Contents lists available at ScienceDirect



Journal of Neuroscience Methods

journal homepage: www.elsevier.com/locate/jneumeth

Computational neuroscience

ICA of full complex-valued fMRI data using phase information of spatial maps



CrossMark

NEUROSCIENCE Methods

Mou-Chuan Yu^a, Qiu-Hua Lin^{a,*}, Li-Dan Kuang^a, Xiao-Feng Gong^a, Fengyu Cong^{b,c}, Vince D. Calhoun^{d,e}

^a School of Information and Communication Engineering, Dalian University of Technology, Dalian 116024, China

^b Department of Biomedical Engineering, Dalian University of Technology, Dalian 116024, China

^c Department of Mathematical Information Technology, University of Jyvaskyla, Finland

^d The Mind Research Network, Albuquerque, NM 87106, USA

^e Department of Electrical and Computer Engineering, University of New Mexico, Albuquerque, NM 87131, USA

HIGHLIGHTS

- ICA of the full complex-valued fMRI data is enabled.
- The SM phases are utilized to identify and suppress the unwanted voxels.
- Our TC-based phase de-ambiguity is more accurate and robust than the SM-based method.
- The phase range of BOLD-related voxels is defined by maximizing TC real-part power.
- Our method can detect much more contiguous activations than magnitude-only ICA.

ARTICLE INFO

Article history: Received 9 March 2015 Received in revised form 30 March 2015 Accepted 31 March 2015 Available online 7 April 2015

Keywords: Complex-valued fMRI data Independent component analysis (ICA) Spatial map phase Phase de-ambiguity Phase positioning Phase masking

ABSTRACT

Background: ICA of complex-valued fMRI data is challenging because of the ambiguous and noisy nature of the phase. A typical solution is to remove noisy regions from fMRI data prior to ICA. However, it may be more optimal to carry out ICA of full complex-valued fMRI data, since any filtering or voxel-based processing may disrupt information that can be useful to ICA.

New method: We enable ICA of the full complex-valued fMRI data by utilizing phase information of estimated spatial maps (SMs). The SM phases are first adjusted to properly represent spatial phase changes of all voxels based on estimated time courses (TCs), and then these are used to segment the voxels into BOLDrelated and unwanted voxels based on a criterion of TC real-part power maximization. Single-subject and group phase masks are finally constructed to remove the unwanted voxels from the individual and group SM estimates.

Results: Our method efficiently estimated not only the task-related component but also the non-task-related component DMN.

Comparison with existing method(s): Our method extracted 139–331% more contiguous and reasonable activations than magnitude-only infomax for the task-related component and DMN at |Z| > 2.5, and detected more BOLD-related voxels, but eliminated more unwanted voxels than ICA of complex-valued fMRI data with pre-ICA de-noising. Our TC-based phase de-ambiguity exhibited higher accuracy and robustness than the SM-based method.

Conclusions: The TC-based phase de-ambiguity is essential to prepare the SM phases. The SM phases provide a new post-ICA index for reliably identifying and suppressing the unwanted voxels.

© 2015 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

* Corresponding author. Tel.: +86 411 84706697; fax: +86 411 84706697. *E-mail address*: qhlin@dlut.edu.cn (Q.-H. Lin).

http://dx.doi.org/10.1016/j.jneumeth.2015.03.036

0165-0270/© 2015 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

1. Introduction

Independent component analysis (ICA) has been widely used to extract spatial maps (SMs) and time courses (TCs) from functional magnetic resonance imaging (fMRI) data (McKeown et al., 1998; Calhoun and Adali, 2006a, 2012; Vigario and Oja, 2008). The vast majority of ICA focused only on the magnitude data of fMRI (i.e., magnitude-only analysis), though fMRI data are initially acquired as complex-valued image pairs. The primary cause is that the phase data of fMRI are ambiguous and noisy. However, a number of previous studies have shown that the phase data contain useful and unique information for better understanding brain function, including blood oxygenation during functional activation (Hoogenraad et al., 1998; Arja et al., 2010), the effect of macro and micro vessels (Menon, 2002; Tomasi and Caparelli, 2007), the orientation of large blood vessels (Klassen and Menon, 2005), and identification of different tissue types (Rauscher et al., 2005). As such, the complex-valued fMRI data are gradually explored via flexible data-driven approaches, such as ICA (Calhoun et al., 2002; Rodriguez et al., 2009, 2010, 2011, 2012; Li et al., 2011) or model-based approaches (Lai and Glover, 1997; Nan and Nowak, 1999; Rowe, 2005; Rowe and Logan, 2004, 2005). In this study, we focused on the ICA approach and blood oxygenation-level dependent (BOLD) fMRI data (Ogawa et al., 1990; Bandettini et al., 1992; Bhaysar et al., 2014).

Calhoun et al. (2002) presented the first application of ICA of complex-valued fMRI data, which demonstrated an increased ability to isolate task-related functional changes, and an average of 12-23% more contiguous activated voxels were detected than magnitude-only ICA at a threshold of Z-score > 2.5. Note that the analysis was restricted to a portion (the posterior half) of the brain due to the noisy nature of whole-brain data. The efforts of follow-up research were mainly directed toward development of complexvalued ICA algorithms for estimating the TC and SM components efficiently (Adali et al., 2004; Calhoun et al., 2004; Calhoun and Adali, 2006b; Adali and Calhoun, 2007; Novey and Adali, 2008; Adali et al., 2008; Li and Adali, 2008; Chen and Lin, 2008) and order selection for complex-valued fMRI data (Wang et al., 2008). Recently, a quality map phase de-noising (QMPD) method enabling whole-brain analysis was proposed (Rodriguez et al., 2009, 2010, 2011, 2012). In this method, the noisy regions in the complexvalued fMRI data were first identified by exploiting the observed phase image and then eliminated before performing individual and group studies using newly developed complex-valued ICA algorithms such as the entropy bound minimization (EBM) algorithm (Li and Adali, 2010; Li et al., 2011). As a result, better sensitivity and specificity than magnitude-only methods were achieved when identifying voxels in an estimated task-related independent component (IC) (Rodriguez et al., 2011, 2012; Li et al., 2011).

Instead of removing some specific voxels in the brain prior to doing ICA, it may be more optimal to perform ICA on the full complex-valued fMRI data, as any filtering or voxel-based processing may disrupt information useful to ICA. However, the biggest challenge is that, since we do not perform pre-ICA denoising of the data, there will be a large number of unwanted voxels with high amplitudes in the SM estimates. As such, we sought to utilize the phase information to perform post-ICA identification and suppression of the unwanted voxels. This is indeed supported by previous studies using phase information of the observed voxels to identify and suppress unwanted macrovascular contributions (Menon, 2002; Klassen and Menon, 2005; Tomasi and Caparelli, 2007; Nencka and Rowe, 2007).

Our method for utilizing the SM phase consists of three parts: phase de-ambiguity, phase positioning, and phase masking. Because the SM phase initially suffers from the inherent phase ambiguity of complex-valued ICA, we first presented an accurate and robust TC-based phase de-ambiguity method to adjust the SM phase for correctly representing the spatial phase changes of all voxels under severe noise conditions. We then introduced the concept of phase positioning to segment the voxels of the SM estimates into BOLD-related versus unwanted voxels, and we defined the phase range of the BOLD-related voxels based on maximization of TC real-part power. Next, we constructed single-subject and group phase masks and provided phase masking algorithms to remove the unwanted voxels from the SM estimates. Finally, we tested the efficacy of our method in individual and group fMRI studies.

2. Methods

2.1. Actual fMRI data

The fMRI dataset used in this study was the same as that used in Rodriguez et al. (2012) and Li et al. (2011). The data were obtained from 16 subjects performing a finger-tapping motor task while receiving auditory instructions. The paradigm had a block design with alternating periods of 30s on (finger tapping) and 30 s off (rest). The experiments were performed on a 3T Siemens TIM Trio system with a 12-channel radio frequency (RF) coil. The fMRI experiment used a standard Siemens gradient-echo EPI sequence modified to store real and imaginary data separately. The following parameters were used: field-of-view = 24 cm, slice thickness = 3.5 mm, slice gap = 1 mm, number of slices = 32, matrix size = 64×64 , TE = 29 ms, TR = 2 s, flip angle = 70 degrees. Preprocessing of the data was performed using the SPM software package. Magnitude data were coregistered to compensate for movements in the fMRI time series images. Images were then spatially normalized into the standard Montreal Neurological Institute space. Following spatial normalization, the data (real and imaginary images) were slightly sub-sampled, resulting in $53 \times 63 \times 46$ voxel. Motion correction and spatial normalization parameters were computed from the magnitude data and then applied to the phase data. Then, the real and imaginary images were both spatially smoothed with a $10 \times 10 \times 10$ mm³ full width at half-maximum Gaussian kernel.

We were interested in the task-related component and the default mode network (DMN), and we utilized their magnitudeonly SM priors to assess the quality of the SM estimates. Considering that GLM (Friston et al., 1995) is a widely used model-based method (directly using the paradigm of the fMRI data), the task-related magnitude mask (named GLM mask), Fig. 11(e), was calculated by performing a one sample *t*-test on the single-subject GLM results (p < 0.05). For the DMN magnitude mask, we utilized the DMN component from Smith et al. (2009) showing close correspondence between the independent analyses of resting and activation brain dynamics, as seen in Fig. 12(e).

2.2. Phase de-ambiguity based on TC estimates

Assuming there are *N* observed signals $\mathbf{X} = [\mathbf{x}_1, \dots, \mathbf{x}_N]^T \in C^{N \times L}$, which are the linear instantaneous mixtures of *N* unknown complex-valued source signals $\mathbf{S} = [\mathbf{s}_1, \dots, \mathbf{s}_N]^T \in C^{N \times L}$ via an unknown mixing matrix $\mathbf{A} = [\mathbf{a}_1, \dots, \mathbf{a}_N] \in C^{N \times N}$, the mixing model of complex-valued ICA is $\mathbf{X} = \mathbf{AS}$. By finding an unmixing matrix $\mathbf{W} \in C^{N \times N}$, complex-valued ICA estimates the source signals as $\hat{\mathbf{S}} = \mathbf{WX} = \mathbf{WAS} = \mathbf{PDS}$ and the mixing matrix as $\hat{\mathbf{A}} = \mathbf{W}^{-1} = \mathbf{A}(\mathbf{PD})^{-1}$, where $\mathbf{P} \in R^{N \times N}$ is a real permutation matrix that causes permutation ambiguity, $\mathbf{D} = \text{diag}(d_1 e^{-j\theta_1}, \dots, d_N e^{-j\theta_N}) \in C^{N \times N}$ is a complex-valued diagonal scaling matrix that causes scaling ambiguity, and d_1, \dots, d_N and $\theta_1, \dots, \theta_N$ are indeterminate scales and angles. Ignoring the permutation ambiguity (Rodriguez et al., 2012), we have:

$$\mathbf{X} = \widehat{\mathbf{A}}\widehat{\mathbf{S}} = (\mathbf{A}\mathbf{D}^{-1})(\mathbf{D}\mathbf{S})$$
(1)

Download English Version:

https://daneshyari.com/en/article/6268232

Download Persian Version:

https://daneshyari.com/article/6268232

Daneshyari.com