Advantage of a Patient-Specific Respiratory Motion Model for the Liver

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Focused Ultrasound Surgery (FUS) has become a frequent tool for non-invasive benign tumour therapy with FDA clearance for the treatment of fibroadenoma in the uterus and obtained CE mark for sonication of bone metastasis. Other tumours are under preclinical (prostate, kidney) and clinical (breast, brain and liver) evaluation. However, FUS is still challenging in terms of reliable therapy planning, monitoring and outcome prediction especially in moving organs with a complex blood supply. The processes involved in FUS are multi-level (ranging from organ morphology, perfusion and motion, down to microscopic and cellular level) and not well understood. To improve this situation, a multi-level model for moving abdominal organs for the use with Magnetic Resonance-guided FUS (MRgFUS) will be developed and evaluated within the FUSIMO project. One key component is the abdominal organ motion model to simulate patient-specific motion. Purely tracking the tumour is not sufficient for FUS, where absorbing and reflecting structures (e.g. bones, gas) can cause thermal injury to neighboring tissue [1, 2]. Observation of the motion for all structures of interest requires real-time 4D image acquisition and processing, which is currently impossible. However, incomplete observations (surrogates) during therapy can be used in conjunction with prior information to provide complete 3D information of the organ. Patient-specific [3, 4, 5, 6] and population-based [7, 8, 9, 10, 11] respiratory motion models have been proposed for this purpose.

Population models are built by gathering data from a number of volunteers or patients. Consequently, the common structures within different subjects are registered and the variance in their location is modeled. A patient-specific approach, on the other hand, adapts to a specific patient using data acquired either through a pre-operative planning session, or shortly before therapy. However, no direct comparison between the performance of population models and patient-specific models has yet been published. In this study, we have investigated the benefit of a patient-specific model by observing the respiratory motion of a patient during a short period before MRgFUS, over the use of a population model.

In our experiments we used 4DMRI [7] data acquired from 12 healthy volunteers (equal number of males and females and an average age of 31). The 4DMR images consist of 25-30 slices taken during the course of 45-70 mins with a temporal resolution of 290-410ms. The liver deformation between the MR volumes were computed using an intensity-based non-rigid registration [7]. To set up inter-patient correspondences, a number of anatomically and biomechanically corresponding landmarks were manually annotated for each patient. By performing a cubic interpolation between these landmarks, the positions of 290 corresponding points in the liver, in addition to 249 points on the surface of the liver were obtained [7]. In the FUSIMO project, ultrasound is used to provide surrogates by tracking visible structures. We assumed in this study that these surrogates include a point on the diaphragm, the entrance point of the portal vein into the liver, and a point in the center of the liver defined by vessel features. To evaluate the benefit of building a patient-specific respiratory model, we used the first 3-5 minutes of the 4DMR images of the subject, typically consisting of 27-84 respiratory cycles.

Von Siebenthal et al. [7] observed a change in exhale position over time (called drift) in addition to the respiratory motion. Arnold et al. [11] showed the benefit of compensating also for this drift besides the prediction of the respiratory motion. Similarly, we have decomposed the displacement of points in the liver into respiratory and drift components. The drift component is defined as the difference in the position of a

point at its most recent exhale from a reference exhale state. The respiratory motion is the displacement of a point with respect to its most recent exhale state. The exhale state in each cycle is defined as the local maxima of the superior-inferior component of the motion trajectory. We have applied the same decomposition for the surrogate signals during therapy, where each component of the surrogate is used to predict the respective component of the motion vector. Finally, we constructed the motion vector by adding the two predicted components. Since the drift is only considerable in relatively long periods of time (15-20 mins), one has to rely on population data for modeling it. Hence, for predicting the drift, we have used a similar approach as von Siebenthal et al. [7] for building a population model.

To predict the respiratory motion, we built two different models, namely a population and a patient-specific one. First, we constructed $3N \times T$ motion matrices for each subject in the population, where N is the number of points in the liver and T is the number of time steps. Next, we combined these matrices to form a $3N \times TM$ matrix which includes the respiratory motion data of the M subjects in the population. Finally we built the population model by applying PCA on this matrix and saving the resulting eigenvectors and eigenvalues. To build patient-specific models, we formed a $3N \times t$ data matrix by using the first t time steps of the 4DMRI sequence of the patient. Similarly to the previous method, we applied PCA on this data matrix. Having created the motion models, we followed the method of Hug et al. [12], to predict the full respiratory motion vectors from the partial motion vectors provided by the surrogates.

	Average Over all Patients	
	mean	95th percentile
Initial Error (no Motion Model)	4.56	11.90
PCA Population Model	1.40	3.38
PCA Patient-Specific Model	1.18	2.97
Improvement by Patient-Specific Model	16%	12%

Table 1: Illustration of the local mean prediction error (mm) for the liver motion in leave-one-out experiments

Table 1 shows the average over all patients of the mean and the 95% prediction error of the temporal sequence for leave-one-out experiments. The improvement can also be appreciated in Figure 1, which shows the spatial distribution of the mean prediction error for patient 1 for the two methods.

In conclusion, we compared population PCA and patient-specific PCA methods for modeling and predicting the respiratory motion of livers within a MRgFUS framework. The patient-specific respiratory model improved the mean prediction error by 16%. Therefore the acquisition of a short 4DMRI sequence shortly before MRgFUS is recommended.

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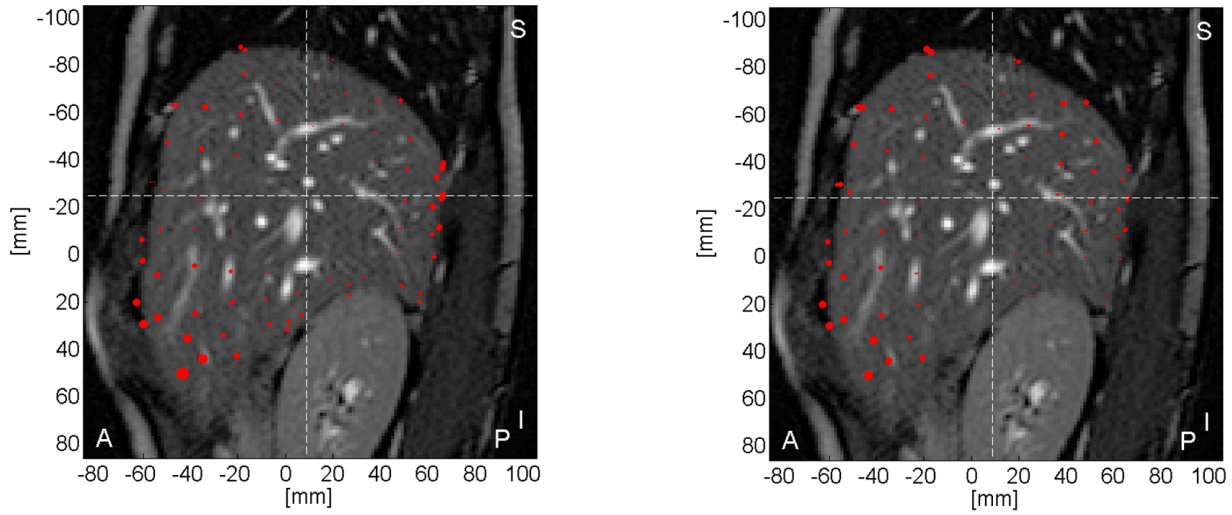

(a) (b)

Figure 1: Example slice showing local mean prediction error (radius of the red circles) for patient 1 using (a) the PCA population model and (b) the PCA patient-specific model for respiratory motion

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