Motion Correction for Improved Characterization of Breast Tumors Using DCE-MRI

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INTRODUCTION

Conventional breast tumor segmentation algorithms of dynamic contrast-enhanced MR images (DCE-MRI) assume no or negligible inter-frame patient motion. However, due to respiratory and cardiac motion and other involuntary motion, the breast does move. In previous work, quantitative breast motion studies using 2D dynamic MRI and fiducial markers [1] illustrated that the breast moves by as much as 3 *mm* (Figure 1), i.e. \geq 3 typical MR image voxels in-plane. The posterior breast is observed to move the most due to its proximity to the diaphragm and heart. The inter-frame spatial mismatch of DCE-MRI degrades the performance of segmentation and contrast-kinetic algorithms. We hypothesize that motion correction prior to segmentation will lead to

improved breast tumor detection and characterization. This work compares outcomes of DCE-MRI segmentation and contrast kinetics with and without motion correction. Performance was evaluated based on visual assessment, sensitivity, and specificity.

MATERIALS AND METHODS

Our study population included 15 patients with a total of 21 suspicious breast lesions (9 malignant and 12 benign, as determined by biopsy and pathology). Patients were scanned on a 1.5 T scanner (Signa LX; GE Medical Systems, Milwaukee, WI) using an SPGR sequence with a temporal resolution of 30 sec. Gd-DTPA (Omniscan, Amersham Health, Princeton, NJ) was injected intravenously (0.1 mmol/kg). We used an



Figure1. Left: sagittal breast MRI with fiducial markers on the skin. Right: anterior/posterior motion of the fiducial marker indicated. The overall motion, i.e. vector sum of superior/inferior, anterior/posterior, and left/right motion, has even greater magnitude than A/P motion alone.

automated segmentation algorithm [2] based on local variation in contrast uptake and arrival time followed by multi-compartmental modeling. Motion correction was performed using the VTK CISG registration toolkit [3], which provides intensity-based image registration algorithms that maximize normalized mutual information (NMI). At current stage, affine registration is preferred to free form deformation (FFD) for its computational efficiency (>10 times faster). Major components of the study include: (1) a pre-processing step of gross polygon ROI definition is necessary for good registration accuracy, which blacks out regions other than the breast that experience significant motion, such as the heart and diaphragm. (2)15-degrees of freedom (DOF—3 translational, 3 rotational, 3 scaling, and 6 shearing parameters) affine registration of inter-frame DCE-MRI, with first frame as reference and subsequent frames as floating images. (3) Automated segmentation of DCE-MRI's with and without motion correction to obtain functional maps (arrival time and permeability). (4) Visual assessment of functional maps, followed by ROC curve comparison of segmentation outcomes with and without inter-frame image registration.

RESULTS AND DISCUSSION

A pair of arrival time maps with and without motion correction (Figure 2) demonstrates that motion correction reduces the noise level of tissue contrast uptake. ROC curve analysis was used for quantitative comparison of segmentation outcomes with and without inter-frame motion compensation (Figure





Figure2. Arrival time map without (left) and with (right) motion correction

multimodal 3D images', Leipzig, Springer-Verlag, March 2002.

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3). The up-left shift of and increased area under the ROC curve after motion correction indicates improved sensitivity and specificity at all threshold levels.

CONCLUSIONS

Our results indicate that inter-frame motion of DCE-MRI can be corrected with good accuracy by 15-DOF affine registration, which leads to improved performance of breast tumor segmentation. Future work will aim to: (1) verify that motion correction improves DCE-MRI segmentation on a larger patient population; (2) optimize FFD-based image registration techniques to compensate for nonuniform nature of soft tissue motion while preserving clinically acceptable computation time; and 3) demonstrate that these techniques improve tumor characterization and diagnosis.

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