Activity-based seed regions for resting-state fMRI analysis are susceptible to large vessels

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Introduction:

Many functional magnetic resonance imaging (fMRI) analyses of the resting state rely on the identification of a seed region based on location of significant activity during a separate task; however, it is known that task-related BOLD fMRI is susceptible to the locations of large vessels [1]. Alternatively, independent component analysis (ICA) approaches identify resting-state networks without the need for seed regions [2]; however, the determination of the appropriate number of components and their final combination is not straightforward. Therefore, in investigations of resting-state connectivity within a specific network, a seed-based approach remains a method of choice. The objective of this study was to compare the location of seed regions for resting-state connectivity based on separate task-related maps to those based on anatomical landmarks.
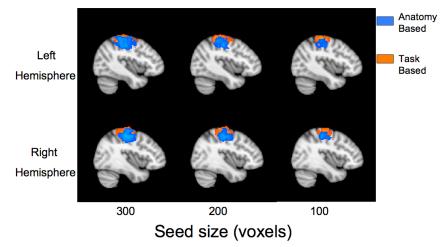
Methods:

Seven healthy volunteers participated in the study after providing informed consent. Resting-state T_2*-weighted images (GRE-EPI: TR/TE = 1500/30 ms, 24-cm FOV; 64x64 matrix; twenty 5-mm thick slices, 110 volumes) were collected while subjects lay still visually fixating on a small black cross at the center of a projection screen (Avotec, Inc., Stuart, FL). Additional images were collected during the performance of a bilateral finger movement task (five visually-cued epochs of 20 seconds of self-paced finger movements and 20 seconds of rest). T_1-weighted anatomical images were also collected. For the fMRI data collected during finger movements, locations of significant brain activity were determined using General Linear Model (FSL: http://www.fmrib.ox.ac.uk/fsl). Two methods of seed and target selection were investigated: 1) using the resulting bilateral finger movement activity map to select the N most significant voxels within each of the left (seed) and right (target) primary sensorimotor cortices (N was decreased from 300 to 200 to 100 voxels); 2) using anatomical images to segment the hand region of each of the left (seed) and right (target) primary sensorimotor cortices based on known anatomical landmarks. The sizes of these anatomical regions were also decreased from 300 to 200 to 100 voxels by successively calculating the correlation between the time course of each voxel within the region with their average time course, and then discarding the voxel exhibiting the lowest correlation. All images and seeds were transformed to the common space of the Montreal Neurological Institute (MNI) brain, and the x, y, and z coordinates of the centre of gravity of each seed region were recorded for each subject. A repeated-measure analysis of variance (ANOVA) was then performed for each of the x, y, and z coordinates of the right and left motor cortex seeds, with method of seed selection (anatomy-based, task-based) and seed size (300, 200, 100 voxels) as within-subject factors.

Results:

The top figure shows the anatomical location of seeds within the motor cortex for task-based and anatomical-based identification, averaged over all subjects. The bottom figure shows the average percentage overlap between anatomical-based and task-based seeds as a function of seed size for left (blue) and right (green) motor cortex, averaged over all subjects. Overlap is not considerable, especially for smaller seeds, suggesting that the two methods do not converge to the same area of motor cortex. As seed size decreases, task-based seeds move to more superior locations in the brain, while anatomy-based masks moves toward inferior regions of motor cortex. In right motor cortex, the ANOVA revealed a significant effect of seed selection method on the z coordinate of the seed [$F_{(1,6)}=13.70$; $p<0.01$]. The same trend was observed for the z coordinate in the left motor cortex [$F_{(1,6)}=5.42$; $p=0.059$].

Conclusion

Task-based seeds for resting-state connectivity analysis are located at more superior locations in proximity to large draining vessels, compared to anatomy-based seeds. Hence, seed regions based on brain activity in response to tasks may not be optimal for analysis of resting-state networks.

Reference:

[1] C-H Moon, et al. *J Neurosci*. 2007;27:6892-6902.

[2] M De Luca, et al. *Neuroimage*. 2006;29:1359-67.