Simultaneous structural and resting functional connectivity using interleaved DTI and BOLD fMRI

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INTRODUCTION

- Diffusion tensor imaging (DTI) and functional MRI (fMRI) have complementary roles in neurological research, but distinct acquisitions.
- Many studies combine information from separate DTI and fMRI experiments, but only one previous attempt has been made to acquire DTI and fMRI simultaneously, by obtaining BOLD contrast from diffusion-weighted images[1].
- We investigated the simultaneous acquisition of DTI and resting-state BOLD fMRI by using navigators in a navigated diffusion sequence[2] to acquire BOLD data.

METHODS

- The 3D-encoded echo planar imaging navigator[1] from the prospective motion corrected diffusion sequence was modified to perform simultaneous DTI-fMRI, by increasing the flip angle, spatial resolution, and TE.

fMRI-DTI acquisition parameters:

- **3D EPI navigator**: TR 65ms per partition, TE 30ms, voxel size 3.91 x 3.91 x 4 mm^3, matrix 64 x 64 x 26, bandwidth 3906 Hz/px, flip angle 7 or 15 degrees.
- **Diffusion imaging**: TR 6500ms, TE 86ms, 34 slices, matrix 112 x 112, voxel size 2 x 2 x 4 mm^3, 30 non-collinear diffusion gradients, b-value 1000 s mm^2, 4 b=0 scans.

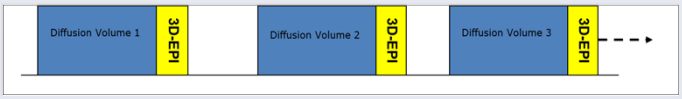


Fig 1. Diagram of the diffusion sequence with 3D EPI navigator. Time between sequential volumes (diffusion TR) is 6500 ms. The total navigator acquisition time for 26 partitions plus fat saturation and phase correction is 1.8s.

Subjects

- 3 adult subjects (aged 25-37 years)

Imaging

- A high-resolution T1 image, 7 fMRI-DTI acquisitions, and 1 non-navigated DTI scan were acquired.
- Both resting data and motor task data were acquired
  - **Motor task data**: 3 fMRI-DTI acquisitions (34 volumes each): two at a 7° flip angle, and one at a 15° flip angle, while subjects performed a right hand finger tapping task in a 26s alternating fixation-tap boxcar design
  - **Resting data**: 4 fMRI-DTI acquisitions (34 volumes each): two at a 7° and two at a 15° navigator flip angle
- All scans were performed on a Siemens Allegra 3T scanner (Siemens Healthcare, Erlangen, Germany)

Image processing

- Functional images were realigned, registered to the subject's T1 image, and smoothed with a 6mm FWHM Gaussian kernel in SPM8.
- **Motor task data**: GLM analysis was performed on the finger tapping data to define a functional ROI for each subject.
- **Resting data**: For each subject the two runs of resting-state data at the same flip angle were concatenated and the mean signal from the functionally defined left sensorimotor cortex (SM1) seed ROI was used in a regression analysis to create a whole-brain map of resting motor connectivity. Independent component analysis (ICA) was also performed on each subject's resting data using the GIFT toolbox.
- **Diffusion data:** Whole-brain, probabilistic tractography was performed on each DTI data set using 3dProbTrackID in AFNI, with a functionally defined left motor cortex ROI.

RESULTS

- Clusters in right SM1 and SMA were connected to the seed ROI at p<0.001 FWE in 5 of 6 resting-state BOLD acquisitions (Figs. 2 and 3).

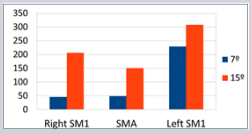


Fig 2. Mean across subjects of number of voxels significantly connected (p<0.001 FWE corrected) to the left SM1 ROI in 3 motor network regions.

- In the ICA, several resting-state networks (RSNs) could be identified through moderate spatial correlation (r>0.2) with GIFT RSN templates, although using this criterion a sensorimotor component could only be identified in one subject's data (Fig. 4).

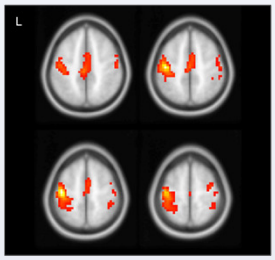


Fig. 3 Regression analysis of resting connectivity to the left SM1 seed ROI in concatenated 7 degree resting state data from subject 1, thresholded at p<0.001 FWE corrected.

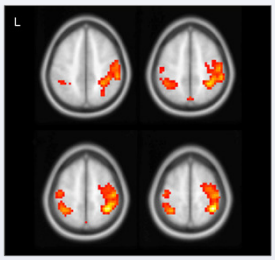
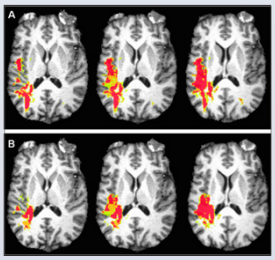


Fig. 4 Independent component from the 7 degree resting state runs from subject 1. Spatial correlation with the GIFT sensorimotor RSN template is r = 0.33. Z-score map is thresholded at z=2.

- Fig. 5 shows the overlap of white matter voxels with a suprathreshold number of reconstructed tracts for three different diffusion scans: 7° flip angle during the motor task, 7° flip angle resting, and non-navigated, overlaid on a T1 image.
- Regions are nearly identical across the three scans; small differences are localized to a single plane and boundary regions.
- Statistics of DTI parameters in the tracked regions are similar; mean FA for each scan is 0.44 ± 0.14, 0.43 ± 0.14, and 0.43 ± 0.13, respectively.

Fig 5. Consistent tract locations across three different scans. Red voxels contained tracts in all three scans; orange in two scans; and yellow, only one. The seed ROI was generated from ICA of a motor task during a 2D EPI BOLD sequence (A) and during the navigated scan (B).



CONCLUSIONS

- Although the quality of the navigator BOLD images is affected by the preceding diffusion gradients, sufficient contrast is present to identify several resting-state networks in individual subjects.
- This method shows potential to perform fMRI and DTI at the same time, without affecting the accuracy of the diffusion tensor reconstruction.
- In future work we plan to refine the sequence to optimize the navigator images and to investigate the possibility of simultaneously measuring diffusion-related and haemodynamic task responses.

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