

Group sparsity reconstruction for physiological noise correction in functional MRI

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Introduction: Functional connectivity studies, which look at low-frequency (<0.1 Hz) temporal correlations in functional MRI, have generated significant interest in recent years. However, these studies sample the cardiac and respiratory rhythms well below their respective Nyquist frequencies, confounding analysis of the underlying temporal correlations. One potential avenue for reconstructing fMRI data with high spatiotemporal resolution is to exploit its sparsity in the temporal frequency domain. Here we propose a modification to the orthogonal matching pursuit (OMP) algorithm [1] that draws from elements of group sparsity. Other group sparsity approaches combined with random sampling and OMP algorithms have been used previously in MRI [2,3], although none for reconstruction and physiological noise removal.

Theory: Mathematically, we assume that $m(x, t) = \sum_{r=1}^R u_r(x) v_r(t)$ where each $v_r(t)$ is a pure complex exponential. This is similar to a low rank model, which has been used in a number of dynamic studies in cardiac MRI [4,5]. In this case, we restrict the temporal basis functions to be pure complex exponentials. The complex exponentials are found through greedy selection: let Φ denote a DFT matrix and let \mathbf{Y} denote a $P \times M$ matrix of measured data where M is the number of k-space points and P is the number of times each k-space point is sampled. We wish to select a small collection of “atoms” φ_i from Φ that best approximates the sampled data in \mathbf{Y} . This is done via the orthogonal matching pursuit algorithm outlined in Figure 1, where $\mathbf{R}^{(j)}$ denotes the residual and Λ_j denotes the index set at iteration j .

The matrix \mathbf{W}_m is a $P \times N$ matrix of 1s and 0s that contains the sampling information for the k-space point indexed by m . The coefficients to the atoms are solved for in a least squares problem by using \mathbf{A}_v , a matrix that contains the elements of the atoms embedded in such a way as to produce the corresponding output data vector. We combine this with random sampling at each k-space position across time (operator denoted by $S(\cdot)$). This would be feasible in a 3D EPI sequence where each phase encode randomly goes to any one of the M k-space locations. In this setting, we could apply the inverse DFT along the frequency encoding direction and reduce the 3D problem to a stack of 2D problems.

Experiments and Results: We examine the potential of this method via a 2D EPI experiment with high spatiotemporal resolution data. One volunteer was asked to perform a resting state connectivity task. The volunteer was scanned with a 2D single shot EPI sequence at a single slice with imaging parameters TR=100ms, TE=30ms, flip angle = 22°, FOV=22x22cm, matrix size=64x64. The data were detrended and low pass filtered with a cutoff of 0.08 Hz and temporal correlations were calculated relative to the posterior cingular cortex (PCC), known to be part of the default mode network. The correlation map obtained from the original high resolution data served as an “ideal” map. The data were then decimated by a factor of 63/64s to simulate a random 3D EPI where the frequency direction is transverse to the slice. The high temporal resolution data set was then reconstructed with the OMP algorithm. Figure 2 shows the ideal correlation map, a simulated 2-second TR correlation map, and correlation maps with different numbers of atoms selected from the dictionary. As more atoms are added, the correlation maps are increasingly blurred. We observed the best results with 20 atoms.

Conclusions: We have demonstrated that using the inherent temporal Fourier sparsity of fMRI data can allow one to reconstruct data sets with high spatiotemporal resolution with as little as 1/64th of the data. In the future we expect to explore other dictionaries besides the Fourier dictionary, along with other methods for selecting the atoms.

References: [1]Tropp et al., Sig Proc. 86:572-588, 2006. [2]Usman et al., Phys. Med. Biol. 56: N99-N114, 2011. [2]Usman et al., MRM 66:1163-1176, 2011. [3]Zhao et al., IEEE-EMBS 2010. pp. 3390-3. [4]Hu, et al., IEEE TIP 21:742-753, 2012.

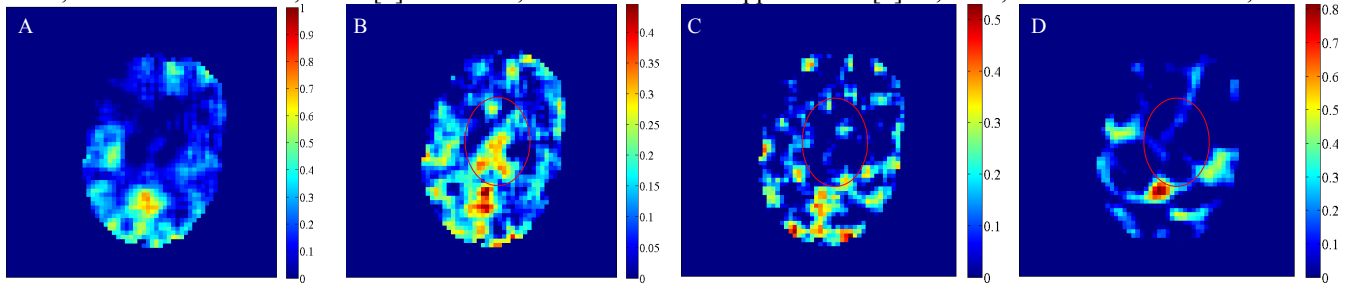


Figure 2: Comparison of ideal correlation map (A), 2-second TR correlation map (B), 20-atom OMP correlation map (C), and 40-atom OMP correlation map (D). Note the removal of correlations from the ventricles in both of the reconstructed maps. Also, the 40-atom map exhibits issues with blurring due to the large number atoms used in reconstruction.

Algorithm OMP

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initialize  $j = 0$ ,  $\mathbf{U}^{(0)}$ ,  $\mathbf{V}^{(0)}$ ,  $\mathbf{R}^{(0)} = \mathbf{Y}$ ,  $\Lambda_0 = \emptyset$ 
repeat
   $\lambda_j = \arg \max_{\omega \in \Omega} \sum_{m=1}^M |\langle \mathbf{R}^{(j-1)} \mathbf{e}_m, \phi_\omega \rangle \mathbf{w}_m|$ 
   $\Lambda_j = \Lambda_{j-1} \cup \{\lambda_j\}$ 
   $\mathbf{V}^{(j)} = \Phi_{\Lambda_j}$ 
   $\mathbf{U}^{(j)} = \arg \min_{\mathbf{U}} \|\text{vec}(\mathbf{Y}) - \mathbf{A}_{\mathbf{V}^{(j)}} \text{vec}(\mathbf{U})\|_2^2$ 
   $\mathbf{R}^{(j)} = \mathbf{Y} - S(\mathbf{U}^{(j)} \mathbf{V}^{(j)})$ 
   $j = j + 1$ 
until stop criterion is met
  
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Figure 1: Outline of OMP algorithm.