Simultaneous fMRI-DTI using the Navigated Diffusion Sequence

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Target Audience: This work is of interest to researchers and clinicians who study functional MRI and diffusion tensor imaging.

Purpose: Although fMRI can show cortical regions that are activated by different cognitive processes, the link between blood oxygenation level dependent (BOLD) fMRI and neural activity is still poorly understood¹. Diffusion Tensor Imaging (DTI) is a powerful technique to map the fine architecture of the white matter. Several studies have recently used region of interest (ROI) of an activated area of fMRI for fiber tracking in DTI². The fMRI and DTI acquisitions are typically performed separately. The purpose of this work is to introduce a novel acquisition technique to perform simultaneous fMRI and DTI using the navigated diffusion sequence³. This was achieved by using the navigators in the navigated diffusion sequence to acquire BOLD data instead of performing prospective motion correction.

Methods: The navigated diffusion sequence has been recently introduced for real time motion correction in DTI using a 3D-encoded echo planar imaging navigator. One of the advantages of this sequence is that the navigator's protocol is separate from the diffusion protocol. As such, the navigator's protocol can be adjusted, modified, and inserted into the diffusion sequence. For motion correction, the navigator's protocol was used with a very low flip angle of 2 degrees, resolution $8 \times 8 \times 8 \text{ mm}^3$ and a very short TR (14 ms) and TE (6.6 ms). For the purposes of fMRI, the navigator's protocol needed to be adapted to optimise BOLD contrast by increasing the flip angle, spatial resolution, and TE. For fMRI-DTI acquisitions, the parameters for the three dimensional navigator were: TR 65 ms for each partition, TE 30 ms, voxel size $4 \times 4 \times mm^3$, matrix size $64 \times 64 \times 26$, bandwidth 3906 Hz/px, flip angles 7 or 15 degrees, total acquisition time for the 26 partitions plus fat saturation and phase correction 1.8 s. The acquisition parameters for the modified navigated diffusion sequence were: TR 6500 ms, TE 86 ms, 34 slices, matrix size 112 x 112, voxel size $2 \times 2 \times 4 \text{ mm}^3$, 30 non-collinear diffusion gradient directions, b-value 1000 s mm⁻², four b=0 scans. All scans were performed on a Siemens Allegra 3T scanner (Siemens Healthcare, Erlangen, Germany). A water phantom was first scanned for different flip angles to validate whether the modified navigator would affect the DTI data. Three fMRI-DTI acquisitions were performed: (i) a baseline acquisition with no navigator in the navigator in the navigator sequence, and acquisitions with (ii) 7 degree, and (iii) 15 degree navigator flip angles.

Three adult subjects (ages 25 - 37 years) were scanned with structural T1 imaging followed by different fMRI-DTI acquisitions. In all fMRI-DTI scans, the real time motion correction mechanism was disabled in the navigated sequence. Two fMRI-DTI acquisitions were acquired for 7- and 15-degree navigator flip angles, respectively, while the subject remained at rest. During another three acquisitions, subjects performed a right hand finger tapping task in an alternating fixation-tap boxcar design. The block length was 26s, so that 4 functional navigator images per block were obtained. For each subject, three runs of 34 volumes were acquired, two at a 7 degree flip angle, and one at a 15 degree flip angle. Two of the subjects repeated the same task during a conventional 2D BOLD EPI acquisition with the same volume TR and resolution, and a 90 degree flip angle. Functional images were realigned to correct for

volume TR and resolution, and a 90 degree Trip angle. Functional images were reangled to correct for motion, registered to the subject's T2 - then T1-weighted structural image, and smoothed with a 6 mm FWHM Gaussian kernel using SPM8. The first 4 BOLD EPI volumes (those corresponding to acquisition of the b=0 volumes) were discarded. Single subject GLM analysis was performed in SPM8 using a boxcar convolved with a canonical haemodynamic response function. The resulting t-statistic maps were visualized on each subject's high-resolution T1-weighted anatomical image. Diffusion tensor reconstruction and whole-brain fiber tractography was performed using Diffusion Toolkit. The area activated by 2D BOLD was used as a mask for fiber tracking.

Results: Figure 1 shows the average MD for different acquisitions for a 4 x 4 mm² region of interest for each slice of the water phantom. Activation in the contralateral primary motor area (M1) was detected for all subjects in each run. Figure 2 shows the maximum t-statistic in M1 for each subject in each run. Figure 3 shows the activated regions obtained for subject 2 in each run at an uncorrected threshold of p<0.001, FWE cluster size corrected p<0.05. Similar results were obtained for the other two subjects. Figure 4 shows for one subject the fibers that pass through the region activated by 2D BOLD for the different acquisitions.

Discussion: Using a water phantom we have confirmed that the modified navigator does not affect the mean diffusivity of the water phantom (Fig. 1). Although the contrast of the BOLD-weighted EPI image is affected by the preceding diffusion gradients, sufficient contrast is present to detect a robust BOLD response to a motor task in individual subjects. Although in each subject the activation strength and extent were greatest in the 2D BOLD images, in terms of maximum t-statistic or activation extent there is no clear difference between the 7 and 15 degree flip angles in the same subject. Figure 4 reflects that the architecture of white matter remains unchanged during BOLD activation when compared to at rest acquisitions.

Conclusion: The results of this work show a promising technique to perform simultaneous fMRI and DTI and moreover the possibility to explore neural connectivity during fMRI activation.

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Figure 1: Comparison of average MD for acquisitions with different flip angles compared to a baseline for a 4x4 mm² ROI for each slice of the water phantom.



Figure 2: Comparison of maximum t-statistic in contralateral M1 for different runs.



Figure 3: Comparison of activation in subject 2 for 2D BOLD to 3D EPI with two flip angles, 7° in (a) and 15° in (b) (p<0.001 uncorrected, FWE cluster size correction p<0.05).



Figure 4: Fiber tracking through the region activated by 2D BOLD for the 7- and 15-degree (D) at rest (R) and task-based (T) fMRI-DTI acquisitions.