

Analysis of Respiratory-induced 3D Deformation of Liver based on Branching Structure of Portal Vein obtained with Time-resolved Volume Acquisitions

Etsuko Kumamoto¹, Tastuhiko Matsumoto², Daisuke Kokuryo³, and Kagayaki Kuroda^{4,5}

¹Information Science and Technology Center, Kobe University, Kobe, Hyogo, Japan, ²Graduate School of System Informatics, Kobe University, Kobe, Hyogo, Japan,

³Molecular Imaging Center, National Institute of Radiological Sciences, Chiba, Japan, ⁴Graduate School of Engineering, Tokai University, Hiratsuka, Kanagawa, Japan, ⁵Center for Frontier Medical Engineering, Chiba University, Chiba, Japan

Introduction: High intensity focused ultrasound (HIFU) treatment of the abdominal organs, such as the liver, requires a tracking technique to “lock on” to the focal spot at the target tissue region during respiratory induced motion. Several target tracking methods based on the vessel of the liver have been proposed^[1–3]. However, deformation in the liver organs caused by respiratory motion leads to the displacement of the estimated target position. To maintain sufficient tracking accuracy, both translation and deformation of the tissue need to be considered. In this study, we analyzed the 3D deformation of the liver under slow breathing on the basis of the morphological changes of the branching vessels by using reconstructed 4D MR images.

Methods and Materials: A series of the multiple sagittal images from a healthy volunteer’s liver was acquired by 3.0T MRI (Signa HDxt, GE Healthcare UK Ltd.) with fast image employing steady state acquisition (FIESTA). The imaging conditions were as follows: TR/TE, 4.85/1.98 ms; slice thickness, 5mm; FOV, 350 x 350 mm²; spatial matrix, 512 x 512; and FA, 90 degrees. 4D MR images were reconstructed from the series of multiple sagittal images because of the time delay in the diaphragm positions of the multiple sagittal planes caused by respiratory motion.

First, the diaphragm positions of each image were extracted with the 3D template matching method^[4]. Template patterns were set in the area that includes the diaphragm in the first image set. The sum of the absolute difference was used for the similarity index between the template and the input pattern. Next, each image set was classified into four categories (inhalation, maximal inhalation, exhalation, and maximal exhalation) depending on the relative displacement with the diaphragm position of the coronal image (Figure 1). The images of each slice position were re-ordered in respiratory order according to the diaphragm position of each category. The re-ordered images were interpolated in the direction of respiration cycle and were assembled to image sets in such a way that the diaphragm positions were fit to the diaphragm line of the coronal image. The rearranged image sets were organized according to the isotropic voxel images with the use of a linear interpolation method.

Several regions of interest (ROI), including branching vessels, were set and tracked with the using 3D template matching method. The center of the extracted region was set as the position of the relevant branching vessel. The distance between the center of the reference ROI and those of other ROI was calculated for each image set. The expansion and contraction of each ROI pair were also computed.

Results: Forty-two image sets of six interleaved slices were acquired under slow-paced free respiration. The images of each slice were reordered and interpolated into 122, 126, 137, 187, 144, and 169 slices and rearranged into 113 image sets of isolated 37 slices with the use of the proposed method. Figure 2 shows the maximum intensity projection display of the reconstructed images and the branching vessels of interest (P_0 to P_3). Figure 3 depicts the Euclidean distance between the reference point (P_0) and other points (P_1 , P_2 , P_3), as well as the linear approximation lines. The horizontal axis shows a phase of respiration from maximum exhalation to maximum inhalation. The gradients of the approximation lines were as follows: P_0 to P_1 : -0.0406 , P_0 to P_2 : 0.1737 , P_0 to P_3 : -0.0744 . The deference of the distance between P_0 and P_1 was small because of the proximity of these vessels to each other. The distance between P_0 and P_2 was extended as the liver fell. The distance between P_0 and P_3 was contracted as the liver fell. The maximum expansion and contraction between P_0 and points P_1 , P_2 , and P_3 were 10.6, 18.2, and 20.1 mm. When the position of the liver falls, the liver organ slides down forward into a narrow space. Therefore, the distance between P_0 and P_2 was extended and the distance between P_0 and P_3 was contracted against P_2 and P_3 , which were both compressed as the diaphragm fell.

Discussion and Conclusions: The effectiveness of the proposed method to reconstruct 4D MR images was demonstrated in a series of multiple sagittal images from a healthy volunteer’s liver. Our measurements showed displacement and deformation in the liver caused by respiration. The results demonstrated that 3D motion tracking of the liver is feasible through observation the vessel branches with the use of rapid MR imaging and the template matching technique.

References [1] Kuroda K, Kokuryo D, et al.: Thermal Medicine; 23(4):181–193, 2007. [2] Kokuryo D, et. al: Proc. of IEEE EMBS 2007; 2614–2617. [3] Kokuryo et al. Magn Reson Med; 67(1):156–163, 2012. [4] Matsumoto T, et al.:Proc. of iMRI; 94, 2014.

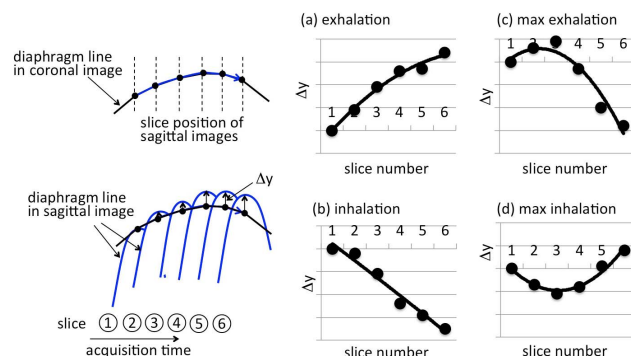


Figure 1 Shift of the diaphragm profiles of sagittal images. (a) In exhalation, the diaphragm profiles shifted upward; (b) in inhalation, the diaphragm profiles shifted downward compared with the diaphragm profile of the coronal image; (c) maximum exhalation and (d) maximum inhalation have a local maximum value and local minimum value.

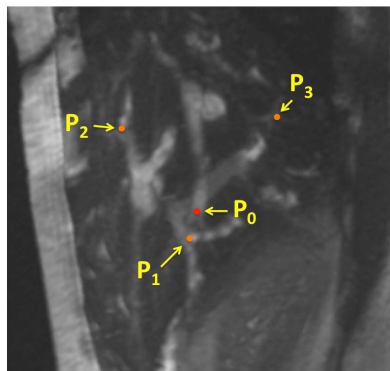


Figure 2 Reconstructed 4D MR images displayed by MIP. P_0 is the reference branching vessel and P_1 , P_2 , P_3 are the branching vessels of interest.

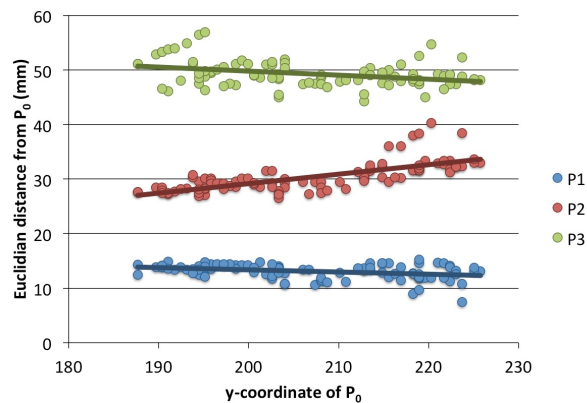


Figure 3 Euclidean distances between the reference point (P_0) and other points (P_1 , P_2 , P_3), as well as the linear approximation lines.