Assessment of the separability of physiologic noise using spatial ICA

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Introduction

Several recent studies have appeared in the literature that demonstrate that spatial ICA can identify components in BOLD-weighted MRI data whose principal temporal behavior is attributable to physiologic noise—either cardiac, respiratory, or an unknown combination of[1-3]. Although these studies do show in a very few subjects that a component is isolated that appears to have strong coupling to cardiac and respiratory rates, they do not demonstrate that the remaining components are unaffected by cardiac and respiratory rate-related effects. In this study, we perform spatial ICA on direct sampled and under sampled BOLD-weighted MRI data and show that, although spatial ICA is capable of separating components with a high correlation to cardiac and respiratory fluctuations, the remaining components still show substantial coupling to cardiac and respiratory effects. Correction methods are investigated.

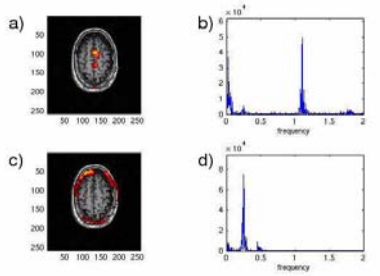

Fig1: ICA components of direct-sampled data selected by procedure to be physiologic in origin. 1a) Spatial map of significantly coupled voxels to selected component. 1b) Fourier power of cardiac-identified component,1c) respiratory map, 1d) Fourier power of respiratory-identified component.

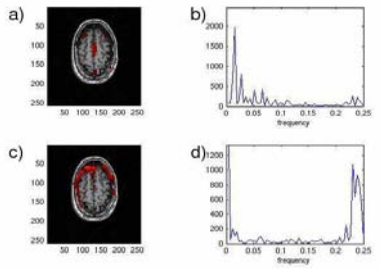

Fig 2: ICA components of whole-brain undersampled data selected by spatial correlation with direct-sampled physiologic components.

Theory

The baseline voxelwise coupling to the physiologic noise sources is calculated using RETROICOR [4] with parallel measured cardiac and respiratory data. RETROICOR finds the peaks of the physiologic sources and converts to the data to a phase, and fits two orders of both a sine and cosine of the phase data to the voxel timeseries. The coupling power for a voxel is the quadrature sum over both orders of these couplings (separate for cardiac and respiration), denoted here by $P_{c,r}$. If there is no physiologic coupling in the timeseries, RETROICOR is fitting noise, and a histogram of $P_{c,r}$ will follow a Rayleigh distribution. If there is physiologic noise present however, the power histogram will have an additional component in the tail at high power that can be determined by fitting the full-width at half-maximum (FWHM) of the histogram to a Rayleigh and subtracting to leave the non-noise coupling. Thus, we characterize the physiologic noise content throughout the brain as the fractional area between the observed distribution of $P_{c,r}$ and a Rayleigh distribution fit to the full-width at half-maximum (FWHM) of the $P_{c,r}$ frequency distribution, denoted here as PN.

Methods

The following three scans were performed on four subjects. Scan1: anatomic whole-brain T1-weighted inversion recovery turboflash (MPRAGE), 120 axial slices, thickness 1.2mm, Field-of-view (FOV) 256mm×256mm, matrix=256×128. Scan 2: undersampled whole-brain EPI scans: 132 volumes of 31-4mm thick axial slices TE/TR/flip=29ms/2000ms/90^o , matrix=64×64, 256mm ×256mm FOV, BW=125KHz. Scan 3 direct-sampled EPI scan, 2 contiguous 4mm axial slices through primary and supplementary motor regions, FOV 256mm×256mm, TE/TR/FA 29ms/130ms/30^0, matrix 64×64, BW=125KHz, 1100 volume repetitions. The locations are chosen such that they correspond exactly to two of the contiguous slices in the pair of whole-brain EPI scans. Physiologic data is measured in parallel for the EPI scans with a finger pulse plethysmograph and a respiratory bellows around the chest. For all subjects, both EPI studies are postprocessed with motion correction, a regression of the second order motion parameters of each voxel[5], and spatially filtered with a 2D hamming filter[6]. The motion corrected and filtered data is analyzed with spatial ICA (FSL Melodic probabilistic ICA)[7]. The number of component in the decomposition of each scan is varied in steps of 4 from 20 to 40, and an additional decomposition using components estimation is performed. The component timeseries calculated from the direct sampled scans (scan 3) are converted to Fourier power and are correlated with the Fourier power of the cardiac and respiratory data to select the spatial component for respiration and the spatial component for cardiac. Within the same subject, the whole volume scan (scan 2) physiologic components are selected by calculating the spatial correlation of the scan 3 physiologic spatial component with the same slice components calculated from scan 2. The scan 2 components with highest spatial correlation to the corresponding physiologic components of scan 3 are selected as the physiologic spatial components for the undersampled data (scan 2). Three separate analyses are performed on the data using these selected components. The first consists of removing only the voxels that have significant coupling to the component found by the aforementioned procedure. If this component contains all voxels with significant coupling to cardiac and respiratory rates, the power in the remaining voxels should be nearly white noise, and the histogram should then follow a Rayleigh distribution. The second analysis consists of removing effect of the components in the undersampled data by the method of Arfanakis et al[6], finding the residual coupling with RETROICOR and calculating Pn. In the third analysis, the remaining components are correlated with the slice-sampled cardiac and respiratory physiologic data to assess the presence of residual correlated noise. The correlation was converted to a z-score and histogrammed.

Results

In all subjects, it was possible to identify a spatial component from the direct-sampled data ICA decomposition similar to that shown in Fig 1, the timecourse of which has Fourier power similar to that of the pulse plethysmograph. Similarly, a respiration-related component was found which had high coupling to the bellows respiration data. A typical spatial map from the whole-volume undersampled data found by correlation with the direct-sampled component is shown in Fig 2. Note aliasing of cardiac ffirst harmonic of respiration, yet spatial maps of both are very similar to Fig1. PN is plotted versus scan and correction applied, shown in Fig 3, but no effect is seen on the fractional coupling power to physiologic noise. The residual component zscores produced by the cross correlation analysis were fit to a gaussian distribution, with standard deviation of 1.1 for cardiac and 2.4 for respiratory, showing that the remaining components have significant coupling to physiologic noise. No effect was observed in varying the number of selected components in the analysis.

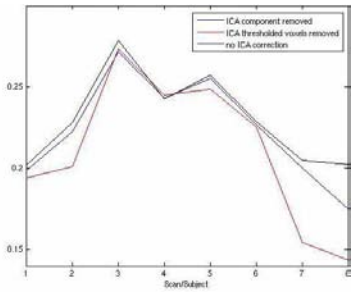

Fig 3: Proportional area between Rayleigh fit to coupling power histogram and the coupling power histogram for uncorrected data, thresholded voxels removed, and data reconstructed without physiologic components.

Conclusion

We have shown that while ICA can reliably separate the temporal and spatial pattern relevant to a particular physiologic process, there remains residual physiologic noise across the remaining components. Incomplete separation of the source signals leads to bias in the correlation maps and correction using parallel measured physiologic data is required.

References

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