Simultaneous acquisition of structural and resting state functional connectivity data using a volumetric navigated diffusion sequence

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Target Audience: This work is of interest to researchers and clinicians using functional MRI (fMRI) and diffusion tensor imaging (DTI).

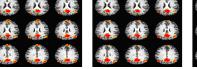
Purpose: FMRI and DTI are two different MRI techniques that complement each other in brain connectivity studies¹ and measure functional and structural connectivity, respectively. They are normally acquired separately and combined during post-processing. Previous attempts to acquire DTI and fMRI simultaneously have typically not been successful due to the mutual interference of DTI and fMRI excitations². Recently, a 3D echo planar imaging (EPI) acquisition was successfully inserted after each DTI volume to perform real-time motion correction³, with the two sequence protocols remaining separate. Here we examine using a 3D EPI protocol modified (e.g. in terms of spatial resolution and flip angle) to acquire BOLD resting state fMRI (rs-fMRI) data and the feasibility of simultaneous DTI-fMRI acquisition. We also investigate inserting a second 3D EPI acquisition in the middle of each DWI volume acquisition to increase fMRI temporal resolution.

Methods: The DTI sequence⁴ uses interleaved multi-slice 2D EPI. In the standard scheme, each slice in DTI is excited with a 90° flip angle rather than exciting the whole DTI volume. If a single 3D EPI volume ("single nav") is inserted each TR, this navigator experiences the same spin history every TR. However, if two 3D EPI volumes are inserted in each TR of a 2D slice-interleaved DTI acquisition, one after the even slices and one after the odd slices ("double nav"), the two navigators experience differing spin histories. To ensure that each DTI slice contributes similarly to the contrast of the navigator, we wanted to ensure that all slices had been excited equally prior to the navigator acquisition. To this end, successive slices were alternately excited and immediately spoiled (fast excitation) or excited and read (normal excitation). This scheme is illustrated in Fig. 1 for 8 DTI slices (slice numbers 0 to 7). Fast excitation plus spoiling takes 3.3 ms and immediately precedes each normal excitation.



Figure 1: DTI excitation scheme to ensure that all DTI slices contribute equally to navigator contrast.

Two adult subjects (aged 25 and 37 years) were scanned with structural T1 imaging and the following three rs-fMRI+DTI combinations: a) standard separate 2D EPI BOLD and DTI acquisitions; (b) combined DTI-fMRI with a single nav, and (c) DTI-fMRI with the double nav. All scans were performed on an Allegra 3T scanner (Siemens Healthcare, Erlangen, Germany). For fMRI-DTI acquisitions, the parameters for the 3D EPI were: TR=79 ms for each partition, TE=30 ms, voxel size 3.9 x 3.9 x 4 mm³, matrix size 64 x 64 x 28, bandwidth 3906 Hz/px, 11 deg flip angle, total acquisition time including fat saturation and phase correction 2.3 s. Standard BOLD data were acquired for 188 volumes with the same spatial resolution, TR 2.3 s, TE 30 ms. The acquisition parameters for DTI were: TR=132.5 ms per slice, TE=86 ms, 40 slices, matrix size 112 x 112, voxel size 2.5 x 2.5 x 2.5 mm³, 30 non-collinear diffusion gradient directions repeated 3 times for DW gradient values of 999, 1000 and 1001 s mm⁻², four b=0 scans to achieve 94 and 188 time points for single and double nav scans, respectively. The rs-fMRI temporal resolution for the standard BOLD sequence, single nav fMRI-DTI and double nav fMRI-DTI were 2.3s, 7.6s, and 4.95s, respectively. Total scan times were 7.2 mins, 11.9 mins, and 15.5 mins, respectively. To compare fMRI-DTI data acquired in the same scan time as the standard BOLD acquisition (7.2 mins), 57 and 87 3D-EPI volumes from single and double nav acquisitions, respectively, were used in analyses. Similarly, four b=0 and 30 DWIs were used for each diffusion analysis. Rs-fMRI pre-processing was performed using AFNI's afni_proc.py tool (regression of WM and CSF; smoothing radius=6mm; bandpass = 0.01-0.1 Hz). For DTI, FSLmcflirt was used for motion correction. Seed based correlation of RS-fMRI data (same seed for all



(a) BOLD (b) Double nav (c) Single nav Figure 2: Default mode network in standard BOLD and 3D EPI images

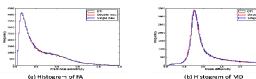


Figure 3: Graphical representation of FA and MD distributions of D images with and without the navigators.



Figure 4 : An example of tracts in the default mode network for different imaging sequences

 $acquisitions)\ was\ performed\ using\ AFNI's\ InstaCorr.\ Tractography\ was\ performed\ using\ AFNI-FATCAT.$

Results: In one subject, five standard resting state networks were visually identified using the double navigator sequence. Figure 2 shows comparisons of the default mode network (DMN; threshold *r*>0.5) in the BOLD and the 3D EPI images. While networks are apparent in the single nav case, they are quite noisy, presumably due to low temporal resolution as well as the relatively small number of total volumes acquired. The FA and MD distributions for all DTI acquisitions are compared in Figure 3. Figure 4 shows the AND-logic tracts connecting the DMN regions (ROIs mapped from the standard BOLD acquisition).

Discussion: We have shown the feasibility of combining BOLD fMRI and DTI data acquisitions. While the single navigator networks appeared to be quite noisy, the resting state networks obtained using standard BOLD and double-3D-EPI-navigated DTI showed quite similar spatial extent and connectivity. Acquired diffusion data showed similar whole brain distributions of tensor parameters, as well as strikingly similar tractographic patterns, suggesting that the presence of two navigators with 11 deg flip angles did not adversely influence the DTI acquisitions. Future work will be performed to increase effective temporal resolution of the fMRI (as well as to decrease total scan time), for example by further insertion of navigators in the DTI acquisition, reducing DTI spatial resolution, or the 3D EPI excitation of a whole DTI volume.

Conclusion: The double 3D-EPI navigated DTI sequence has shown great potential for simultaneously acquiring DTI and fMRI data, and therefore for investigating brain structural and functional connectivity simultaneously.

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