EXTRACTION OF COMMON TASK SIGNALS AND SPATIAL MAPS FROM GROUP FMRI USING A PARAFAC-BASED TENSOR DECOMPOSITION TECHNIQUE

Bhaskar Sen, Student Member, IEEE and Keshab K. Parhi, Fellow, IEEE

Department of Electrical and Computer Engineering
University of Minnesota, Twin-Cities, USA

ABSTRACT

Blind source separation (BSS) using independent component based analysis (*e.g.*, probabilistic ICA and infomax ICA) have been studied in-depth to extract common hemodynamic sources for a group of functional magnetic resonance images (fMRI). The inherent assumption here is that the sources must be non-Gaussian. For most of the real world data, the decomposition is non-unique. Furthermore, there is no quantitative way to determine the component(s) of interest common for the group. This paper shows that using a novel *constrained* Parallel Factor Analysis (PARAFAC)-based tensor decomposition, one can extract the common task signals and spatial maps from a group of noisy fMRI as rank-1 tensors. The extracted hemodynamic signals have very high correlation with ideal hemodynamic response. A quantitative algorithm to extract common components for a group of subjects is also presented. The modified decomposition preserves the uniqueness under mild conditions which is the most attractive feature for any PARAFAC-based tensor decomposition approach.

***Index Terms*—** fMRI, tensor decomposition, PARAFAC, spatial map, task signal

1. INTRODUCTION

Functional magnetic resonance imaging (fMRI) provides a non-invasive way to measure activity of brain during resting state (r-fMRI) or task (t-fMRI). Specifically, when a subject is scanned, the change of blood-oxygen level density (BOLD) in the brain over time is measured. The resultant scan is a 4-D image where the first three dimensions are spatial and the fourth dimension is temporal. This provides an indirect way to measure the activities of the brain regions. When a subject performs a task, the corresponding regions involved with the task have a high inflow of oxygenated blood. This in turn gives rise to the so-called hemodynamic response in fMRI time series for the input impulse excitation.

During task fMRI, the subject is asked to perform a repetitive task to understand which part of the brain is involved in that particular task. For example, one experiment may investigate the brain regions involved while tapping the fingers. In this case, a healthy person while in scanner, is asked to perform finger tapping at a particular interval (15 or 30 secs). This repetition ensures that we are able to filter out false positives found during non-repetitive task by investigating the fMRI time series and extracting parts involving the hemodynamic response corresponding to the repetitive task. In addition to a task, when a person is awake (even in rest condition), there are some regions in the brain that are always activated. In those regions, fMRI signal will have hemodynamic response of different characteristics. fMRI scans can consist of other signals (considered noise from neuroscience perspective), that involves breathing artifacts and eye-blinking etc.

Extracting the common hemodynamic signal from group-fMRI is of utmost importance for further analysis of the data. For example, some of the signals detected during a task may be indicative of a psychiatric disease state and can be used to discover an objective biomarker for diagnosis of the disease. In addition, the signals and their corresponding spatial components may associate the regions of brain involved in a particular task. The group level exploratory BSS analysis using PCA and ICA have found success and become popular in the last decade in the analysis of fMRI [1] [2]. This success can be attributed to their ability to extract biologically meaningful spatial maps of hemodynamic sources and the rich history of these techniques being applied to a number of biological signals [3]. However, since ICA is based on matrix decomposition, it is unique under very restrictive conditions. Source separation using PCA introduces orthogonality between extracted time courses [4]. Also, there is no quantitative way to extract common components of interest for a group of subjects from fMRI data. A tensorial extension of ICA for fMRI has been proposed [5]. However, the uniqueness of PARAFAC decomposition [6] that makes the tensor decomposition most attractive has not been fully utilized for fMRI.

Tensors are functions of three or more indices (i, j, k). Conceptually they are similar to matrices that are functions of only two indices (r, c). Even though tensor decomposition techniques have been known for a long time, their penetration to biomedical signal processing community have been slow. They are gradually becoming popular for biomedical data [7]. For example, tensor decomposition has recently been applied to EEG signals in [8].

The contribution of this paper is twofold. First, it presents a novel *constrained* PARAFAC-based tensor decomposition

approach to extract the task related common hemodynamic signals and the activated spatial maps from a group of subjects in a relatively *straight-forward* way as rank-1 tensors. This takes advantage of the possible unique decomposition for PARAFAC. Second, it also describes a quantitative algorithm to extract the common task signals across a group of subjects. This can find application in the plethora of fMRI studies including filtering fMRI of various individual noises to keep the common group signal, group level task activation studies between patient and control groups etc.

2. PARAFAC-BASED DECOMPOSITION MODEL

The goal of a tensor decomposition technique is to decompose a multi-way array (tensors) to a number of rank-1 multi-way arrays (tensors). There are a number of approaches for the decomposition – the most prominent among them being *Parallel Factor Analysis (PARAFAC)* [6] and *Tucker Decomposition* [9]. The main advantage of rank-1 PARAFAC based decomposition is its uniqueness in relatively mild conditions. Commonly used rank-1 matrix decompositions (*e.g.*, ICA) are essentially non-unique unless the rank is actually one or under some very specific constraints. Traditional PARAFAC-based tensor decomposition model for fMRI was studied in [10] [5]. The authors found that this model was not suitable for fMRI as it introduces *cross-talk* between spatial components. In this paper, we modify the traditional PARAFAC with simple constraints that capture the essential properties of fMRI decomposition. We present the traditional PARAFAC model at first and then discuss our proposed modified *constrained* PARAFAC model.

2.1. Preliminaries

Each fMRI scan is reshaped to a matrix (dim1 $=$ $spatial$, dim2 $=$ $temporal$). The scans from a group of subjects are concatenated to form a 3-way tensor where the dim3 $=$ $subject$. We denote the 3-way tensor of size $I \times J \times K$ as $X_{I,J,K}$.

2.2. Traditional PARAFAC

The traditional PARAFAC [11] modeling to decompose the tensor X_{IJK} into F number of rank-1 tensors can be described as

$$X_{I,J,K} = \sum_{f=1}^{F} a_f \circ b_f \circ c_f, \; \underline{X} = (\underline{A}, \underline{B}, \underline{C}) \quad (1)$$

where A, B, C are of size $I \times F$, $J \times F$ and $K \times F$ respectively. $a_f = A_{:,f}$, $b_f = B_{:,f}$, $c_f = C_{:,f}$ where $A_{:,f}$ is the f^{th} column of A and $\circ$ denotes outer product. For PARAFAC decomposition, each rank-1 tensor will consist of one time signal for task (each column of B), a corresponding spatial map (corresponding column in A) and the loading of the spatio-temporal map for each subject (column in C). The decomposition optimizes the following function:

$$\min_{A,B,C} ||X_1 - (C \odot B)A^T||_F^2 \quad (2)$$

where $X_1 = X_{JK,I}$ and $\odot$ denotes *Khatri-Rao product*. More specifically, X_1 is tensor X reshaped as a matrix with number of rows $J \times K$ and columns I. Likewise we also define $X_2 = X_{KI,J}$ and $X3 = X_{JI,K}$ where X_2 and X_3 correspond to reshaped matrix form of tensor X. It can be shown that PARAFAC decomposition is unique under very mild conditions. For a detailed analysis of PARAFAC uniqueness see [6][11][12].

2.3. Constrained PARAFAC

Traditional PARAFAC tensor decomposition may introduce components that are hard to interpret from a biological perspective. For example, one common empirical hypothesis is that different regions in the brain will be responsible for different tasks. Hence in a healthy brain, the cross-talk between spatial components should be as small as possible. We can satisfy this by using $A^T A = \Sigma$. Here Σ is a diagonal matrix such that $\Sigma_{ij} = 0$, when $i \neq j$. Incorporating this constraint is a key contribution of this paper. Also, for interpretability, we can assume the weighting of spatio-temporal maps in each subject to be non-negative ($C \geq 0$). Hence the corresponding optimization is stated as:

$$\min_{A,B,C} ||X_1 - (C \odot B)A^T||_F^2 \; s.t. \; A^T A = \Sigma, \; C \geq 0 \quad (3)$$

This can be solved using alternating optimization technique by keeping two matrices constant and minimizing for the third. Notice that for A, B, C, respectively, the alternating optimization problem can be stated as:

$$\min_{A} ||X_1 - (C \odot B)A^T||_F^2 \; s.t. \; A^T A = \Sigma \quad (4)$$

$$\min_{B} ||X_2 - (C \odot A)B^T||_F^2 \quad (5)$$

$$\min_{C} ||X_3 - (B \odot A)C^T||_F^2 \; s.t. \; C \geq 0 \quad (6)$$

These three equations can be optimally solved, respectively, by using *orthogonal least squares solution to the PARAFAC model* [6] [13] [14], *least square* and *non-negative least square* [15]. The unique solution for the sub-problem described by (4) also normalizes the columns of A.

Interestingly, for exploratory matrix decomposition of fMRI, the ICA method is regarded as more preferable to (only) de-correlation techniques like PCA. The spatial independence of components by ICA enforces that their time courses not be highly co-linear. This results in a more biologically plausible system model than PCA decomposition which enforces orthogonality between time courses thus excluding the detection of hemodynamic signals which correlate with each other in the temporal domain [4]. Our objective function (3) preserves the advantages of ICA as it does not enforce any orthogonality between time courses. At the same time, it is computationally simple and provides meaningful factors corresponding to specific applications. One of the main advantages of constrained PARAFAC model compared to ICA is that the model can be unique under more relaxed conditions than traditional PARAFAC conditions [16][17].

2.4. Extract Common Task Signal

The factor C (matrix size $K \times F$) includes the weightage of each separated component for every subject in its columns. In a group level analysis of task fMRI, every subject performs the same task. In the decomposition, the extracted component corresponding to the task(s) will have relatively same weightage in each subjects. The subject-level variations and noises will be captured in other components. A simple procedure to find the task signal(s) from F number of components is described in Algorithm 1.

Algorithm 1: Extracting Task Signal Components

Data: C matrix from fMRI PARAFAC
Result: Component IDs for Task Signals in Vector I
$I = [\,]$;
for $1 \leq i \leq F$ **do**
  C_{min} = *minimum*$(C_{:,i})$;
  C_{max} = *maximum*$(C_{:,i})$;
  if $\frac{C_{min}}{C_{max}} \geq \omega$ **then**
    $I = [I; i]$;
  end
end

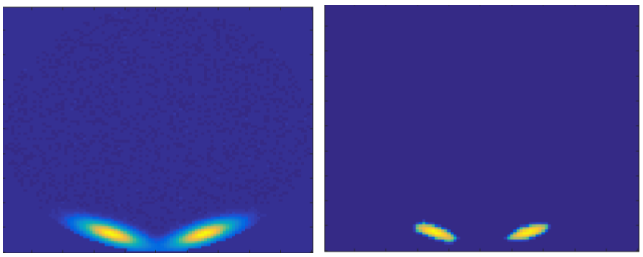
Based on empirical results ω is set to 0.1. This algorithm can be extended to systematically extract the task signals from the data based on prior knowledge. In this case, the value of F can be increased from 1 until the required number of task-signals are found using the algorithm.

3. RESULTS

In order to validate our model, we used three small fMRI datasets (one simulated, two real-world). We also compare our extraction result with previous models for the real-world datasets. For implementing fMRI−PARAFAC, we used *n-way* toolbox for MATLAB freely available from [1]. Spatial maps from tensor decomposition were overlaid using *caret* software available from [2].

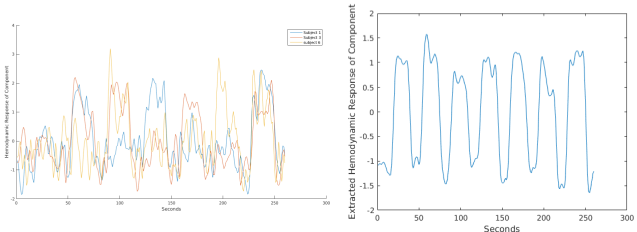
3.1. Simulated Data

For our first experiment, we used simTB [3] toolbox to generate task-fMRI data for 9 subjects. The already available MATLAB script ($experiment\_params\_block.m$) was modified to accommodate 5 independent components. Two blocked conditions are used. The hemodynamic response corresponding to these two blocked conditions will give rise to two common signals across subjects. The other 3 components represent undesired signals that are common for few of the subjects. We do not consider them as components of interest even though our algorithm is able to generate those components. The decomposed rank-1 tensors were able to capture the common task signal and individual hemodynamic responses. One common spatial map extracted from the data is shown in Fig. 1. We have also shown the hemodynamic time course corresponding to the spatial map in Fig. 2. The algorithm was able to extract the seven task blocks from the generated fMRI data in columns of matrix B.



(a) Spatial map ground truth (b) Extracted spatial map

Fig. 1: Performance of proposed model in extracting the spatial maps



(a) Hemodynamic time courses for three subjects for task condition

(b) Extracted common time course

Fig. 2: Performance of proposed model in extracting time course. It captures 7 task blocks.

3.2. Real Data

3.2.1. Visuomotor Task

The second dataset is a visuomotor task [18] data available from fMRI GIFT toolbox [4]. The dataset consists of three subjects. Here we briefly describe the experiment. The task consisted showing of *motor-free visual perception test, revised* (MVPT-R) figures an average of 17 s apart using the computer program E-Prime. For each item, a central target test image was presented above four other images (out of which one matches the test image) numbered 1 through 4, from left to right, as in the MVPT-R test. The task was first to look at the image and match the image with correct number among the choices. The task consists of visual perceptions involving spatial relationships, visual discrimination, figure-ground, and visual closure. Buttons 1 and 2 were controlled by the index and middle fingers of the right hand, respectively, and buttons 3 and 4 were controlled by the index and middle fingers of the left hand, respectively. Here hemodynamic responses represent visuomotor tasks corresponding to visual discrimination-right hand coordination and visual discrimination-left hand coordination, respectively. In our experiment, these two signals are separated into two compo-

[1] http://www.models.life.ku.dk/nwaytoolbox
[2] http://brainvis.wustl.edu/wiki/index.php/Caret:Download
[3] http://mialab.mrn.org/software/simtb/
[4] http://mialab.mrn.org/software/gift/

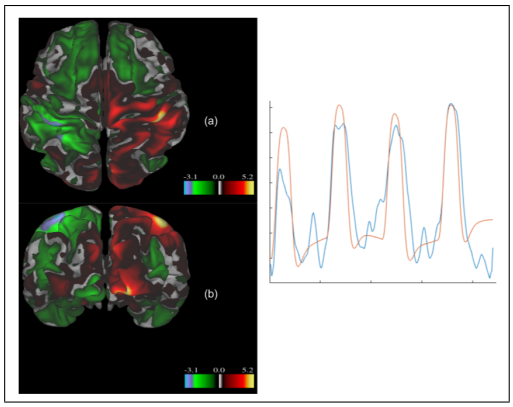


Fig. 3: **Visuomotor Component 1**, *left*: spatial maps (a) axial and (b) posterior view, *right*: ideal hemodynamic response in *red*; extracted hemodynamic response in *blue*; *correlation* 0.86

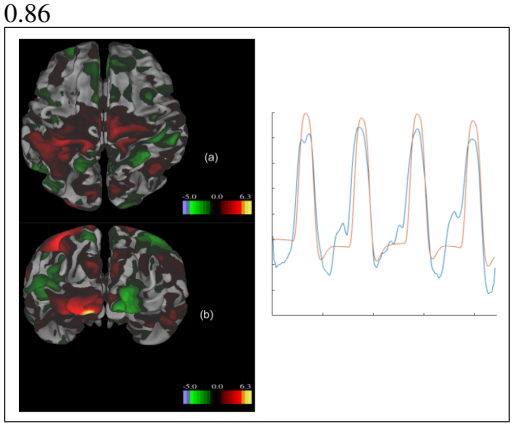


Fig. 4: **Visuomotor Component 2**, *left*: spatial maps (a) axial and (b) posterior view, *right*: ideal hemodynamic response in *red*; extracted hemodynamic response in *blue*; *correlation* 0.90

nents as shown in Figs. 3 and 4. Both the components were able to identify the corresponding visual and motor areas.

3.2.2. Working Memory Task

Our third dataset is taken from Human Connectome Project [19]. Specifically, we used scans of three subjects from the *working memory* task-fMRI. The preprocessed fMRI data is available from [5]. The task consists of four blocks each representing a different type (places, tools, faces and body parts) visual cue for 0-back and 2-back memory tasks. Within each run, half of the blocks use a 2-back working memory task and half use a 0-back working memory task. A 2.5 second cue indicates the task type (and target for 0-back) at the start of the block. Each of the two runs contains 8 task blocks (10 trials of 2.5 seconds each, for 25 seconds) and 4 fixation blocks (15 seconds). On each trial, the stimulus is presented for 2 seconds, followed by a 500 ms inter-task interval (ITI). Our main goal here is to extract the hemodynamic response responsible for working memory. This consists of a combination of 0-back

[5] https://www.humanconnectome.org/

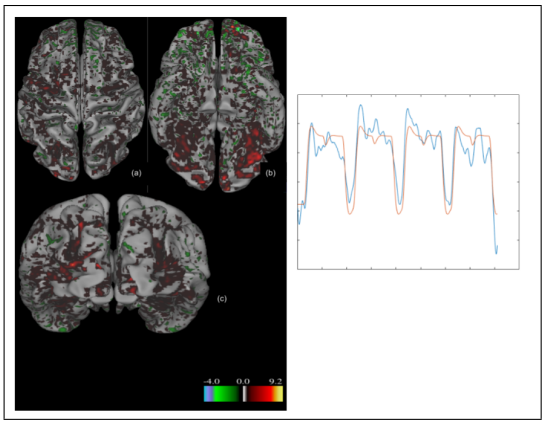


Fig. 5: **Working Memory**, *left*: spatial maps (a) axial (b) ventral and (c) posterior view, *right*: ideal hemodynamic response in *red*; extracted hemodynamic response in *blue*; *correlation* 0.90

and 2-back responses. In order to reduce the computational complexity, we only used voxel corresponding to *grey matter* from the brain. The ideal response was calculated using MATLAB toolbox SPM [6] and compared with the extracted signal in Fig. 5.

3.3. Comparison with Previous Results

The comparison between proposed model, group-ICA [1] and tensor-ICA [5] in terms of average correlation of extracted time series with ideal hemodynamic response is shown in table below. Here higher correlation means better performance.

	Visuomotor	Working Memory
Group-ICA [1]	0.91	0.90
Tensor-ICA [5]	0.86	0.85
proposed model	0.88	0.90

Although our proposed method was able to extract the signals with high correlation, the main advantage is its inherent simplicity and the uniqueness of decomposition under relatively mild conditions. Also, we have provided an algorithm to extract common task signals from a group quantitatively.

4. CONCLUSION AND FUTURE WORK

In this paper, we have developed a PARAFAC-based tensor decomposition for blind source separation of group-fMRI data. We introduced a systematic way to find components of interest for the group. We also showed that fMRI task signals can be decomposed as rank-1 tensors. In future, we plan to use this work to compare task activations in psychiatric patients vs healthy for extension of our previous work [20]. Also, we plan to devise an iterative algorithm to find the underlying true tensor rank for group-fMRI data.

5. ACKNOWLEDGMENT

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[6] http://www.fil.ion.ucl.ac.uk/spm/

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