Group independent component analysis reveals consistent resting-state networks across multiple sessions

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Introduction. Brain connectivity maps in the absence of task performance have been revealed in several brain circuits, including sensorimotor, visual, auditory, and language processing networks[1-4]. Among these observations, the existence of a brain network including posterior cingulate cortex (PCC) and medial prefrontal cortex (MPF) has been observed[2,4], which supports previous suggestions that there is a functionally significant default brain mode in awake resting-state[5]. Since the brain expends a considerable amount of energy in neuronal signaling processes in the absence of a particular task[6], it is further argued that, in pursuit of better understanding of brain functions, observation of intrinsic brain activity may be at least as important as that of evoked activity[7]. With growing interest in resting brain activity, it becomes increasingly important to fully understand and characterize the intrinsic brain function. Consistency of resting-state activity along time and across subjects is crucial for longitudinal studies, but is not well established quantitatively over extended periods thus far.

Methods. To address consistency of resting-state connectivity, we used group Independent Component Analysis (gICA), a multivariate data-driven method[8], following an extension of Calhoun et al.[9] FMRI images from 14 normal subjects (all male, 30±6 y.o.), scanned 5 times each over 16 days, were reduced and aggregated in 3 steps using Principle Components Analysis (PCA, within scan, within session and across session) and subjected to the gICA procedure. The amount of reduction was estimated by an improved method that utilizes an AR(1) fitting technique to the PCA spectrum[10,11]. The gICA analysis produced 55 spatially independent maps. Obvious artifactual maps were eliminated and the remainder divided into groups based upon perceived physiological relevance. Across-session consistency was examined by three methods, all using back-reconstruction of the single session or single subject/session maps from the grand (5 session) maps. First, spatial correlation was performed between the single-session and the grand (5-session) maps. Second, a conjunction analysis was performed across the 5 sessions to look at overlap of thresholded maps. Finally, voxel-wise ANOVA was performed to investigate amplitude differences across sessions.

Results. The gICA analysis produced at least 9 (of 55) physiologically relevant maps, including bilateral motor and sensory cortices, left- and right-lateralized frontal-parietal attentional networks, and the so-called default-mode network (see Figure 1). These maps showed remarkable consistency across sessions, with correlations between single-session maps and the grand maps in the 0.5-0.95 range and striking overlap between the single-session maps. Furthermore, the components with the most obvious physiological relevance showed statistically greater consistency than those apparently artifactual in nature, such as eyes, CSF, or edge-of-brain indicating head motion, see Figure 2. The ANOVA results were in good agreement with the correlation results.

Discussion. The gICA analysis technique seems to be well suited to the analysis of resting-state data where the networks may be stationary but the fMRI timecourses may not. The gICA component maps we found agree well with the literature[12] and consist of well-known anatomical and/or functional networks. Even in the absence of task or overt exogenous stimuli, these networks appear robust and repeatable both over time and across individuals. The consistency of these maps suggests that, at least over a period of weeks, these networks would be useful in longitudinal treatment related studies.

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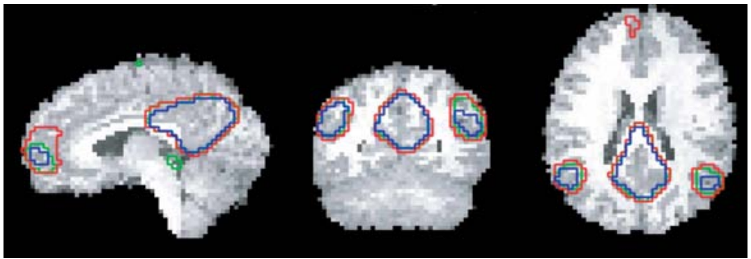

Figure 1. Group ICA map of the default-mode network (red), regions of overlap in all 5 sessions (blue) or 3/5 sessions (green) showing the striking consistency.

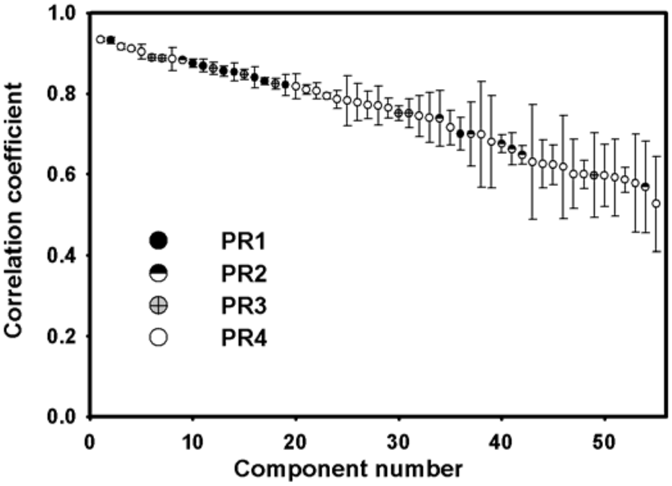

Figure 2. Average correlation between single-session and grand component maps. PR=physiological relevance; PR1 are clearly relevant whereas PR4 are clearly artifact. Note that the PR1 group is more consistent (higher average CC)