Co-registration of inspiratory and expiratory datasets for treatment planning for robotic-assisted liver thermal ablation

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Purpose

Introduction

Recent developments in thermal ablation, e.g. radiofrequency ablation (RFA), microwave and cryoablation, have expanded the treatment options for certain oncology patients. In the treatment of hepatocellular carcinoma (HCC), less than 40% of patients are candidates for surgery, and the rate of recurrence after curative surgery is high. Minimally invasive, image-guided therapy may now provide effective local treatment of isolated or localized neoplastic disease, and can also be used as an adjunct to conventional surgery, systemic chemotherapy, or radiation therapy. In the procedure, the tumours are located with ultrasound, computed tomography (CT), or magnetic resonance (MR) imaging modalities.

This study focused on the challenges in accurately targeting the liver tumour in CT-guided RFA procedure. There may be changes in liver morphology between the baseline and treatment scans affecting the location of the targeted lesion. Respiratory motion during a baseline contrasted CT may lead to mis-registration of location of tumour targeting. According to previous research (Shimizu, et al., 1999; Suramo, Paivansalo, & Myllyla, 1984), the liver might be moved as much as 2 cm in the cranio-caudal direction resulting from normal respiratory motion.

In order to minimize artifacts caused by respiratory motion, 3D non-rigid registration has been applied. This implementation of deformable registration uses conservation of organ volume because differential tissue contrast enhancements at each time point have the tendency to lead algorithm to mis-register areas with the same contrast but different anatomical location. The image registration algorithm used (Jensen, et al., 2013) generally only shifts images rigidly in the axial direction only and does not correct organ rotation or translation in the axial plane or organ deformation; these alter changes leading to residual apparent organ motion. This is especially so at the dome of the liver where the motion of the diaphragm can cause significant organ deformation at different phases of respiration.

Studies using Pre-RFA and post-RFA CT data have also been used to create fusion images (automatic rigid registration and manual correction referring to intra hepatic structures and hepatic contours around a tumour) to determine a minimal ablative margin (MAM) measured on fusion images to prove risk factors for local tumour progression (LTP) have been reported with good results.
In the present study, we aimed to evaluate the changes in the location of tumours in the liver by combining two different datasets (end inspiration and end expiration) to determine the exact and direction of movement of these tumours. Subsequently, we aimed to explore if a baseline dataset, which is used for offline treatment planning, can be then fused/combined with the online dataset for a quick and effective real-time treatment plan. A commercial available software (Maxio workstation, Perfinth Healthcare, USA) was used in this study.
Methods and materials

Material / Data:

The computed tomography (CT) images of 16 patients underwent radiofrequency ablation (RFA) of the liver were used in this study. The end-inspiration and end-expiration images were obtained for each patient using a triphasic liver imaging protocol. It was assumed that the end-inspiration images corresponded to the arterial phase while the end-expiration images corresponded to the venous phase. The reconstructed slice thickness of 0.7 mm was used for all the images.

For image registration, the end-inspiration/arterial phase image was used as the "source image" and the end-expiration/venous phase was used as the "target image". A commercial available image processing software (Maxio workstation, Perfinth Healthcare, USA) was used to register the target image to the source image.

Methods:

Step 1: Liver Segmentation

For each patient, liver was segmented in both the end-inspiration and end-expiration images by marking the base and apex points in each image volume. For the purposes of this study, manual editing of the segmented contours was limited to removing inconsistencies between the segmented contours of both the series. Figure 1 shows an example of a segmented liver surface overlaid on the patient's abdominal scan.

Step 2: Registration

After segmenting the liver surfaces, the end-inspiration and end-expiration images were registered to each other. Figure 2 illustrates the alignment between liver surfaces before and after registration for two patients.

Registration accuracy was evaluated by computing registration error at sub-surface points by picking corresponding anatomical landmarks between the end-inspiration image and the registered end-expiration image. The pairs of sub-surface points were either picked manually (at major vessel bifurcations) or automatically (tumor centroid) between the end-inspiration image and the registered end-expiration image. The 2D as well as 3D distances between these points was measured.
2D registration error calculation:

2D distances represent distance between the points along the three cardinal image planes - axial or inferior-superior plane, coronal or ventral-dorsal plane and sagittal or anterior-posterior plane. The target registration error (TRE) was computed using the following formulas.

\[
\text{TRE (along Sagittal)} = \text{Absolute}(S_2 - S_1) \\
\text{TRE (along sagittal)} = \text{Absolute} (S_2 - S_1) \\
\text{TRE (along coronal)} = \text{Absolute} (C_2 - C_1) \\
\text{TRE (along axial)} = \text{Absolute} (A_2 - A_1)
\]

3D registration error calculation:

\[
TRE = S_1 - S_2 + C_1 - C_2 + A_1 - A_2 \\
TRE = \#(S_1 - S_2)^2 + (C_1 - C_2)^2 + (A_1 - A_2)^2
\]

where:

- \( S_1 \) and \( S_2 \) = corresponding points picked in the sagittal/anterior-posterior plane;
- \( C_1 \) and \( C_2 \) = points picked in the coronal/ventral-dorsal plane;
- \( A_1 \) and \( A_2 \) = points picked in the axial/inferior-superior plane.

Figure 3 shows an example of manual sub-surface point localization (at major vessel bifurcation) in end-inspiration and end-expiration images for a patient. Point pair selection was performed for all 16 patients and TRE was computed.

Tumor centroid sub-surface point localization was done by manually segmenting the tumor surfaces on both end-inspiration and end-expiration images. Tumor centroid was then computed automatically using an algorithm.

Figure 4 depicts the tumor segmentation on liver surfaces. The distance between tumor centroids of source image and target image before and after registration were noted and 2D.
3D registration error was computed for 13 patients only, as the tumor was not visible in one patient, tumor was outside of the liver in another patient, and tumor was almost covering the entire liver in another patient. This made it impossible to segment the tumor and compute centroids for these three patients.
Fig. 1: Example of end-inspiration image and its corresponding liver surface. Region shaded in grey is the segmented liver contour generated using the commercial registration software (MAXIO workstation, Perfinth Healthcare, USA). The patient’s abdomen is illustrated in magenta shade.

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Fig. 2: Images showing the overlay of "source image" (coloured) and "target images" (grey scale) before and after registration for Patients A and B.

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Fig. 3: Images showing corresponding point localization at a major vessel bifurcation for a patient data.

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Fig. 4: Three cardinal views showing segmented tumors in the "source image" (yellow outline) and "target image" (solid green) before and after registration.

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Results

Results:

(A) Distances measured between the vessel bifurcation

Distances between the segmented liver contours were computed by finding bi-directional/symmetric closest points (closest points from source to target and from target to source) between the images.

Averaging across 16 patients, registration improved the average symmetric surface distances by 45% (5.3 ± 4.1 mm before registration and 2.9 ± 1.1 mm after registration).

A total of 85 sub-surface vessel bifurcations were localized to compute registration error (in 2D and 3D), as seen in Table 1.

The average distances (after registration) between the vessel bifurcation points in the three cardinal image planes are follows:

2.3 ± 1.8 mm along the axial axis;
1.5 ± 1.3 mm along the coronal axis; and
1.9 ± 1.5 mm along the sagittal axis.

Whearas the average 3D distances between vessel bifurcations was 3.7 ± 2.0 mm.

(B) Distances measured between the tumour centroids

Distances were obtained between the tumour centroids to compute registration error at those points. For a few patients multiple tumours were present and for those patients 2-3 tumours were picked randomly and analysed. A total of 21 tumor centroids were localized to compute registration error as shown in Table 2.

The average distances (after registration) between the tumour centroids in the three cardinal image planes are follows:
2.5 ± 2.7 mm along the axial axis;
1.6 ± 1.6 mm along the coronal axis; and
1.0 ± 0.8 mm along the sagittal axis.

Whereas the average 3D distances between tumour centroids was 3.5 ± 2.8 mm.
### Table 1: 2D distances and 3D distances between corresponding pairs of points manually localized at vessel bifurcations. The distances between the points is a measure of the registration error.

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Table 2: 2D distances and 3D distances between tumour centroids. The distances between the points is a measure of the registration error. Patients 1, 3, 5, 9, 11 and 13 had only one tumour, therefore the distances are not presented as mean +- standard deviation. For the remaining patients with multiple tumours, 2-3 tumours were selected randomly to compute centroids and registration error.

<table>
<thead>
<tr>
<th>Patient #</th>
<th># of tumors used for analysis</th>
<th>2D registration error (mm)</th>
<th>3D Registration error (mm)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Axial</td>
<td>Coronal</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>0.4</td>
<td>0.9</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1.8 ± 0.5</td>
<td>0.8 ± 0.5</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>1.2</td>
<td>2.4</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>6.2 ± 5.2</td>
<td>1.5 ± 1.0</td>
</tr>
<tr>
<td>5</td>
<td>1</td>
<td>3</td>
<td>6.1</td>
</tr>
<tr>
<td>6</td>
<td>2</td>
<td>1.9 ± 0.6</td>
<td>4.3 ± 0.4</td>
</tr>
<tr>
<td>7</td>
<td>2</td>
<td>5.0 ± 2.4</td>
<td>0.8 ± 0.8</td>
</tr>
<tr>
<td>8</td>
<td>2</td>
<td>0.6 ± 0.1</td>
<td>0.2 ± 0.1</td>
</tr>
<tr>
<td>9</td>
<td>1</td>
<td>0.8</td>
<td>1.7</td>
</tr>
<tr>
<td>10</td>
<td>2</td>
<td>1.8 ± 2.4</td>
<td>1.9 ± 0.9</td>
</tr>
<tr>
<td>11</td>
<td>1</td>
<td>2.8</td>
<td>0.4</td>
</tr>
<tr>
<td>12</td>
<td>2</td>
<td>0.6 ± 0.7</td>
<td>0.3 ± 0.2</td>
</tr>
<tr>
<td>13</td>
<td>1</td>
<td>2.5</td>
<td>0.6</td>
</tr>
</tbody>
</table>
Conclusion

Conclusion:

The registration algorithm used in this study showed that the mean registration error was less than 5 mm, however the software can be further improved to achieve smaller registration errors in both 2D and 3D registration.
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