subjects having had an abdominal MRI performed over a period of six months in 2010-2011 (11 men, 10 women, ages between 33-75 years, average age 60 years). Study patients were chosen by a radiologist to include a large spectrum of hepatic morphologies (Figure 1).

![Diagram of liver morphologies]

Fig. 1: Varying morphology of livers in study subjects (n=21).

References: Radiology, Université de Montreal - Montreal/CA

MRI Protocol

MRI was performed using a 1.5T superconducting system (Discovery MR 450; GE Healthcare, Wauksha) and a phased-array torso coil. The MRI liver protocol included coronal T2-weighted single shot fast spin echo (SSFSE), axial T2-weighted fast spin echo (FSE), axial T1-weighted gradient-recalled echo (GRE) in-phase and out-of-phase, and axial T1-weighted 3D GRE before and after dynamic gadolinium injection. The axial T1-weighted 3D GRE sequence 60 seconds after gadolinium injection was used for segmentation (Table 1).

Table 1. MRI 1.5T Parameters

<table>
<thead>
<tr>
<th>Sequence</th>
<th>Ax LAVA 60 seconds</th>
</tr>
</thead>
<tbody>
<tr>
<td>Repetition Time/Echo Time</td>
<td>4.8ms / 2.1ms</td>
</tr>
<tr>
<td>Matrix</td>
<td>320 x 224</td>
</tr>
<tr>
<td>Field of view</td>
<td>350 mm</td>
</tr>
<tr>
<td>Flip angle</td>
<td>12°</td>
</tr>
</tbody>
</table>
Thickness | 4.4 mm
Number of Excitations | 0.69
Echos | 1
Bandwidth | 244 Hz

**Manual method**

The axial T1-weighted 3D GRE sequence images acquired 60 seconds after gadolinium injection were saved as DICOM files and uploaded onto an imaging post-processing software (SliceOMatic, TomoVision, Montreal, Canada). A Radiology resident with 4 years of experience performed the manual segmentations. For a given axial slice, the image analyst outlined the liver using a large cursor then manually deformed the curve to contour the liver, a tool usually referred to as "snakes". The curves could be projected upward or downward to simplify segmentation of adjacent slices. Large vessels abutting the liver periphery such as the main portal vein and inferior vena cava, but not vessels surrounded by liver parenchyma, were excluded (Figure 2).

![Reference Standard. Manual segmentation performed by a senior radiology resident using image processing software (SliceOMatic). For a given axial slice, the image analyst outlined the liver using a large cursor then manually deformed the curve to contour the liver. Large vessels abutting the liver periphery such as the main portal vein and inferior vena cava, but not vessels surrounded by liver parenchyma, were excluded.](image-url)
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. A senior Radiology resident performed the segmentation using MATLAB® computational software and recorded the interaction time required.

Initialization:

First, the liver is delineated manually on 4-6 multi-planar slices using the mouse cursor and assisted by a "snapping" effect [7]. Those contours are then used to interpolate a smooth surface by variational interpolation [8]. The interpolation results in a smooth surface mesh composed of vertices and quadrangular faces intersecting the contours initially delineated. This surface mesh represents a rough segmentation solution to be further refined (Figure 3).

Fig. 3: Initialization. The liver is initially delineated on 4-6 multi-planar slices using a cursor. The liver contours undergo variational interpolation to generate a smooth surface mesh representing an initial segmentation solution.
Deformation:

The initial mesh obtained during the initialization phase is iteratively deformed in an elastic manner by the user until it converges to actual patient anatomy. The surface is displaced in 3D until it is aligned with the liver contours (Figure 4).

Fig. 4: Deformation. The rough surface mesh obtained during the initialization phase is deformed in an elastic manner by the user. The surface is displaced in 3D until it is aligned with the liver contours.

References: Radiology, Université de Montreal - Montreal/CA

Fine segmentation:

The surface model is then subject to a "snapping" process, based on an adaptation of the minimal path algorithm where the model snaps around the organ to represent finer details. If the resulting surface is unsatisfactory, further manual deformations can be applied and the surface mesh can be "snapped" again.

Volumetry:
The number of pixels within each mesh 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 provided the total liver volume for each patient.

**Inter-method agreement**

Agreement between the semi-automated segmentation method and the manual 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:

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

**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.

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

**Fig. 6**: 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.

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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 [8].
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.

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Interaction time

Interaction time was recorded for both the semi-automated and manual segmentation methods.
Images for this section:

**Fig. 1:** Varying morphology of livers in study subjects (n=21).

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**Fig. 2:** Reference standard. Manual segmentation performed by a senior radiology resident using image processing software (SliceOMatic). For a given axial slice, the image analyst outlined the liver using a large cursor then manually deformed the curves to contour the liver. Large vessels abutting the liver periphery such as the main portal vein and inferior vena cava were excluded. Video edited to shorten duration.

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Fig. 3: Initialization. The liver is initially delineated on 4-6 multi-planar slices using a cursor. The liver contours undergo variational interpolation to generate a smooth surface mesh representing an initial segmentation solution.

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**Fig. 4:** Deformation. The rough surface mesh obtained during the initialization phase is deformed in an elastic manner by the user. The surface is displaced in 3D until it is aligned with the liver contours.

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

**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.

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

**Fig. 6:** 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.

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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.

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Results

Inter-method agreement

The mean volume difference between semi-automated and manual segmentation was -124 +/- 212 mL (bias +/- repeatability coefficient). The 95% limits of agreement were found to be -336 and 88 ml using the Bland Altman analysis. (Figure 8)

Fig. 8: Bland-Altman analysis to verify the agreement between the semi-automated and manual segmentation method 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 evaluated using 3 error measures.

Table 2. Results of error measures between two segmentation methods (n = 21)
<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>10.7%</td>
<td>2.9%</td>
</tr>
<tr>
<td>2) Relative Volume Difference</td>
<td>-6.5%</td>
<td>3.0%</td>
</tr>
<tr>
<td>3) Average Symmetric Surface Distance</td>
<td>2.5mm</td>
<td>0.5mm</td>
</tr>
</tbody>
</table>

**Interaction time**

Mean interaction time was 5:11 ± 1:15 min:s per case for the semi-automated method and 29:15 ± 4:16 min:s per case for the manual method.
Fig. 8: Bland-Altman analysis to verify the agreement between the semi-automated and manual segmentation method for accurate liver volumetry.

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Conclusion

In this IRB-approved, proof-of-concept study we introduce a novel semi-automated liver segmentation method developed for MRI. We have validated the method by comparing with volumes obtained from manual segmentation, the current gold-standard method.

As summarized by Campadelli et al. [9], there are a variety of segmentation approaches that have been developed including live-wire methods, grey-level based methods, model-fitting methods and level-set methods. However, these methods have mostly been validated for CT imaging and may not be directly applicable for MRI-based volumetry. Yet, there is an inherent benefit to perform liver segmentation based on MRI due to its accurate quantification of liver fat, portrayal of vascular/biliary anatomy, and lack of ionizing radiation. However, there are few MR-based volumetry methods described in the literature. Here, we describe a method developed at our institution that combines minimal path surface segmentation, variational interpolation [8] with elastic and rigid model deformation.

In our study, mean volume difference between the semi-automated segmentation method and the manual segmentation reference was -124 +/- 212mL with limits of agreement of -336 and 88mL. In a similar study examining hepatic volumetry in living liver transplant donors, Hermoye et al. found that volume difference between semi-automated segmentation and volume from surgical specimen ranged from -214 to +86 ml [10]. The mean volume difference between the two methods (0.047 +/-0.211ml) and 95% limits of agreement (-0.377, 0.471) were expressed in logarithmic scale and are thus difficult to compare with ours. Though we used manual segmentation as the reference standard and Hermoye et al. used surgical specimen volume, the studies showed similar range in terms of method agreement.

In terms of segmentation accuracy, our segmentation method obtained a mean volumetric overlap error of 10.7 +/- 2.9%, a mean relative volume difference of -6.5 +/- 3.0% and a mean average symmetric surface distance of 2.5 +/- 0.5mm. Heimann et al. [6] described similar but better results in a liver volumetry competition where 16 teams evaluated their liver segmentation algorithms on a database of 20 CT studies. 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. The higher error in our study may be attributable to the increased section thickness of MR images versus CT, which has been shown to influence measurements [10].
The mean interaction time was found to be 5:11 +/- 1:15 min:s per case for semi-automated segmentation and 29:15 +/- 4:16 min:s per case for the manual method. These results are similar to those obtained by Hermoye et al. [10]. Thus, semi-automated segmentation was found to be roughly 6 times faster than the manual method demonstrating the efficiency of semi-automated volumetry.

Our proof-of-concept study had certain limitations. First, the study was conducted on 21 patients and thus the number of cases we could utilize for segmentation was limited. While the cases contained a variety of segmentation difficulties, they were not necessarily reflective of what may be seen in common clinical practice. As mentioned in [10], section thickness can directly affect volume measurement, thus using thinner slices may have increased segmentation accuracy. The use of manual segmentation as our reference rather than CT-based segmentation or surgical specimen volume, more widely accepted reference standards, may also have influenced accuracy. Finally, our study only examined a single MRI sequence from the liver studies clinical protocol.

Manual segmentation is a time-consuming process used clinically to extract liver volumes for use as a prognostic biomarker. Semi-automated volumetry represents a faster means to obtain this important information with satisfactory accuracy. Future studies may evaluate segmentation accuracy using thinner 3D MR sequences and more rigorous reference standards such as CT-based segmentation.
References


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