Improved Detection of BOLD-like Independent Components with Multi-Echo Simultaneous Multi-Slice Acquisitions and Multi-echo ICA

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Introduction: Resting-state functional connectivity magnetic resonance imaging (fcMRI) has emerged as a popular approach to characterize the functional connectivity of the brain at rest. The recent advent of simultaneous multi-slice (SMS) fcMRI acquisitions allows for higher sampling rates over conventional acquisitions[1]. This benefits resting state fcMRI analysis in terms of tSNR, statistical power, increased spectral bandwidth for resting state networks[2] and reduced aliasing of higher frequency signal and noise sources. In a parallel line of work, multi-echo acquisitions analyzed with an independent component analysis framework (ME-ICA), which decomposes fcMRI data into BOLD and non-BOLD weighted components, have been shown to be effective for automatic identification and removal of physiological noise and motion artifacts, with concomitant increases in tSNR and statistical power[4]. By combining the two approaches, ME-ICA analysis of data acquired with multi-echo and simultaneous multi-slice acquisitions[3] (MESMS) has the potential to improve the identification of BOLD weighted components that contain high-frequency information. Here we investigate this potential gain by comparing the performance of MESMS data to multi-echo single-slice (MESS) data.

Methods: Resting state fMRI data were collected from twelve subjects on a 3T GE MR750 system with a 32 channel receive coil (Nova Medical). Resting state acquisitions (10 minutes per run; eyes open; fixation cross) were either MESMS and MESS (3 echoes) echo-planar imaging (EPI) in two separate runs per session. Both acquisitions used a 1.33-fold phase encode acceleration factor. The resolution was 3.75x3.75x4mm and had whole brain coverage (FOV 24cm, 64x64 matrix, 36 slices). A blipped-CAIPI EPI k-space trajectory[5] was used, with 3 sagittal slices per RF excitation[6]. Other acquisition parameters (MESMS/MESS) were: TR=0.87s/2.61s (690/230 volumes), TEs=13.9ms, 33ms, 52.1ms, FA=56°/80°. To reconstruct the images, we used a SENSE reconstruction with a fast Conjugate Gradient Toeplitz-based iterative algorithm and a spatial roughness penalty[7]. For the ME-ICA analysis, the multiple echoes were optimally combined[8] and then decomposed using spatial independent components analysis (ICA). Each IC's time series was fit to the original multi-echo data and the resulting spatial maps were statistically tested for BOLD and non-BOLD properties[4]. A goodness of fit metric automatically categorized each IC as BOLD (accepted) or non-BOLD (rejected). ME-ICA analysis was run on both the MESMS and MESS data. It was also run on subsampled MESMS data generated by taking every third volume of the original MESMS data, with the first, second and third volume as start volumes. Subsampling was performed without and with low-pass filtering (LPF; fc=0.19Hz), yielding 3 datasets (1 per start volume) of subsampled (ssamp) MESMS and 3 datasets of MESMS LPF+ssamp, respectively.

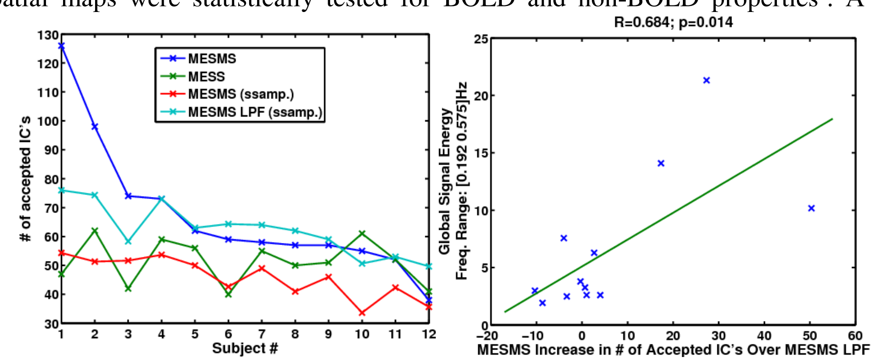

Figure 1: (Left) Number of accepted IC's from ME-ICA per subject ordered from highest to lowest number of MESMS accepted IC's. (Right) Correlation between high frequency global signal energy and the increase in the number of accepted IC's for MESMS compared to MESMS LPF+ssamp.

Results & Discussion: Figure 1 (Left) shows, for each subject, the number of accepted ME-ICA components for MESMS, MESS and the two subsampled MESMS datasets (both averaged across the three start volumes). Table 1 shows results from t-tests of the difference in means of selected pairs of curves. From this we see: 1) *MESMS vs MESS*: MESMS data allows for finer parcellation (more BOLD IC's) and thus better characterization of resting state networks due to the benefits of the higher sampling rate; 2) *MESS vs MESMS (ssamp)*: The number of ICs identified by subsampled MESMS (w/o LPF) is similar to that of MESS, indicating that the properties of MESS are well represented by subsampling of the MESMS data; 3) *MESMS (ssamp) vs MESMS LPF+ssamp*: MESMS LPF+ssamp performs better than MESMS (ssamp), indicating that the presence of aliased high frequency components can interfere with the ability to detect BOLD-like components; 4) *MESMS vs. MESMS LPF+ssamp*: On average, MESMS LPF+ssamp data have a similar number of accepted IC's as the MESMS data. The exceptions are the first three subjects, which exhibit a larger number of components in the MESMS data. Figure 1 (Right) shows that these subjects have a greater amount of high frequency energy in the global signal (average BOLD signal across the brain) and that this energy is correlated with the number of additional components observed in the MESMS data (as compared to MESMS LPF+ssamp). Overall, our results show that some subjects can exhibit high frequency resting state BOLD-like activity that is not captured at conventional sampling rates and that MESMS and ME-ICA analysis can be used to detect and characterize these BOLD-like components.

MESMS vs MESS	MESS vs MESMS (ssamp)	MESMS (ssamp) vs MESMS LPF+ssamp	MESMS vs MESMS LPF+ssamp
0.0386	*0.0755*	**2.663e-07**	0.3218

Table 1: P value of t-tests comparing means of curves in Figure 1.

References: [1]Smith et al, Neuroimage, 2013. [2]Niazy et al, Prog Brain Res, 2007. [3]Olafsson et al, ISMRM 2013, 3318. [4]Kundu et al, PNAS, 2013. [5]Setsompop et al, MRM 2012. [6]Wong, ISMRM 2012, 2209. [7]Fessler et al, IEEE TSP, 53:3393, 2005. [8]Posse, MRM, 1999.