Free-Breath DCE MRI for Solitary Pulmonary Nodule with Motion Correction Based on Non-Rigid Image Registration

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Introduction

Dynamic contrast-enhanced (DCE) MRI has proven valuable to characterize tissue of interest in solitary pulmonary nodule (SPN) [1], especially for delineating malignant from benign tumor. In DCE MRI studies, the kinetics of signal variation at lesions following the administration of the contrast agent is analyzed from time-intensity curve. Thus, it is crucial to measure the signal intensity at the corresponding regions in each frame in the time-series of images for accurate signal intensity curve analysis. However, the respiratory motion of the subjects during scans causes misalignment of anatomical regions among the frames resulting inaccuracy of time-intensity curve. Furthermore, the misalignment makes it impossible to perform pixel-by-pixel analysis to obtain distribution of kinetic parameters. To overcome the issue, several studies have demonstrated free-breath lung DCE MRI incorporating motion correction based on rigid image registration techniques [2,3]. We examined a free-breath lung perfusion analysis of patients with SPN using motion compensation technique based on deformable registration.

Materials and Methods

Five patients (2 males, 3 females, 27-81 years old, average 61 years old) with a SPN between15 to 30mm were enrolled. The study was conducted under the guideline of the institutional review board and a written informed consent was obtained from the participants. The initial diagnosis of SPN was made by CT and chest X-ray, and all patients underwent MRI study. The perfusion study was carried out on a 3T scanner (Siemens Trio, TIM system, Erlangen, Germany) using a body array coil. DCE MRI was performed using a 2D turbo FLASH (TR/TE=2.79/1.6msec, FOV=400mm, 192x180, 1 excitation, BW=360kHz, FA=10, 5mm slice thickness, oblique sagittal orientation, Temporal resolution=2s, scan time=4min, Gd-DTPA iv. 0.1 mmol/kg). Approx. 120 frames of images were acquired for each patient. Three intensity curves obtained from each series were compared: (i) an intensity curve measured at the fixed region throughout the series of frames without correcting inter-frame misalignment due to patient's respiration; (ii) an intensity curve measured at the fixed region throughout the series of frames, after applying automatic motion correction; (iii) an intensity curve measured at the lesion manually segmented in each frame by a radiologist. For automatic motion correction, each frame is registered to a 'key frame,' which is selected prior to the registration process. We used Diffeomorphic Demons image registration proposed by Vercauteren et al [4]. We analyze kinetics of the contrast agent based on the model proposed by Tofts and Kermode [5]. In our study, the plasma concentration after the bolus injection of Gd-DTPA was assumed to be a biexponential decay, which is expected from the compartmental theory. The kinetic parameters K^{trans}, v_e and k_{ep} were calculated from each intensity curve. All image processing and curve analyses were performed on medical image processing and visualization software, 3D Slicer [6] with 4D Analysis plug-in module developed for this study.

Results

The intensity curves from one of the cases are shown in Figure 1. The mean standard deviation error of kinetic parameters between (i) and (ii), and between (ii) and (iii) are listed in Table 1. We also generated parameter maps from motion corrected DCE images, which are shown in Figure 2.

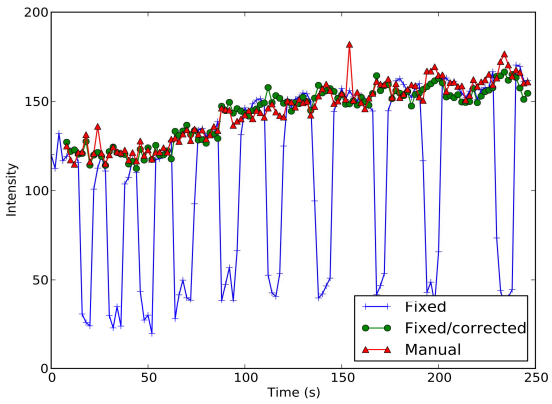
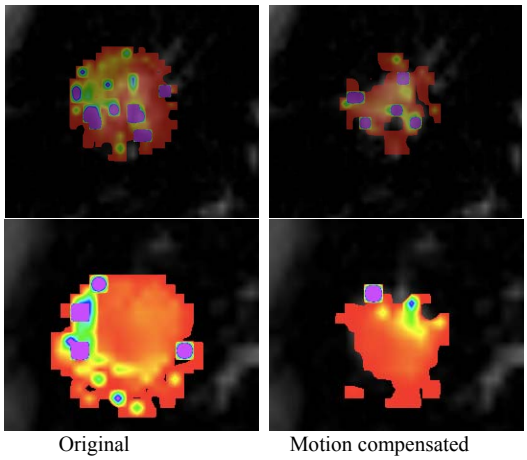


Fig. 1. Example of time-intensity plots measured in (i) fixed region, (ii) fixed region after motion correction and (iii) manually segmented region in the lesion.

Discussion and Conclusion

Our preliminary experiences with 5 patients show that free-breath lung DCE MRI with motion correction using non-rigid image registration significantly improved the fitting of the model curves to the signal intensity curves, and the results are comparable with the intensity curves generated from manually measured data. The pharmacokinetic parameters obtained from the motion corrected DCE MRI comparable to the parameters calculated from the manually measured intensity curves. Although the number of subjects is still limited in this preliminary study, the result indicates that the proposed method enables the pharmacokinetic analysis of free-breath DCE MRI. This is an important step to bring the DCE MRI analysis into future clinical routine for diagnosis of SPN, since it is not practical to manually measure the signal intensity at the suspected lesion on each frame of DCE MRI data, which usually consists of more than hundreds of frames. The technique also allows us to generate parameter distribution maps from free-breath lung DCE MRI. The parameter mapping may add information of the tumor structure, which helps to diagnose potential malignant portion of the SPN. For example, in the case of mixed type adenocarcinoma shown in Figure 2 upper, only 10% of the tumor was solid based on the histology diagnosis; the K^{trans} map shows about 10% of relatively high areas in peripheral, which agree with the histology finding. In conclusion, the proposed method provides a practical way to perform kinetic analysis of SPN based on free-breath DCE MRI, thus it enables future diagnostic applications.



Original Motion compensated

Fig. 2. Distributions map of Ktrans around SPN region are calculated from original (left) and motion-corrected (right) DCE MRI for two cases (upper and lower) and mapped to the structural MR images. The Ktrans map calculated from original DCE MRI does not match to the actual SPN area.

Table 1. Error of calculated kinetic parameters between (i) and (ii) and between (i) and (iii)

	K^{trans}	v_e	K
(i) – (ii)	-0.1 ± 0.2	-0.2 ± 0.6	-0.5 ± 1.1
(i) – (iii)	0.0 ± 0.0	0.0 ± 0.2	0.0 ± 0.3

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