

Template free identification of resting state networks based independent component analysis

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Introduction:

The "default mode of brain function" has gained considerable interest in human neuroimaging studies, as it has been suggested that changes in the default network may be associated with neurologic and psychiatric diseases [1]. Independent Component Analysis (ICA) is one of the most important explorative data analysis methods for resting state networks, as it represents a purely data-driven statistical approach that enables decomposing high-dimensionality data into discrete signal and noise components. Still, it remains unclear how resting state components of interest may be evaluated appropriately, as no group analysis approach of ICA single subject results has become generally accepted in the scientific community today.

Data acquisition and analysis:

Images were acquired on a 3 Tesla Medspec S300 system (Bruker Biospin, Germany) using single-shot gradient-recalled EPI. 14 axial slices (6mm thickness, 1mm gap) were aligned to the connection line between anterior and posterior commissure) with a matrix size of 64 x 96, an FOV of 230 x 190 and TE/TR of 40/1000 ms. Ten healthy subject underwent 360s resting-state scans. Subjects were instructed to relax, stay awake and lie still without moving, while keeping their eyes closed at all times.

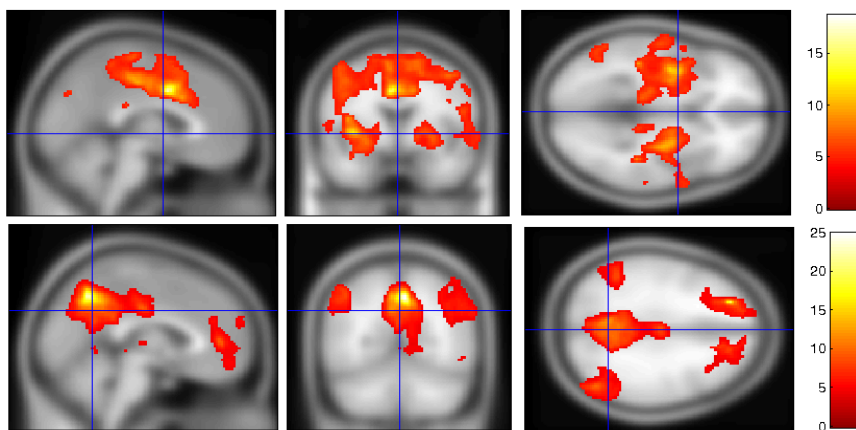
Image preprocessing was performed in SPM5 including correction for slice-timing differences, motion correction, spatial normalization and spatial smoothing using a Gaussian kernel (FWHM=9mm). ICA was performed using Probabilistic ICA [2] as implemented in MELODIC (Multivariate Exploratory Linear Decomposition into Independent Components) Version 3.05, part of FSL (FMRIB's Software Library, www.fmrib.ox.ac.uk/fsl).

Pre-processed data were whitened and projected into a lower-dimensional subspace using probabilistic Principal Component Analysis where the number of dimensions was estimated using Minimum Description Length (MDL) [3]. The whitened observations were decomposed into sets of vectors which describe signal variation across the temporal domain (time-courses) and across the spatial domain (maps) by optimising for non-Gaussian spatial source distributions using a fixed-point iteration technique [4]. Estimated Component maps were divided by the standard deviation of the residual noise and thresholded by fitting a mixture model to the histogram of intensity values [2].

Evaluating resting state components:

A correlation matrix over all subjects and components was derived and the maximal correlations coefficients were calculated. On the basis of the top 20 highest spatial correlations, seed component maps were calculated by averaging the spatial maps. Then these seed maps were spatially correlated with all subjects and components and the map with the highest correlation within each subject was determined. One sample t-tests were then performed over the resulting components in order to allow group inferences.

Results:



For fast calculation of the correlation matrix over all subjects and components MATLAB's "corrcoef" function was used.

Components obtained after correlating all subjects' components with the derived averaged spatial seed component maps were exported to SPM5 for one sample t-test and visualization.

Figure: Two default mode networks detected with template-free identification analysis. Components are overlaid onto a standard template.

Discussion:

The standard evaluation of resting-state components that are spatially consistent over all subjects leads to problems using a predefined spatial template for correlation with the single subjects components as other default mode networks might be disregarded due to the template definition. The novel evaluation analysis approach for identifying spatially consistent default mode networks across a given group of subjects as reported here requires neither component templates nor manual inspection/selection of single subject components allowing for a truly explorative way of assessing resting state networks.

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