Our laboratory has worked with Yoshio Takane of McGill for the past 10 years on development of functional magnetic resonance imaging (fMRI) software that, from our perspective, improves on standard procedures in a number of ways. Namely, fMRI-CPCA (1) is multivariate (networks are the focus of the analysis as opposed to individual regions), (2) is exploratory (brain networks of interest emerge from strong patterns of intercorrelations between brain regions, rather than being imposed on the data when restricting to so-called “regions of interest”), (3) is flexible (blood oxygen dependent, or BOLD signal, is not required to match a rigidly imposed hemodynamic response shape to be detected as task relevant), (4) is conducive to group comparisons (i.e., straight-forward values reflecting network integrity for each subject emerge from the analysis), (5) is optimized to produce functional networks that relate to stimulus presentation timing (as opposed to exploring post-hoc for associations with task timing), (6) allows a significance test of the reliability of each functional network that can be carried out in a straightforward fashion using familiar statistical testing methods and software, such as repeated-measures ANOVA (as opposed to using software-specific methods such as bootstrapping, or voxel-based p value corrections for tens of thousands of voxel-specific t-tests), and (7) allows a visual check of the hemodynamic response shape associated with a derived functional network to ensure biological plausibility (as opposed to assuming this for any brain region or network passing the threshold for significance). This software is publicly available, free of charge (www.nitrc.org/projects/fmricpca), and is now gaining popularity. Our lab designs all in-house experiments such that the data can be analyzed as an event-related design, but the software can also be used to analyze block design data, but would not, in that case, allow visualization of the network-associated hemodynamic response shape.

Briefly, CPCA combines principal component analysis and regression analysis. When applied to fMRI data, three main steps are carried out. In the first step, referred to as the external analysis, a multivariate least-square multiple regression is carried out to separate the BOLD signal into variance that is and is not predictable from stimulus timing model (the finite impulse response, or FIR model. FIR models do not assume a BOLD signal shape, but estimate BOLD changes in post-stimulus time). In the second step, the predicted scores from the multivariate multiple regression are submitted to principal component analysis (PCA with rotation). In a third step, weights are computed that, when applied to the stimulus timing model, would produce the component scores (the latter run over scans and subjects, as does the FIR model). This produces subject-, condition-, and perstimulus-time-point-specific predictor weights for each functional network, which reflect the intensity of each functional network over peristimulus time, and as such, estimate the hemodynamic response (HDR) associated with each functional network. Predictor weights can be interpreted as the importance of each extracted component to each combination of peristimulus time point, subject and scan. Predictor weights can be used to test the effects of the experimental condition on estimated BOLD response and to compare these responses between groups using repeated-measures ANOVA. Predictor weights also provide estimates of the HDR associated with a particular functional network; therefore, a significant effect of peristimulus time in ANOVA combined with a biologically plausible HDR shape provides evidence that the component is reflecting a reliable BOLD signal.

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fMRI-CPCA papers


