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Deconvolution of fMRI Data using a Paradigm Free Iterative Approach based on Partial Differential Equations

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Introduction

Functional magnetic resonance imaging (fMRI) is a technique which indirectly measures neural activations via the blood oxygenated level dependent (BOLD) signal [1]. So far, few approaches have been proposed to regularize the fMRI data, while recovering the underlying activations at the voxel level. In particular, for task fMRI, voxels time courses are fitted on a given experimental paradigm [1]. To avoid the necessity of a priori information on the pattern, supposing the brain works with blocks of constant activation, Farouj et al. [1] has developed a deconvolution approach which solves the optimizations problem by splitting it into two regularization problems, i.e. spatial and temporal. Starting from this idea, we propose a paradigm-free iterative algorithm based on partial differential equations (PDEs) which minimizes the image variations, while preserving sharp transitions (i.e. brain activations), in the space and the time dimensions at once.

Methods

We minimized image variations by iteratively smoothing the data with a gradient descent based on PDEs such that: $\partial I / \partial t = (1 - \lambda) \cdot H' * (I_0 - H * I) / A + \lambda \cdot \text{div}(\nabla I) / B$, where the first term on the right is the data fitting term, which measures the correlation of the residual with the hemodynamic response function (H) [4], and the second term minimizes image variations. Moreover, I_0 and I are the acquired fMRI and the denoised image respectively, λ is the regularization parameter, H' is the time-reversed H ,

$A = \|\nabla I\|$ and $B = \|\text{div}(D\nabla I)\|$ are normalization factors and $D = \nabla I \nabla I^T / \|\nabla I\|^2 * G$ is the structure tensor of I , smoothed by a gaussian kernel G ($\sigma_G = 1$). The convolution with H and H' were computed only along the time dimension. Then if the gradient of the image was big ($\|\nabla I\| > 0$), we performed an anisotropic smoothing to smooth the image while preserving sharp edges, which can occur both in space and in time; whereas if the gradient was small ($\|\nabla I\| \rightarrow 0$), we isotropically smoothed the image in all the four dimensions. The validity of this approach has already been shown on simulated data [5]. Similarly to [1, 6] the study was conducted on the preprocessed and normalized motor task-fMRI data of a subject taken from the Human Connectome Project (HCP) database (TR=0.72 s) [7]. The reconstructed signals, $u^*(t)$, were averaged in two regions of interest (ROIs) of $6 \times 6 \times 6$ mm³. We selected the task related to the tongue, and we chose one ROI centered in the Brodmann Area 4p (rBA4p; MNI coordinates: 62, -14, 30) which is supposed to be active in a tongue motor task, and another centered in the primary auditory cortex (TE1.2; 56, 4, 10) [8] in order to prove that our approach is able to differentiate between a region which is activated and one that is not. We compared the results obtained using our approach (PDEs) with the ones given by the total activation (TA) method, implemented in the iCAPs toolbox [1, 9]. To evaluate the results, Pearson correlation coefficients were computed between the tongue activation, simulated as a piecewise constant signal, and the recovered $u^*(t)$ for each voxels, and then averaged among the voxels belonging to the gray matter (GM)-masked ROIs.

Results

Fig.1 shows the considered ROIs. Fig.2 shows the reconstructed signal $u^*(t)$ and the correlations values using our approach and the TA. We show a higher correlation between the tongue activation and the rBA4p recovered activation $u^*(t)$, which we expect to be involved in the motor task, while a low correlation is shown with the rTE12 which is not involved in the task. Whereas, the TA approach showed low correlation values for both ROIs.

Conclusions

Our findings show that the iterative approach based on PDEs allowed us to recover brain activations of the fMRI data without a priori knowledge on the experimental paradigm. This is promising for resting-state fMRI image which measures spontaneous activity of the brain, in order to improve brain dynamics recovery for future clinical application.

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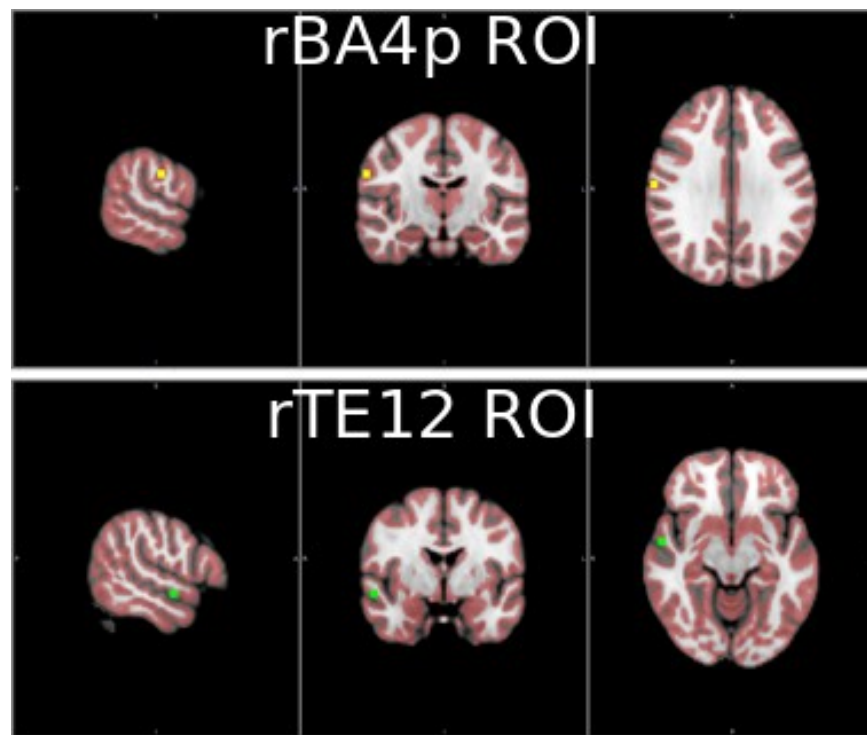


Fig.1. Regions of interest (ROIs) of $6 \times 6 \times 6 \text{ mm}^3$ centered in the right Brodmann Area 4p (rBA4p, MNI coordinates: 62, -14, 30) in yellow and in the primary auditory cortex (rTE1.2, MNI coordinates: 56, 4, 10) in green, superimposed to the gray matter (GM) map (in red).

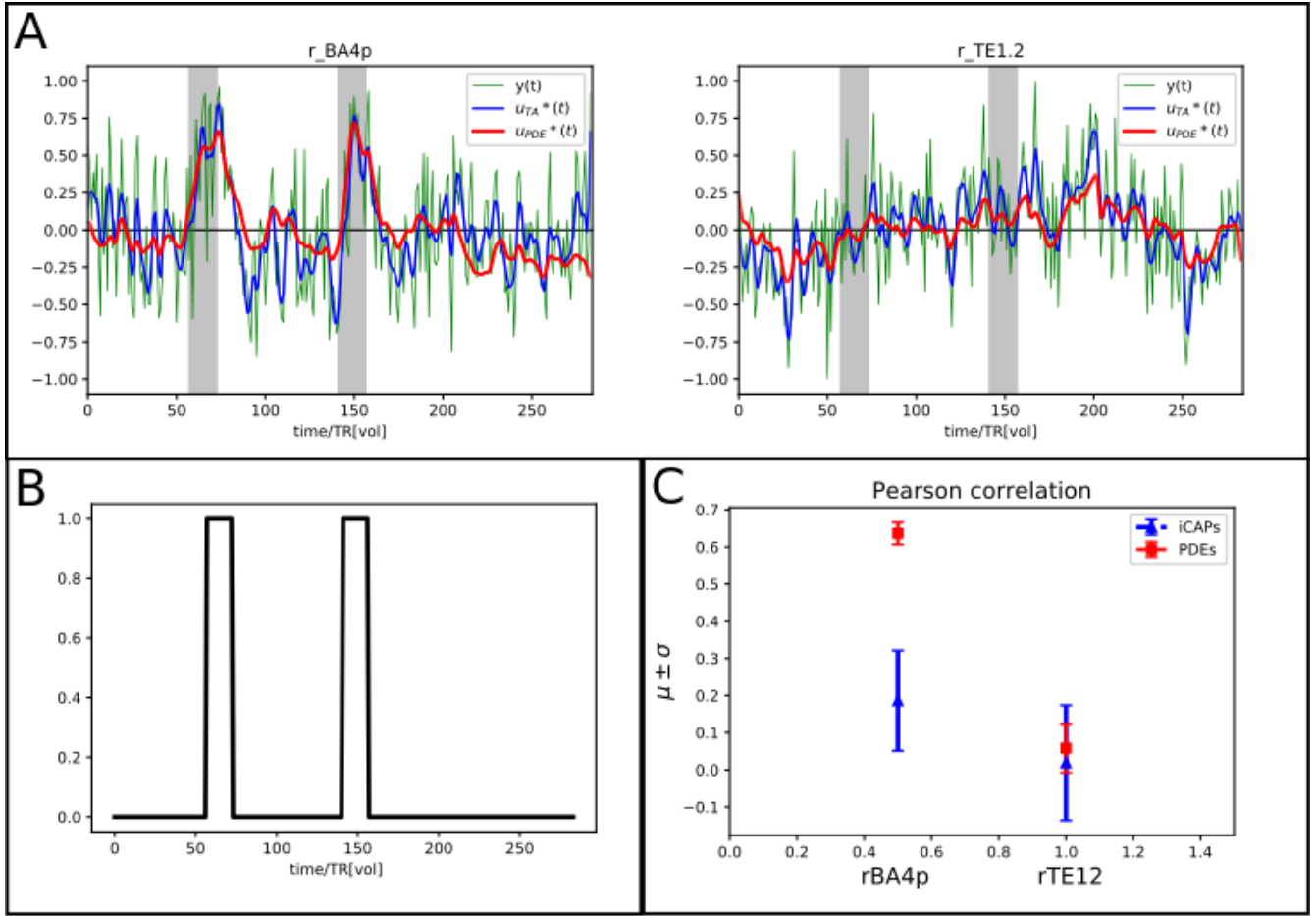


Fig.2. (A) Reconstructed signals $u^*(t)$ obtained with our approach (PDEs, red) and the total activation tool (TA, blue) superimposed on the fMRI signals (green). The plot on the left is related to the region of interest (ROI) located on the Brodmann Area 4p (rBA4p), the plot on the right is associated to the ROI positioned on the primary auditory cortex (rTE1.2). All the signals were averaged among the voxels belonging to the gray-matter (GM)-masked ROIs. The grey areas represent the occurrence and the duration of the tongue movements. **(B)** Simulated tongue activation. **(C)** Mean Pearson correlation coefficients (μ) and their associated standard deviations (σ) computed between the tongue activation and the recovered signals $u^*(t)$ averaged among the voxels belonging to the GM-masked ROIs (rBA4p on the left, rTE1.2 on the right). The blue curves are related to the TA approach, while the red ones to the PDEs approach.

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