ROI atlas generated from whole brain parcellation of resting state fMRI data

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Introduction

Connectivity analyses and computational modeling of human brain function from fMRI data require the specification of regions of interests to be employed in the analysis. Several methods have been used that either rely on a neuroanatomist's ability to reliably identify targeted brain regions, or atlases derived from anatomical or cyto-architectonic boundaries. Neither of these approaches incorporates functional data into region specification and likely result in functionally heterogeneous regions. We introduce a method for parcellating the whole brain based on fMRI resting state data into contiguous regions of functional homogeneity.

Methods

Twenty-four healthy control subjects (mean age 29, std. dev. 6.83, 9 females) were recruited in accordance with Emory University Institutional Review Board policy. Subjects were scanned on a 3.0T Siemens Magnetom TIM Trio scanner (Siemens Medical Solutions USA; Malvern PA, USA) using a 12 channel head matrix. Resting state fMRI data were acquired with the Z-SAGA sequence to minimize susceptibility artifacts [1]. One hundred and fifty functional volumes were acquired in thirty 4-mm axial slices using the parameters: TR 2920 msec, TE^1/TE^2 30 msec/66 msec, FA 90°, 64 x 64 matrix, in-plane resolution 3.44x3.44 mm^2.

All preprocessing of MRI data was performed using SPM5 [2] running in MATLAB 2008a (The Mathworks; Natick MA, USA). fMRI volumes were slice timing corrected, motion corrected, written into ICBM462 space at 4x4x4 mm^3 resolution using the transformation calculated on the corresponding anatomic images, and spatially smoothed using a 6-mm FWHM Gaussian kernel. fMRI data were restricted to grey matter and de-noised by regressing out motion parameters, WM time-course, as well as CSF time-course [3, 4]. Each voxel time-course was band-pass filtered (0.009 Hz < f < 0.08 Hz) to remove frequencies not implicated in resting state functional connectivity [3, 5] and then z-score normalized.

Normalized cut (ncut) [6] spectral clustering was performed using custom scripts written in Python. An affinity matrix was constructed for each subject where each element in the matrix contains the similarity between the corresponding voxel time-courses. Similarity was measured by the eta^2 statistic between time-courses [7]. Similarity was only calculated between voxels in a 3-D neighborhood. This ensures that the resulting clusters contain contiguous voxels. Each subject's affinity matrix was submitted to ncut clustering to generate clusterings of K ($50 \le K \le 300$) clusters. The resulting subject-specific clustering was used to construct a group-level coincidence matrix. Each element of the matrix contains the percentage of subjects for which the corresponding voxels reside in the same cluster. A coincidence matrix was constructed for each K and then submitted to ncut clustering to produce a group level clustering with K clusters. Leave-one-out cross-validation (LOOCV) was used to evaluate the quality of each clustering (K). In each iteration of the LOOCV procedure group clustering was performed excluding a single subject. The result of this clustering was compared to the clustering obtained for the left out subject. This was performed leaving out each subject, and the LOOCV accuracy was averaged across iterations.

Results/Discussion

Figure 1 shows the learning curves for the LOOCV procedure. For K<80 the clusters are very reproducible, but this is a trivial situation in which cluster homogeneity is low. As the number of clusters increase, reproducibility tends to decrease until a peak is reached around K=130. Figure 2 illustrates the clustering obtained for K=130. The clusters tend to be symmetric across hemispheres and align well with known neuroanatomical boundaries.

Conclusions

A whole brain parcellation was achieved by cluster resting state fMRI data. The resulting clusters are contiguous and exhibit homogenous functional connectivity. This technique reduces whole brain data into 130 ROIs that can be used to further study the functional connectivity and network structure of resting state fMRI data.

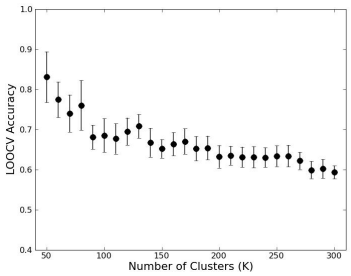

Figure 1 LOOCV learning curve

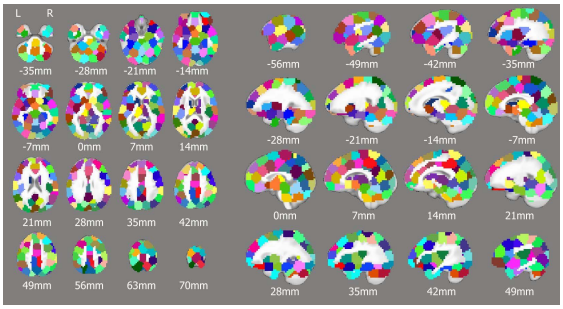

Figure 2 Resulting 130 cluster ROI map

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Acknowledgements: Data collection and salary support was provided by P50 MH077083 (HSM), R01 MH073719 (HSM), K23 MH077869 (PEH) and a NARSAD Young Investigator Award (PEH). Salary support was also provided by NIH R01 EB002009 (XPH).