
fMRI-based decoding of the modified default-mode network in mild cognitive impairment

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Introduction. The diagnostic tool to detect early stages of Alzheimer’s Disease, a progressive neurodegenerative disease, is lacking until today. FDG-PET (Fluorodeoxyglucose-Positron Emission Tomography) shows hypometabolic areas in the brains of pre-demented, i.e. patients suffering from mild cognitive impairment (MCI). The reduced activity may be attributed to disrupted connectivity of the resting-, or default-mode network of the brain [1]. In this contribution, we study the detection of such a network using the framework of blind signal processing, a technique to identify hidden sources within a multivariate mixture using source characteristics such as statistical independence or sparseness. The results are compared to FDG-PET data.

Methods. Blind source separation (BSS) in its simplest setup denotes the task of recovering a source random vector $s(t)$ from observations $x(t)$ following a linear mixture model $x(t) = As(t)$, possibly deteriorated by white Gaussian noise. If the sources are statistically independent (\rightarrow independent component analysis, ICA), it can be shown that the sources can be uniquely recovered except for scaling and permutation, if not more than one Gaussian is contained in $s(t)$. In the context of fMRI, corresponding algorithms provide a nice framework for hypothesis-free analysis of hidden features, possibly unrelated to the functional task [2].

Commonly, temporal BSS is performed to separate data set. However, if the data possess both spatial and temporal structures such as scans from fMRI, we can require the transformed data to be as independent as possible in both domains, which leads to spatiotemporal BSS [3]. Recently, we have proposed two efficient algorithms for performing spatiotemporal BSS by jointly diagonalizing varying conditions of the mixtures — such as autocovariances or quadri-covariance matrices — both in time and in space. This provides a robust method for fMRI analysis, taking into account both spatial and temporal patterns [4]. Since the default-mode network and its MCI-related disease modification do not provide a well-defined activation pattern, the model-free approach is the most viable technique for this task.

Presented here are preliminary results of two MCI patients and two healthy controls. 4 minutes of fMRI scanning ($TR=3s$, 77 scans) were performed using a Siemens Symphony 1.5T-scanner. Data were analysed after preprocessing (skull-stripping, slice-mean-normalisation, realignment, smoothing) using two ICA-tools: MELODIC¹, a tool based on probabilistic ICA, and b) mfBox² a toolbox for SPM, developed at the University of Regensburg, that allows for the usage of various BSS algorithms, among others spatiotemporal BSS.

Results. Comparison of the default-mode network component with FDG-PET maps determined within one and the same patient show common features in the two patients investigated up to now (Fig.1). Hypometabolic areas determined with FDG-PET agree well with the parietal areas of the default mode network as determined with fMRI. The comparison of MCI patients and healthy controls

¹FSL-MELODIC: <http://www.fmrib.ox.ac.uk/analysis/research/melodic>

²mfBox: <http://mfbox.sourceforge.net>

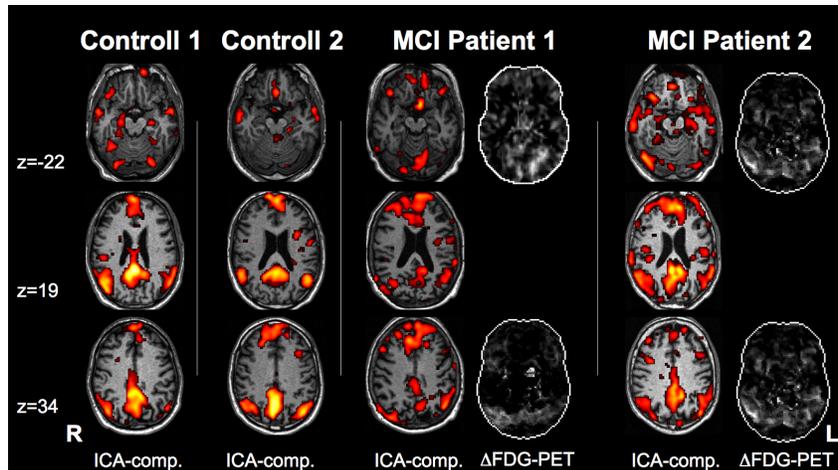
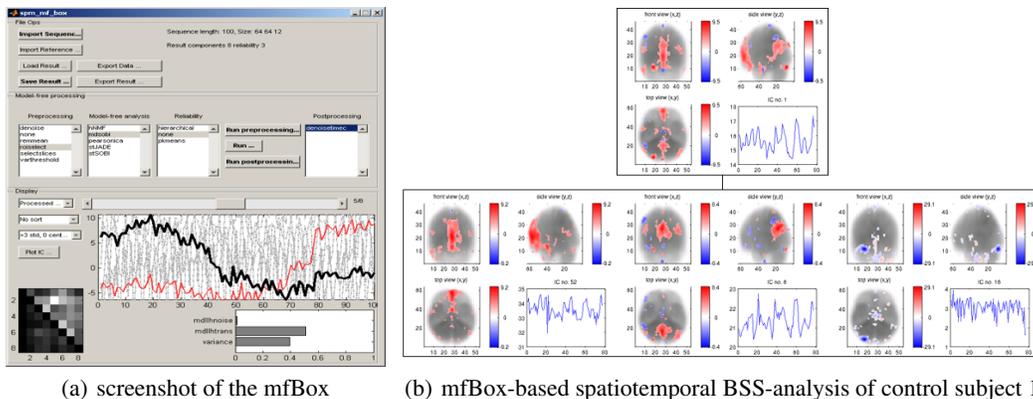


Figure 1: Comparison of default mode network and hypometabolic areas: The default-network-components as defined from ICA(MELODIC)/fMRI in health control subjects and in MCI-patients superimposed onto the patients/subjects anatomical images are shown. For the patients plots of areas in which the individual FDG-PET signal deviates (Δ FDG-PET) from the signal measured in a collective of healthy control subjects are added. All images were normalized to a template. Z-coordinates in MNI-space for the slices are indicated. Note that Δ FDG-PET images were only coregistered manually.



(a) screenshot of the mfBox

(b) mfBox-based spatiotemporal BSS-analysis of control subject 1

Figure 2: mfBox. (a) shows a screenshot when using mfBox as SPM-plugin. In (b), the resting-state component of control subject 1, extracted by spatiotemporal ICA using the mfBox is plotted.

in this preliminary analysis indicates that in MCI patients larger parts of the frontal lobe are integrated into the default mode network than in healthy controls (Fig. 1). Ordering of ICA-components according to hierarchical criteria (Fig. 2) helps identifying and classifying default mode components within a subject. We are currently studying how to provide statistically meaningful choices of BSS parameters such as number of extracted sources and model using the component validation, clustering and post-processing tools provided by mfBox.

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