Segmentation of Thalamus by Clustering of Resting-State fMRI

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Introduction

Resting-state functional MRI (rsfMRI) examines spatial synchronization of spontaneous fluctuations in blood oxygenation level dependent (BOLD) signals arising from neuronal and synaptic activity that is present in the absence of entrained task performance. Using a temporal cross-correlation method, Biswal et al. first demonstrated functional connectivity in somatomotor networks [1]. Subsequently, a rising number of studies have shown that cortical and subcortical brain regions engaged during various cognitive tasks also present coherent functional connectivity that could be demonstrated using rsfMRI [2]. Furthermore, Zhang et al. segmented the thalamus based on the correlations in resting-state activity between the human thalamus and the cerebral cortex [3]. In this study, we hypothesized that voxels belonging to the same partition of thalamus should be provided with the similar temporal cross-correlation values to other voxels. Finally, the segmentation the thalalmus based on the clusters of the rsfMRI data would be demonstrated in the results.

Materials and Methods

Normal, healthy participants were recruited in this study, and were provided full informed consent before experiment. The image data were acquired on a 3T Siemens Trio MRI scanner. Prior to the rsfMRI scan, the volunteer was instructed to rest with eyes closed, not to think of anything in particular, and not to fall asleep during data acquisition. A single shot EPI sequence was performed to acquire the high resolution rsfMRI data with parallel to the AC-PC line to cover from the upper corpus callosum to the subcortical brain regions. Twenty-fourth axial slices were acquired with the parameters sensitive to BOLD signal change, TR/TE = 2000/30 ms, field of view = 192 * 192 mm^2, in-plane matrix size = 96*96 and voxel size = 2*2*2 mm^3.

To avoid the disappearance of differences between the BOLD signals of all voxels of thalamus during the preprocessing schemes of fMRI, all rsfMRI analyses were applied in the native space (not MNI space) to keep the original BOLD signal. Only normalization function of SPM2 (Wellcome Department of Cognitive Neurology, London, UK) was used for motion correlation and provide the covariables for further time cross-correlation calculation. The registration function of SPM2 was also applied to map the AAL template (Anatomical Automatic Labeling) to EPI image to delineate the contour of thalamus and obtain all voxels in the thalamus [4]. This correlation calculation was done by REST toolkit (http://restfmri.net/forum/index.php). Each voxel of thalamus was then defined as the seed point with radius =2 mm individually to obtain the temporal cross-correlations with other voxels of thalamus.

To cluster the voxels of thalamus, we transferred the correlation matrix (N by N, N means the points of thalamus) to a meta-data with N instances and N attributes. Weka 3, a opensource data mining software was then applied to cluster this data based on the k-median clustering algorithm. Finally, we presented the segmentations of thalamus according to the clustered results.

Results

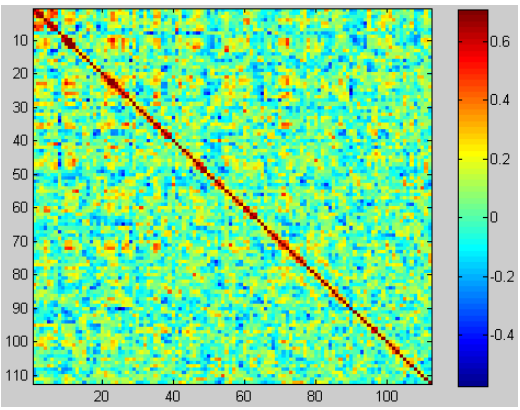
Fig.1 presented the N by N temporal cross-correlation Z-score map (N=109) of resting-state BOLD signal in the slice #10 of left thalamus. Based on this map, we could transfer each row as an instance and each column as an attribute for the clustering algorithm. Fig. 2 showed the segmentation of thalamus by the clustered results with k=4. It should be noted that the results were processed in right (N=112) and left (N=109) thalamus respectively and drawn with 4 kinds of color (red, orange, yellow and green) together.

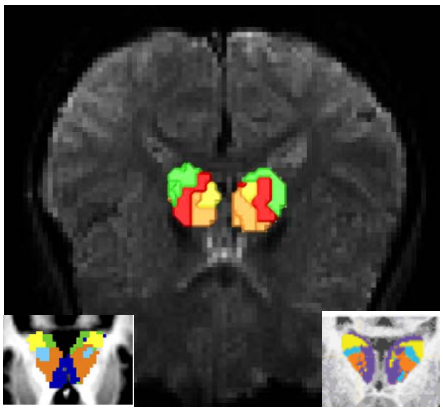
Discussions

From our results, resting-state fMRI could provide not only the functional connectivity network between cortical and subcortical brain regions, but also local characteristic within thalamus. Using the cross-correlation map derived from rsfMRI analysis, the segmentation map presents the high consistence between two hemispheres. In comparison with the parcellation results by DTI tractography and segmented partitions based on rsfMRI shown in the right and left lower corner of Fig.2 respectively[3][5], the results show higher similarity with the latter. The reason might be caused by that structural connectivity could not reflect the functional connectivity completely. Although the SNR of high resolution rsfMRI data is lower, the results still showed that high resolution rsfMRI data seems to provide more information to highlight the differences or similarity with other voxels than common dataset (3 mm isotropic voxel). In next step, more numbers of cluster and more slices will be demonstrated to evaluate the workability using rsfMRI results for separating the localized nuclei in thalamus.

References

[1] Biswal B. et al., Magn. Reson. Med. 34: 537–541, 1995. [2] Smith S. M. et al., Proc. Natl. Acad. Sci. 106:13040–13045, 2009. [3] Zhang D. et al., J Neurophysiol. 100:1740-48, 2008. [4] Tzourio-Mazoyer N. et al., NeuroImage, 15(1):273-89, 2002. [5] T E J Behrens et al., Nat. Neurosci., 6:750-7, 2003





◄◄**Fig. 1** The cross-correlation Z-score map in the slice #10 of left thalamus. By registering AAL template to the native EPI space, the localization of thalamus could be delineated. In the slice #10, 109 voxels were assigned as the voxels of left thalamus. Each voxel was then defined as the seed point to get the 109 cross-correlation value. In the right side, the color bar presented the corresponding Z-score.

◄**Fig. 2** The segmentation of thalamus. The center graph was drawn based on the clustering results with 4 kinds of color (k=4), and the left lower and right lower graphs were cited from the references respectively [3][5].