Fully Automated fMRI Denoising Using Multi-Echo fMRI and TE-Dependent Properties

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Introduction

Noise from motion, cardiac pulsation, and other sources severely reduces signal fidelity in many parts of the brain, in both activation and resting-state BOLD fMRI. There has been a recent focus on using multi-echo (ME) fMRI to denoise fMRI data. ME-fMRI acquires T2*-weighted images at several echo-times (TE) after excitation within approximately the same TR as for conventional fMRI. These are reconstructed to provide each voxel with a set of timecourses for the different TEs. BOLD signals, which are fluctuations in T2*, are equivalently expressed at all TEs, however scaled by a TE-dependent magnitude. Non-BOLD signal manifests differently across TEs. This can be used to denoise ME data by averaging the normalized signal of all TEs, or modeling the optimal combination of the timecourses to produce one contrast-enhanced signal. In this study, the opposite approach was taken. ME data were decomposed with ICA to identify both BOLD signal components and noise components and evaluate their modulation with TE. ICA of conventional fMRI provides no criteria to distinguish artifact from BOLD components, but with ME data, BOLD components were identified with TE-dependent component scaling. Remaining components were determined to be noise. Noise component timecourses were then used as baseline regressors for activation and resting-state mapping.

Methods

Activation was studied with 10 blocks of a 25-second passive face viewing condition alternated with right-handed finger tapping with no interleaving rest. Resting-state fixation was separately scanned. Multi-echo fMRI was acquired with the SPEP sequence, in the gradient-echo (GE) echo-planar-imaging (EPI) mode, with parameters: 3 TEs=14,37, and 60ms; TR=2500ms; FA=90 degrees, A/P frequency encoding; FOV=300mm with 64x64 in-plane (4.7mm^2) resolution and ASSET-2 in the phase direction; 4.7mm slice thickness, 0.3mm gap, and 24 slices spanning the full cerebrum and a fraction of the cerebellum for all subjects. ME k-space data was reconstructed offline with in-house software to three 3D+time datasets, one for each TE.

Functional scans were preprocessed with standard methods including slice-time correction, volumetric alignment, and minimal spatial smoothing (5mm FWHM). The set of image series of the three TEs were then spatially concatenated, so that each image of the resulting aggregate image series had three brain images, and the resulting image series had the same number of images as the input. A customized configuration of FSL's MELODIC was used for ICA decomposition of the concatenated ME image series. Probabilistic PCA was used for automated dimensionality estimation. Each output component was expressed as three "stacked" spatial patterns, which together encoded each voxel's component amplitude at the different TEs. An amplitude model based on the canonical signal decay was then used to compute an F-statistic for the TE-dependence of the component at every voxel. To determine BOLD components, voxelwise F-statistics were then averaged for each spatial component, weighted by the variance of signal magnitudes, to providing a component-ranking score, Gamma.

Results and Discussion

Components split into two groups when ranked by Gamma score (Fig A). This was consistent between subjects and conditions. Typically, between 17 and 30 components had high Gamma scores (70-200). These were verified as BOLD components based on timecourses corresponding to task-activation and localization to primary motor and visual cortices, or otherwise timecourses with low-frequency oscillations (<0.08 Hz) and localization to known functional networks. The remaining components all had low Gamma scores, between 17 and 30. Low-gamma spatial maps consistently showed artifactual localization and noisy component timecourses. Components with lowest Gamma scores were found to be to be high-frequency oscillations. The Gamma distribution was used to fully automate artifact component identification, independently of subject motion or physiology timecourses, and without anatomical references.

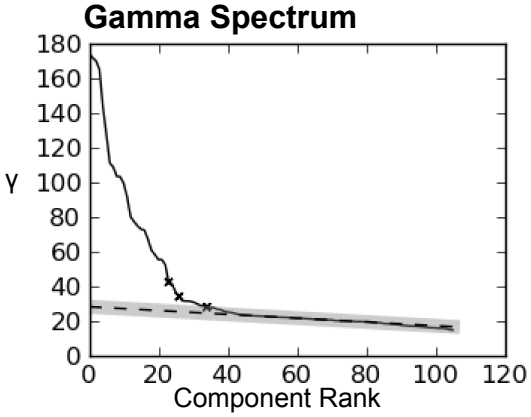

Fig A The distribution of Gamma (G) scores, when plotted as a rank-ordered spectrum, was a distinct L-curve with a long, flat, tail. This is shown in Figure A. Low-Gamma components were selected by fitting a line to the flattest part of the tail, and all components with Gamma scores below the line (and its spread) were selected as artifacts.

Timecourses of low Gamma components were used as baseline regressors for both activation mapping and for seed-voxel connectivity for the hippocampus (Fig B). T-maps were computed on unfiltered input data of the highest contrast, at TE=37ms,. Along with polynomial drift terms, 'Before' maps use motion parameters as baseline, and 'After' includes only low-Gamma component timecourses as baseline. T-values are REML-corrected for autocorrelation in noise, and thresholded to FDR corrected q=.001 for activation, and q=0.0001 for resting state.

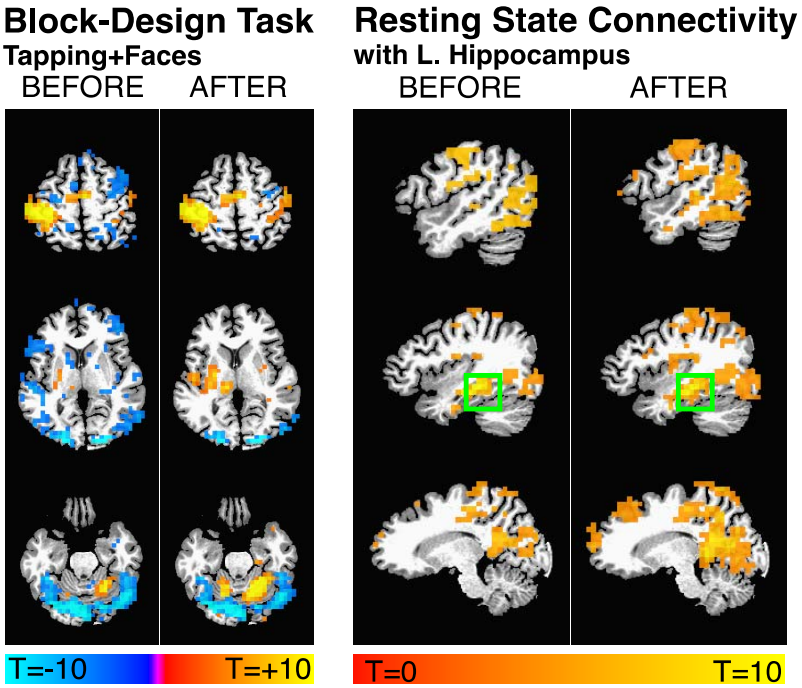

Fig B ME-ICA denoising improves SPMs for both task-activation and resting-state connectivity. Positive activation from tapping is enhanced in SMA, S1, left putamen and vetrolateral thalamus, and cerebellum. It preserves expected anti-correlation for the interleaved face-viewing in V1 and FFA, while removing spurious anticorrelations elsewhere. Hippocampal connectivity is generally improved across the brain, while revealing correlations in frontal cortex (seed in green box).