Improved detection of subcortical resting state networks in functional MRI using multi-echo simultaneous multi-slice acquisition

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Introduction

Resting-state functional connectivity magnetic resonance imaging (fcMRI) has emerged as a key approach for characterizing the functional connectivity of the human brain. Functional connectivity of subcortical structures is of a particular interest and has been shown to play a role in verbal episodic memory function and Alzheimer's disease[1,2]. A recent method called multi-echo ICA (ME-ICA) has shown that collecting multiple echoes facilitates automatic identification and robust removal of physiological noise confounds[3] in fcMRI. This has the potential of increasing the detection performance of subcortical resting-state functional connectivity. However, collecting additional echoes can reduce the number of volumes per scan time, which reduces detection performance. One way to increase the number of volumes per scan is by using simultaneous multi-slice RF pulse excitation[4]. In this study, we investigated the detection performance of subcortical resting-state functional connectivity using multi-echo simultaneous multi-slice (MESMS) with a TR=0.92s. The performance was evaluated by comparing it to a subsampling of the same data.

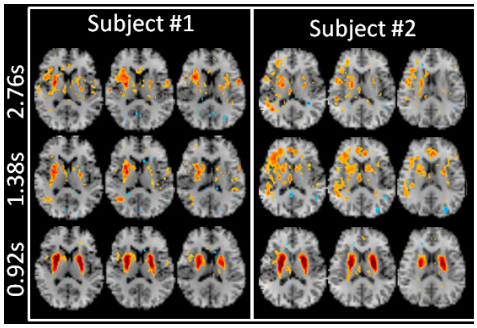

Figure 1. Representative functional connectivity maps for two temporal subsampling schemes and the original data for a seed voxel in the left Putamen. Results are shown for both subjects.

	Accepted BOLD ICs	
TR	**Subject #1**	**Subject #2**
2.76s	25, 20, 19	30, 15, 18
1.38s	32, 32, 34	30, 27, 29
0.92s	39	31

Table 1. Number of accepted BOLD ICA components used in the correlation analysis.

Methods

fMRI resting state data were collected from two subjects on a 3T GE MR750 system with a 32 channel receive coil (Nova Medical). Resting state scans (10 minutes, 26 seconds; eyes open with fixation cross) were performed using MESMS (3 echoes) echoplanar imaging (EPI) acquisition, where the acquisition used a 1.33-fold phase encode acceleration factor. The resolution was 3.75x3.75x4mm with whole brain coverage (FOV 24cm, 64x64 matrix, 36 slices). We used a blipped-CAIPI EPI k-space trajectory[5] with 3 sagittal slices per RF excitation[4]. Other acquisition parameters were: TR=0.92s (680 volumes), TEs=13.9ms, 33ms, 52.1ms, FA=56°. To reconstruct the images, we used SENSE reconstruction with a fast Conjugate Gradient Toeplitz-based iterative algorithm, where we regularized with a spatial roughness penalty[6]. Using the previously described ME-ICA approach[3], the multiple echo data from the MESMS scan were spatially concatenated and decomposed using spatial independent components analysis (ICA)[7]. The weights of each component were then fit to a BOLD signal model and a goodness of fit metric was used to automatically differentiate BOLD components from non-BOLD components. The BOLD ICA component coefficients were optimally combined across the multiple echoes to form single-echo BOLD ICA component coefficients[8]. To generate the functional connectivity maps, a seed signal from the left putamen ROI (generated using Freesurfer anatomical segmentation) was computed from the BOLD ICA component coefficients and correlated with every voxel in the brain. We also generated data with longer effective TR values and performed the same ICA analysis. This was done by either sampling every third volume of the original MESMS data (TR=2.76s) or sampling every 2-out-of-3 volumes (TR=1.38s). Both sampling schemes can be done three different ways for a total of 6 subsampled data sets.

Results & Discussion

Figure 1 shows the functional connectivity maps obtained with a seed placed in the left putamen. The figure shows how the bilateral connectivity for the putamen becomes more visible for lower TR due to the increase in the number of volumes per scan time. We also see that the putamen functional connectivity map is very consistent across both subjects for TR=0.92s, which is not the case for longer TRs. This indicates that fcMRI data with an increased number of volumes per scan time are able to improve the detection of subcortical functional connectivity maps in a robust manner. Importantly, the MESMS approach achieves high temporal resolution but does not sacrifice tSNR in deep brain artifact-prone areas such as the subcortex, and ME-ICA can extract BOLD components from simultaneous multi-slice data. This detection improvement is further supported in results shown in Table 1, where the number of accepted BOLD ICA components for different TRs are listed. Table 1 shows that the number of accepted BOLD ICA components is the highest for the data with the most number of volumes per scan time (shortest TR). As the number of volumes per scan time decreases the average number of accepted components decreases also. This indicates that the number of accepted functional networks increases as the number of volumes per scan time is increased. To summarize, by using MESMS we are able to collect more volumes per scan time compared to the multi-echo single-slice acquisition (where a typical TR is on the order of 2s), which effectively increases the detection performance of subcortical resting state networks.

References: [1]Ystad et al, Neuroimage, 2010. [2]Allen et al, Archives Neurology, 2007. [3]Kundu et al, Neuroimage, 2011. [4]Moeller et al, MRM, 2010. [5]Setsompop et al, MRM 2011. [6]Fessler et al, IEEE TSP, 53:3393, 2005. [7]Beckmann & Smith, IEEE TMI, 23:137, 2004. [8]Posse et al, MRM, 42:87, 1999.