Task-Free Functional MRI Summary Metric of Atlas Based DMN Regions of Interest

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Sept 1	All data downloaded from LONI
Oct 31	Results uploaded

Summary

The human brain forms a complex network to exchange information that is dependent on multiple scales spanning the genetic/molecular to the systems/behavioral level. Alzheimer's disease (AD) disrupts this highly interdependent, multi-scale organization. This AD-related disruption has been investigated at the functional systems-level using task-free fMRI (TF-fMRI) [1], demonstrating increased connectivity in frontal networks (e.g. anterior default mode network, aDMN) and decreased connectivity in parietal networks (e.g. posterior default mode network, pDMN) [2,3]. These reciprocal AD-related changes are also present during normal aging [2,4] and in cognitively normal elderly apolipoprotein E Ɛ4 allele carriers [5]. These systems-level changes can be demonstrated using a variety of analysis techniques (see [6] for a recent review). However, given the uncertain effect of the variability in the temporal signal-to-noise in lateral hemispheric regions related to the ADNI TF-fMRI acquisition (i.e. the so called "pencil artifact"), we have elected to focus on metrics that are not dependent on connectivity information present in lateral hemispheres, instead focusing on the intrinsic integrity of midline regions which tend to be free from this artifact. Therefore we have developed a TF-fMRI summary metric that exploits the reciprocal relationship between the aDMN and pDMN using only connectivity from midline cortical regions of interest (ROIs), which we refer to as the DMN RV-ratio. We computed the DMN RV-ratio for all the available TF-fMRI scans that have not failed quality control.

Method

Image Preprocessing

Preprocessing was performed utilizing a combination of the Statistical Parametric Mapping (SPM5) software (http://www.fil.ion.ucl.ac.uk/spm/software/spm5/) (Wellcome Department of Cognitive Neurology, University College London, UK), the Resting-State fMRI Data Analysis Toolkit (REST) v1.5 (http://www.restfmri.net) [7], Data Processing Assistant for Resting-State fMRI (DPARSF) v2.0 (http://www.restfmri.net) [8], and in-house developed software implemented in MATLAB v7.11 (Mathworks Inc., Natick, MA, USA).

Preprocessing steps included discarding the first 3 volumes to obtain steady state magnetization, slice time correction, realignment, normalization to SPM5 EPI template, smoothing with 4 mm full-width half maximum Gaussian kernel, linear detrending to correct for signal drift, and 0.01–0.08 Hz bandpass filtering to reduce non-neuronal contributions to blood-oxygenation-level-dependent (BOLD) signal fluctuations. In addition, linear regression correction for spurious variables included rigid body transformation motion effects and the first seven principle components of the voxel-wise time courses within white matter and cerebral spinal fluid regions of interest derived from their respective template space priors [9].

Anterior and Posterior DMN Regions of Interest

A complete description of the methods used to create the population based functional atlas was recently reported [3]. In brief, 892 healthy elderly subjects from the Mayo Clinic Study of Aging [10] who had undergone TF-fMRI of adequate quality were used in a group independent component analysis (GICA) [11]. This GICA was used to create 68 functional regions, which were categorized based on network of origin, anatomic locations, functional meta-analysis, and community structure (i.e. dynamic modularity). The GICA aggregate component maps and 68 functional ROIs are freely available for download (http://mayoresearch.mayo.edu/mayo/research/jack_lab/supplement.cfm). Given the current uncertainty surrounding the effect of the "pencil artifact" on various TF-fMRI metrics, we elected to only extract the BOLD signal from midline aDMN and pDMN edge eroded ROIs. Right and left ROIs were combined into single bilateral regions (Figure 1).

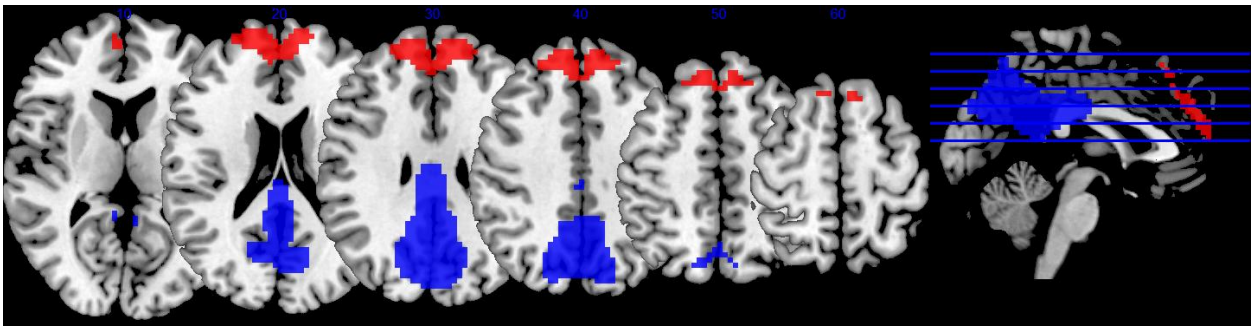

Figure 1: Anterior (red) and posterior (blue) DMN regions of interest overlaid on template brain.

Anterior and Posterior DMN Regions of Interest to Voxel Correlation

For each ROI, the average time course was extracted and compared to the time course of every voxel within the respective ROI using Pearson's product-moment correlation coefficient. Fisher r-to-z transformation was then computed for each of these values. The median z(r) within each ROI is then extracted and referred to as the ROI-to-voxel (RV) correlation. To capture the reciprocal relationship between the aDMN and pDMN within one summary metric, the aDMN RV is divided by the pDMN RV and referred to as the DMN RV-ratio. Our RV correlations are related to other measures of regional integrity of intrinsic activity, such as regional homogeneity (ReHo)[12]. Specifically, the DMN RV-ratio is highly correlated with coherence based ReHo calculations of the same aDMN-to-pDMN ratio (r = 0.81).

Results

We pre-processed all available ADNI2 and ADNIGO TF-fMRI scans that have not failed quality control through our pipeline and computed the DMN-RV ratio. In the uploaded file the aDMN RV, pDMN RV and DMN-RV ratio are provided for each task-free fMRI scan that passed minimum quality standards.

Version Information

Version 1.1 is the initial version.

Dataset Name	Date Submitted
Jack Lab – DMN RV-ratio Version 1.1	31 October 2012

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