IMPROVING SENSITIVITY AND SPECIFICITY FOR RS FMRI USING MULTIBAND MULTI-ECHO EPI AT 7T

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Target audience: MR physicists, Neuroscientists, Data analysts

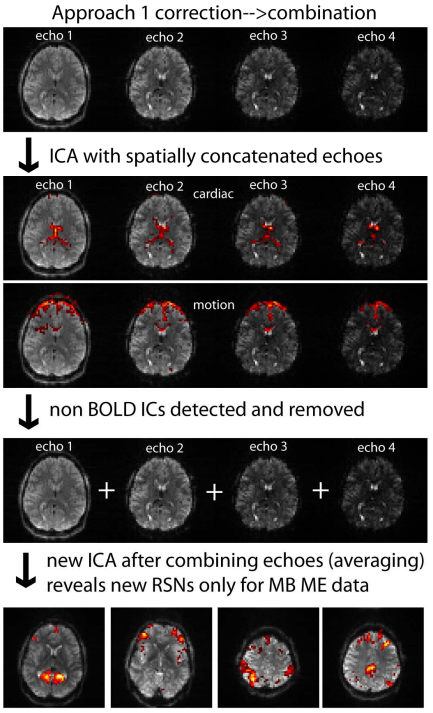
Purpose: Recently we implemented a multiband[1] (MB) multi-echo (ME) sequence to investigate the potential improvement in sensitivity at 7T for resting state (RS) fMRI. The power of ME for the detection and removal of non-BOLD (physiological noise, motion related) signal variance from fMRI data has been convincingly shown for RS[2] and task[3] fMRI. In this study we investigated two different approaches for cleaning ME and MB ME RS fMRI data to fully exploit the rich temporal information of MB ME data.

Methods: RS data (eyes open, 5 min. both acquisitions) were collected for 10 subjects (with informed consent) at a 7T Siemens scanner (Siemens Healthcare, Erlangen, Germany) with a 32 channel head coil. Acquisition parameters are summarized in Table 1. The sequences are matched in terms of spatial resolution and FOV. Reconstruction of MB data is done offline in Matlab using a SENSE/GRAPPA reconstruction[4].

Table 1. Acquisition Parameters

	TR (s)	TEs (ms)	In plane GRAPPA	SMS factor	Excitation FA	BW (Hz/Px)	Slice gap	Res.(mm)
ME	2.22	11,23	3	-	40	2520	17%	3.5 isotropic
ME SMS	0.74	36,48		3				

Prior to ICA the following preprocessing steps were applied: spatial smoothing (5 mm kernel), drift removal, MCFLIRT motion correction. All ICAs were carried out with Melodic (v3.14, http://www.fmrib.ox.ac.uk/fsl/) with 70 components. Two different analysis pipelines are illustrated in Figure 1. Manual detection and removal of non-BOLD ICs was carried out with FSL_FIX (http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FIX). The same procedure was followed for ME and MB ME data. The ICs for each of the three possible scenarios (no correction and the two analysis pipelines) were manually categorized and linked to corresponding ICs in the other two scenarios.



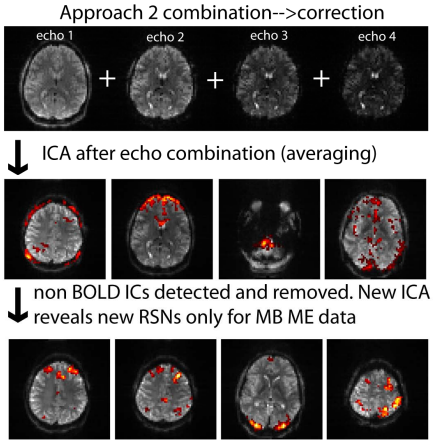


Figure 1. The two analysis pipelines

Results & Discussion: Figure 2 shows the IC corresponding to the motor network from different analysis pipelines for a single subject. Comparing the first and second row the RSNs show reduced false positives similar to results from Ref.5. With respect to differences between ME and MB-ME data, after correction with either of the techniques, 10 to 12 additional RSNs (last rows in Fig. 1, mostly in the vicinity of regions associated with artifacts before the correction) were discovered for MB-ME data whereas ME data resulted in approximately the same number of RSNs. This improvement is most likely due to the better separation of physiological based noise sources such as respiration and the interaction of cardiac and respiration into individual ICs for MB ME data.

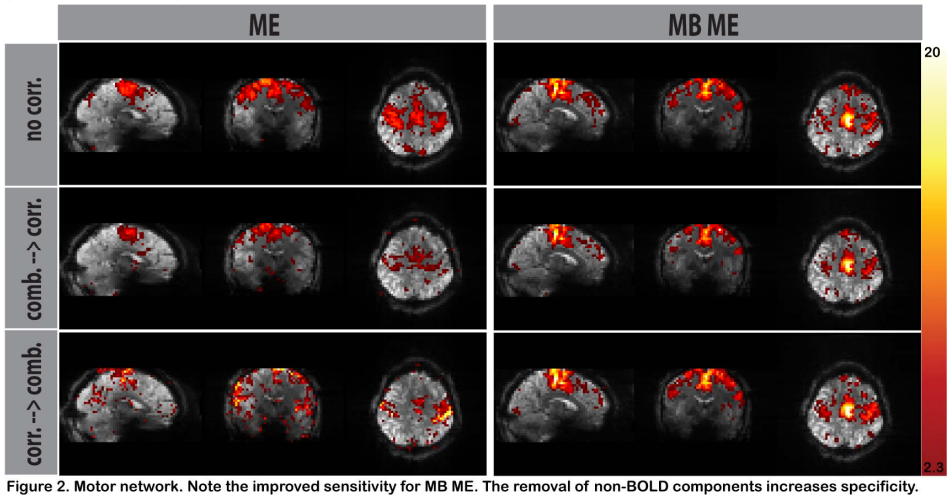


Figure 2. Motor network. Note the improved sensitivity for MB ME. The removal of non-BOLD components increases specificity.

Removal of non-BOLD ICs before combination results in larger clusters. With regards to the differences between the two analyses it can be argued that MB ME data is less sensitive to the analysis strategy whereas ME requires a detailed and careful correction procedure. Using a commonly employed spatial resolution, MB ME offers improvements in the analysis of resting state connectivity next to the commonly known advantages such as low distortion, the potential to acquire data over a broad range of T2* values and automatic regression of non-BOLD ICs[2].

Conclusion: We have implemented a high temporal resolution (0.74s) MB ME EPI sequence and showed that MB acquisition improves functional connectivity compared a standard ME sequence after the removal of non-BOLD related artifactual signals.

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References: 1) Larkman et al., JMR 2001. **2)** Kundu et al., NeuroImage 2012. **3)** Buur et al. NMR Biomed 2009. **4)** Blaimer et al., JMRI 2006. **5)** Kundu et al., PNAS 2013.