Independent Vector Analysis for Group fMRI Processing

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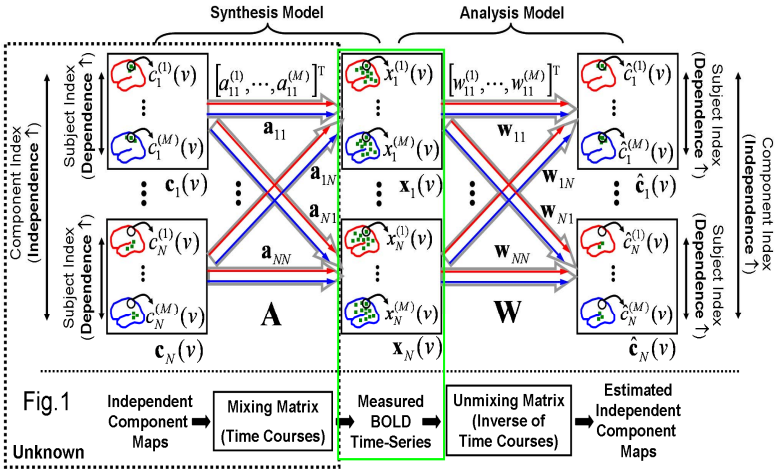
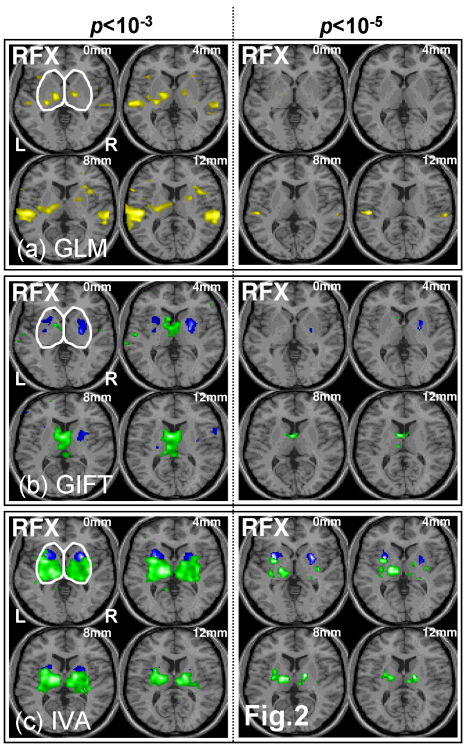
Introduction: Among multivariate analysis methods of functional MRI (fMRI) data, independent component analysis (ICA) has frequently been adopted because of its excellent ability to extract blood oxygenation level dependent (BOLD) signal components along with its spatial features [1]. Due to inherent restrictions on the spatial, temporal, and subject domains [2-4], however, group-inference based on the ICA approach may not fully analyze the individual-specific activation patterns, especially those arising from small cortical/subcortical areas. In order to improve upon this limitation, we propose a novel group fMRI analysis technique based on independent vector analysis (IVA) [5]. To demonstrate the efficacy of IVA for detecting activation arising from small subcortical areas, we applied IVA to fMRI data during a hand motor task and compared the results to those from general linear model (GLM) and from the ICA-based concatenating scheme, GIFT [2].

Method: We modeled the group fMRI data within the IVA framework [5] as shown in Fig. 1. In the figure, the BOLD signal at the v^{th} voxel across M subjects (green box) is generated within the synthesis model and is analyzed within the subsequent analysis model. In the synthesis model, the measured BOLD signal is assumed to be a linear combination of N independent vector components $\mathbf{c}_i(v)$ (i.e. the v^{th} voxel's activation patterns of the i^{th} unknown component map across M subjects; i=1,…,N) through a mixing matrix $\mathbf{A}$. In the analysis model, the estimation of $\mathbf{c}_i(v)$, can be obtained through an unmixing matrix $\mathbf{W}$. In order to derive a learning rule of $\mathbf{W}$, the Kullback-Leibler (KL) divergence between a joint probability density function (p.d.f.) and factorized marginal p.d.f.s of the estimated vector components was employed as a cost function (i.e. the mutual information MI among vector components) [5]. By using a gradient decent scheme to the MI, an iterative learning rule was obtained (please see detailed derivation in [5]): $\Delta\mathbf{W}^{(m)} \propto \left[\mathbf{I} - \varphi\left(\hat{\mathbf{c}}^{(m)}(v)\right)\left(\hat{\mathbf{c}}^{(m)}(v)\right)^{\mathrm{T}}\right]\mathbf{W}^{(m)}$, (1) $\varphi\left(\hat{\mathbf{c}}^{(m)}(v)\right) = \left[\varphi\left(\hat{c}_1^{(m)}(v)\right) \cdots \varphi\left(\hat{c}_N^{(m)}(v)\right)\right]^{\mathrm{T}}$, $\varphi\left(\hat{c}_j^{(m)}(v)\right) = \hat{c}_j^{(m)}(v) \Big/ \sqrt{\sum_{l=1}^{M}\left|\hat{c}_j^{(l)}(v)\right|^2}$. where $\mathbf{I}$ is an N×N identity matrix, and



12 right-handed subjects (aged 24.7±4.5, 5 females) performed a right hand clenching (2Hz) task based on a trial design (65s; task period: 15~18s). A 3T scanner (Signa,GE) was used (EPI, TR/TE=1s/40ms; FA=80°; 64×64, 3.75×3.75mm^2 in-plane; 5mm thick; 13 axial slices). Prior to group processing, individual EPI data was standardized to the Montreal Neurological Institute space. For GLM, a default canonical hemodynamic response function (HRF) in SPM2 was employed as a regressor to detect task-related activations. For GIFT, the number of independent components (ICs) was set at 50 (out of 65 total) and the default parameters were adopted (Infomax, learning rate≈0.0038, and iterations=512). For IVA, after applying a PCA-based dimension reduction scheme [1], the 50 ICs (same as GIFT) were estimated based on Eq. (1), for a learning rate of 10^{-3} and with 500 iterations. From the results of GIFT and IVA, two ICs showing activations within the thalamus and basal ganglia were manually chosen from all 50 ICs. The resulting individual maps (contrast images from GLM and z-scored normalized IC maps from GIFT/IVA) were further processed using a random effect analysis (RFX) model [6].



Results & Discussion: Fig. 2 shows the group inference results (two statistical values: p<10^{-3} & p<10^{-5}; thalamus in green and basal ganglia in blue). Overall, the localized group activation areas identified by IVA showed substantial activation regions with higher z-scores and the distinct activation loci within the anterior putamen and ventral posterolateral/mediodorsal thalamus. The activation remained even for the very stringent threshold condition of p<10^{-5}. We conjecture that this is because the IVA approach can estimate maximally flexible individual- and region- specific hemodynamic responses of the measured data compared to the GLM and GIFT approaches. The current IVA-based approach is achieved at the cost of extensive computational demands, (e.g. ~10 hours processing using Intel Pentium IV 2.8GHz with 3GB RAM). Thus, alleviation of the computational load along with optimization of model parameters would be necessary.

References: [1] McKeown, HBM (1998) 6:160-88. [2] Calhoun, HBM (2001) 14:140-51. [3] Svensen, Neuroimage (2002) 16:551-63. [4] Beckmann, Neuroimage (2005) 25:294-311. [5] Lee, LNCS (2007) 4666: 633–640, [6] Friston et al., Neuroimage (1999) 10:1-5. The work was partly supported by the grant from NIH U41 RR019703 and 5R01NS048242-03.