DETECTION OF FUNCTIONAL BRAIN CONNECTIVY BY INDEPENDENT COMPONENT ANALYSIS

Martin Havlíček
Doctoral Degree Programme (1), FEEC BUT
E-mail: havlicekm@phd.feec.vutbr.cz

Supervised by: Jiří Jan
E-mail: jan@feec.vutbr.cz

ABSTRACT

Spatial independent component analysis (sICA) is a technique that attempts to separate data into spatially independent groups and is meaningful for application in functional magnetic resonance imaging. Data that were observed during specific experiment of visual stimulation were analyzed by ICA using Infomax algorithm. Based on correction time courses of head movement we marked the components that are closely related to this artifact. Finally we presented the common component map that figure a contribution from the most dominant components in particular voxel across whole brain volume.

1. INTRODUCTION

Functional magnetic resonance (fMRI) has become the most commonly used method for the investigation of human brain function. There are two major concepts assessing human brain organization. The functional specialization [3], which is the most widely used, assumes the local specialization of human brain but allows that this specialization can be anatomically segregated across different cortical areas. However, this explanation is incomplete as long as no insight is provided into how the locally specialized activations are bound together by context-dependent interactions among these areas, i.e. their functional integration. One way how the functional integration can be characterized is by the functional connectivity [2]. Functional connectivity is defined as the correlations between spatially remote neurophysiologic events and can be represented by the pattern of temporal correlations (or more generally, deviations from statistical independence) that exists between distinct neuronal units. Independent component analysis (ICA) is one of the methods that are able to evaluate functional connectivity in exploratory fashion [5]. Even though this method is already in use for few years, there are still many questions how to handle the analysis in correct way and many options how to extend consequent processing of its results.

2. DATA AND METHODS

2.1. EXPERIMENT AND MEASUREMENT PROPERTIES

Data set used in this work was used from a study [1], where can be found more detailed information about the experiment organization. Briefly, measurements were performed on healthy, right-handed subjects with normal vision. Two types of visual stimuli were presented to the subjects: standard stimuli represented by white characters ”OOOOO” on a dark background; and target stimuli represented by white characters ”XXXXX” on a dark background. The standard event occurred more frequently than target events. The subjects were instructed to mentally count the target stimuli and report the total number at the end of the experiment.

Functional and anatomical measurements were performed on a 1.5 T MRI tomograph Siemens Symphony. Functional images were acquired using a gradient echoplanar imaging (EPI) sequence: TR (scan repeat time) = 1600 ms; TE= 45 ms; FOV=250 mm; flip angle=90; matrix size 64×64; slice thickness = 6 mm; 15 transversal slices per scan; and 256 scans in total. High-resolution structural T1-weighted images were acquired using a 3D sequence: 160 sagittal slices with resolution 256 × 256 resampled to 512 × 512; slice thickness=1.17 mm; TR=1700 ms; TE=3.96 ms; FOV=246 mm; flip angle=15°. High-resolution images were consequently used during pre-processing operations and as a background matrix for the results from functional analysis.

2.2. FUNCTIONAL CONNECTIVITY ANALYSIS

Following pre-processing steps were applied in the Statistical Parametric Mapping (SPM5) program (http://www.fil.ion.ucl.ac.uk/spm) to time-series of fMRI data: realignment for the correction of any head motion artifacts; spatial normalization to fit into a standard anatomical space (MNI); interslice time correction; spatial smoothing using a Gaussian kernel with a FWHM of 8 × 8 × 8 mm. The voxel size was resampled to 3 × 3 × 3 mm.

After preprocessing in SPM program, time series of functional images were reduced as in spatial domain by selecting only non-zeros voxels that belong to brain volume, as in temporal domain, when this operation was implemented by Principal Component Analysis (PCA).

Functional data X, i.e. $p \times v$ matrix of the observed time courses (p = number of scans, v = number of voxels), were first centered by subtracting its mean [4]:

$$X = X - E\{X\}, \tag{1}$$

and then underwent PCA decomposition into m mutually orthogonal components, in our case m = 50. At the end of PCA we also included whitening (or sphering) of the data [4]. For this purpose we calculated whitening matrix B from sorted eigen vectors contained in matrix V and eigen values in matrix λ that we got from covariance of centered data:

$$B = \left(\sqrt{\lambda}\right)^{-1} V^T . \tag{2}$$

The resulting principal components (PCs) were established as:

$$X^{PC} = XB^T . \tag{3}$$

The whitening operation is very useful for later independent component analysis, because after whitening X^{PC} data has a feature that $X^{PC}(X^{PC})^T = D$, where D is diagonal matrix, and thus further estimation problem in ICA is considerably simplified.

Functionally connected patterns of activity were estimated using spatial ICA. Formally, ICA attempts to separate independent sources that have been mixed together. Assume that data $X = [x_1,. . ., x_n]$ are observed and modeled as a linear combination of *n* random variables $S = [s_1,. . .,s_n]$:

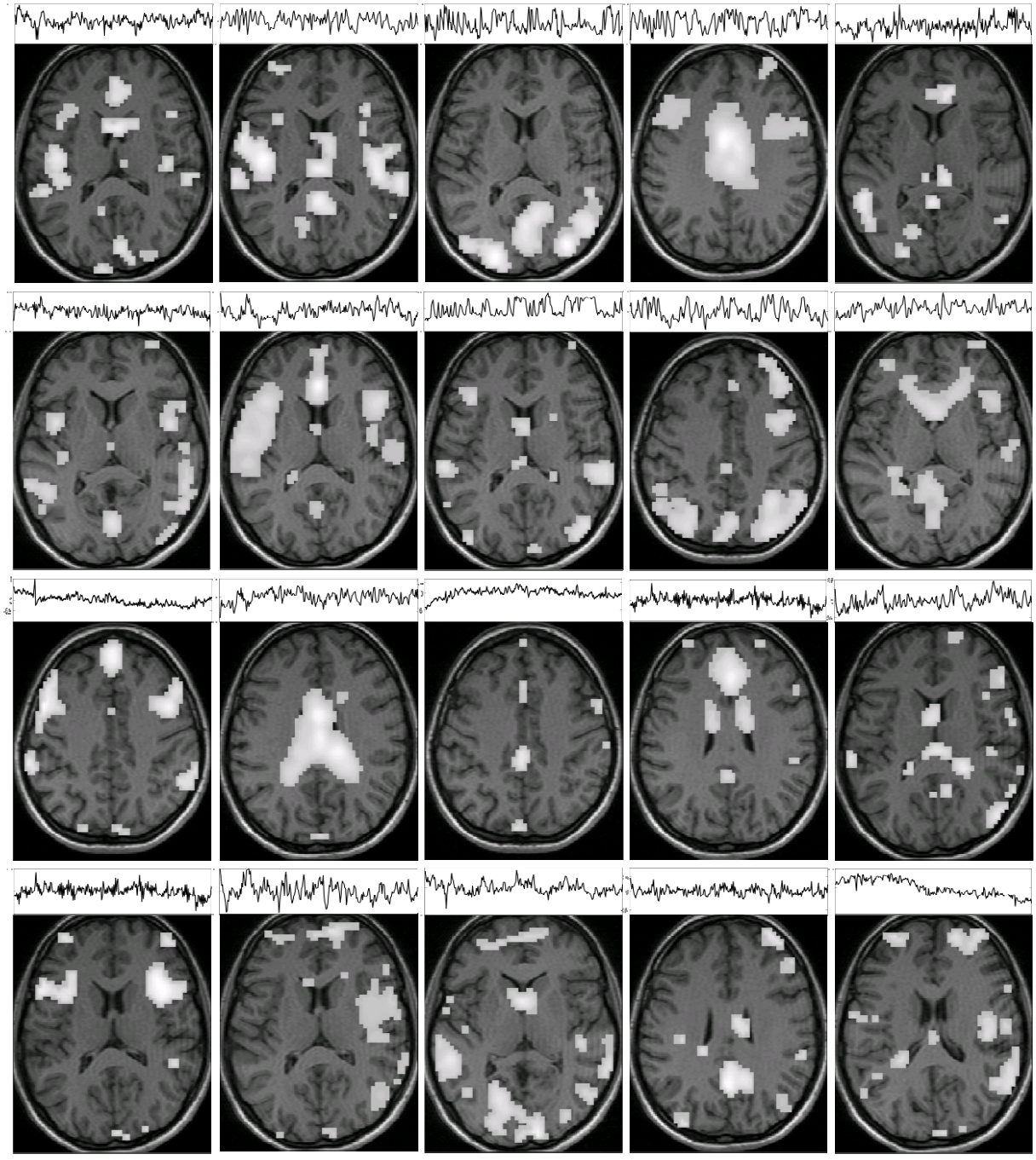

Figure 1: 20 spatially independent components depicted on high-resolution structural background with appropriate time courses (sorted from left to right and from up to down). Component maps were thresholded by $p = 0.05$ and the negative values are not shown.

$$X = WS\,, \tag{4}$$

where S is the $m \times v$ matrix whose rows are filled with the (unknown) realizations of spatial components, and W is $n \times m$ "mixing" matrix. Here we already consider observed data X that were previously reduced by PCA, i.e. $X = X^{PC}$.

The independent components s_i (ICs) are latent variables, meaning that they cannot be directly observed. Also the mixing coefficients w_{ij} are assumed to be unknown. We can only observe the random variables x_i, and must estimate w_{ij} and s_i using x_i. The ICA model assumes (i) the ICs are statistically independent and (ii) they have non-Gaussian distributions. Under these assumptions, after estimating the matrix W, we can compute its inverse W^{-1}, and obtain the ICs simply with:

$$S = W^{-1}X\,. \tag{5}$$

It is important to mention that if the functional data have Gaussian distribution then components received after the application of ICA are the same as these with PCA, i.e. components are only mutually orthogonal. Therefore, at the beginning data were checked for their non-Gaussianity by calculating kurtosis. The result (k = 2.3) pointed out that data have sub-Gaussian distribution (Gaussian distribution has k = 3) and that the using of ICA is reasonable.

The Infomax algorithm [4] with the natural gradient feature was used to estimate coefficients of mixing matrix W, and subsequently according an equation (5) we got 20 spatially independent components. Each spatially independent component is also connected with its unique time course that is derived as:

$$T_c = \left(V\sqrt{\lambda}W^{-1}\right)^T, \tag{6}$$

where the term $V\sqrt{\lambda}$ can be understood as a dewhitening matrix. The independent components are depicted on Fig. 1.

2.3. POST-HOC ANALYSIS OF COMPONENTS

Independent components were sorted by mean variance in descending order. In addition, each component time course was mean-corrected, linearly detrended, and correlated with the six head motion time course that were obtained during the pre-processing step of realignment [5]. Components whose time courses were highly correlated ($r > 0.5$) with the estimated motion time courses were discarded from further analysis. It concerns components with number 13, 14, 15, 20. Afterwards, components were again sorted according to mean variance in descending order.

In the next step of our analysis we wanted to find the dominant component (from all components) in each voxel of the whole brain volume, and in this way depict common component map. We did not want to consider too small blobs of activity in the components. Therefore we checked the final common component map with cubic cluster of size $3 \times 3 \times 3$ voxels and compact blobs whose size covered in this cluster less then 6 voxels were discarded. The result can be seen on Fig.2.

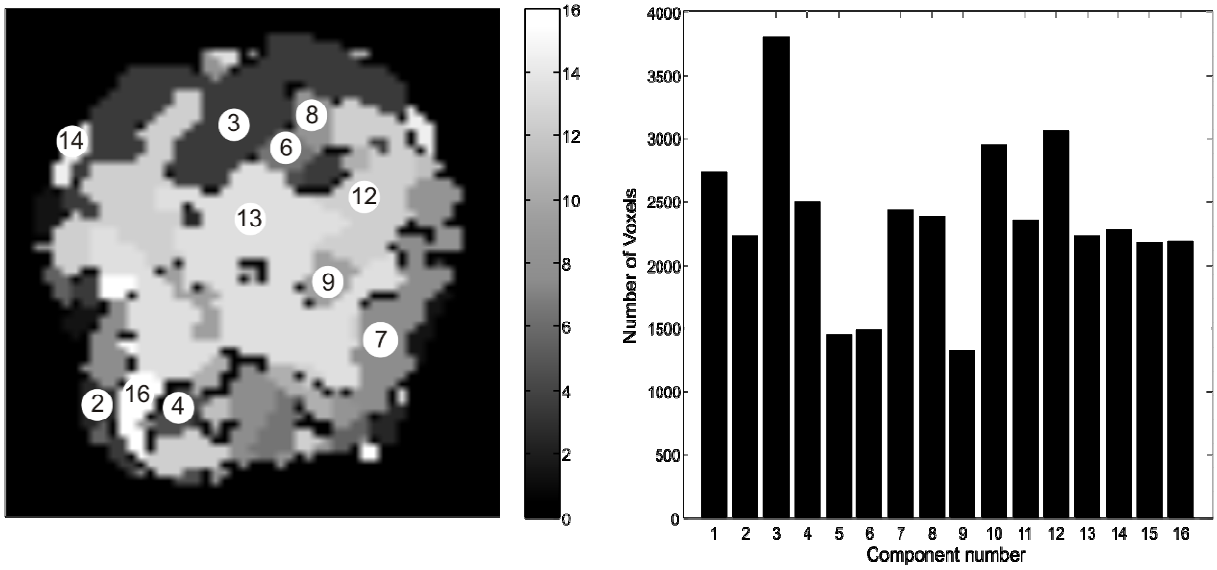

Figure 2: One slice of the common component map (left side) and histogram depicting number of voxels in the brain volume that belongs to particular component (right side).

3. DISCUSSION AND CONCLUSION

We performed all steps that are needed for basic analysis of functional connectivity, i.e. necessary pre-processing procedures; data reduction in spatial and temporal domain for memory less demanding manipulation with entire data set; and ICA decomposition into spatially independent components by which a different pattern of activated regions in the brain that are functionally connected can be already seen.

Subsequently, we marked components that are closely connected to head motion artifact. At the end, we proposed a way how to jointly depict the most dominant components across one brain volume.

Our next aim is focused on the causal relationship among individual components.

REFERENCES

[1] Brázdil, M., et al.: Effective connectivity in target stimulus processing: A dynamic causal modeling study of visual oddball task. NeuroImage 2007:35:827-835.

[2] Sporns, O., Tononi, G.: Structural Determinants of Functional Brain Dynamics. Springer 2007:117-148.

[3] Rajapakse, J.C.: Exploratory Analysis of Brain Connectivity with ICA. IEEE Med. and Biol. 2006:25:102-111.

[4] Hyvärinen, A., Karhunen, J., Erkki, O.: Independent Component Analysis. Wiley-Interscience 2004.

[5] Ven, V.G., Formisano, E., et al.: Functional Connectivity as Revealed by Spatial Independent Component Analysis of fMRI Measurements During Rest. Human Brain Mapping 2004:22:165-178.