#### Resting-state fMRI Segmentation in Spatio-temporal Domain Using Supervoxels

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## Introduction:

Functional segmentation of human brain in resting state is an important task. It can be used as a baseline for constructing brain networks as well as diagnosing diseases. State-of-the-art methods that are used for this task are usually computationally expensive (Thirion, 2014). We propose a computationally more efficient framework (Fig.1) for functional segmentation and validate it by comparing to AAL parcellation both visually and by measuring in-cluster and between-cluster correlations, where larger in-cluster and smaller between-cluster correlations indicates better segmentation performance.

#### Methods:

Temporal smoothing of 4D fMRI data is performed using cosine series representation (CSR) - a Fourier transform involving only orthonormal cosine basis in [0,1] (Chung, 2010). Fig.1b depicts two fMRI signals from different voxels (Fig.1a) and their resampling with 120 cosine basis functions (Fig.1c, solid lines).

In image segmentation, supervoxel algorithms group voxels into meaningful atomic regions to replace rigid structure of voxel grid. Simple Linear Iterative Clustering (SLIC) supervoxel algorithm adopts k-means clustering but has lower computational complexity O(k) (Achanta, 2011). First, 3D image of N voxels is divided in k equal size supervoxels by a regular grid with interval  $S=(N/k)^{1/3}$ . A search for similar voxels is done in a region 2Sx2Sx2S around supervoxel center. In practice, each voxel falls in the local neighborhood of at most 26 cluster centers. Algorithm uses distance D=  $((d_g/3S)^2+((1-\rho)/2)^2)^{1/2} \in [0,1]$ , where d<sub>s</sub> is a Euclidean distance in spatial domain, and  $\rho$  is correlation between a voxel and a supervoxel's center. Clusters smaller than S<sup>3</sup>/10 are merged to the closest cluster.

Given sample correlations  $\rho_i$ , i=1...n, we are interested in the average of correlations  $\rho_0$ . First, transform  $\rho_i$  using Fisher's z-transform  $z_i$ =arctanh( $\rho_i$ ). Then, inverse Fisher transform applied to the mean of  $z_i$  will give an estimate of the population correlation coefficient (Corey, 1998).



Fig.1 Framework for functional segmentation of human brain



Fig.2 Computing average in-cluster and between-cluster correlation coefficients. For each pair of clusters we build a correlation matrix. Using direct and inverse Fisher transform, we computer in-cluster and between-cluster correlation coefficients from corresponding highlighted areas of correlation matrices. Here, we consider only those voxels that present in AAL parcellation ROIs. Now, a subject is represented by a matrix of cluster correlations. We again apply Fisher transform to obtain average in-cluster and between-cluster correlation coefficients for each subject that are used to estimate population in-cluster and between-cluster correlation coefficients



Fig.3 Influence of number of supervoxels on the performance of SLIC algorithm. Blue lines show difference between population in-cluster (a, dashed line) and between-cluster (b, dotted line) correlation coefficients calculated for SLIC segmentation (obtained for 300, 500, 700 and 1000 number of supervoxels, respectively) and AAL parcellation. Red lines show corresponding p-values under the null hypothesis  $H_0: \mu_{SV} - \mu_{AAL} = 0$ 

# **Results:**

The proposed framework (Fig.1) is applied to a subset of 100 BOLD resting-sate fMRI scans from the Human Connectome Project dataset (Van Essen, 2012). The data is preprocessed using CSR with 120 cosine basis functions (to reduce size of data to 10%).

Correlation between fMRI signals is used as a measure of closeness to evaluate the quality of segmentation. Fig.2 shows how in-cluster and between-cluster correlations are calculated from correlation matrices employing Fisher direct and inverse transformations. Using AAL as a ground-truth we consider only positive correlation coefficients corresponding to voxels from AAL regions to compute in-cluster and between-cluster correlations. From resulting clusters correlation matrix, average in-cluster and between-cluster correlation coefficients are calculated. For 100 subjects, sample in-cluster and between-cluster correlation coefficients are  $0.249\pm1.9*10^{-5}$  and  $0.186\pm9.8*10^{-7}$  for SLIC algorithm with 1000 supervoxels, and  $0.205\pm1.1*10^{-5}$  and  $0.187\pm1.2*10^{-6}$  for AAL parcellation. We performed two-sample t-test separately for incluster and between-cluster correlation coefficients are 0.027, respectively. Additionally, Fig.3 presents corresponding test results for 300, 500, 700 and 1000 supervoxels.

#### **Conclusions:**

Although segmentation obtained with proposed framework doesn't follow macroscopic brain structures perfectly (compared to AAL parcellation), there's a well-marked correspondence between them (Fig.4). SLIC segmentation tends to retain similar structure across different subjects that can be used to construct resting-state brain activity network for the whole dataset.



**Fig.4 Correspondence between AAL structural parcellation and SLIC functional segmentation.** For given two subjects we present results of AAL and SLIC segmentation for horizontal and coronal plane cuts (voxels that do not present in AAL parcellation are ignored for visualization). The first row presents original fMRI signal at time step 1. For rows presenting results of SLIC segmentation for different number of supervoxels, each cluster is colored according to the average fMRI signal across the cluster

# **References:**

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# Categories

BOLD fMRI fMRI Connectivity and Network Modeling<sup>2</sup> Segmentation and Parcellation<sup>1</sup> Task-Independent and Resting-State Analysis Cortical Anatomy and Brain Mapping

## Keywords

FUNCTIONAL MRI, Machine Learning, Segmentation