

A MODIFIED K-MEANS ALGORITHM FOR RESTING STATE FMRI ANALYSIS OF BRAIN TUMOR PATIENTS, AS VALIDATED BY LANGUAGE LOCALIZATION

Naresh Nandakumar*, Niharika Shimona D’Souza*, Haris Sair†, Archana Venkataraman*

* Department of Electrical and Computer Engineering, Johns Hopkins University, USA

†Department of Neuroradiology, Johns Hopkins School of Medicine, USA

ABSTRACT

We propose a modified K-means algorithm to accurately cluster data with missing values. We applied our model to resting state fMRI data of 20 brain tumor patients and assessed the coherence of language clusters. Our model shows higher correlation between language areas of the brain than the Automated Anatomical Labeling (AAL) atlas does.

Index Terms— K-means Clustering, rs-fMRI Analysis

1. MODIFIED K-MEANS FOR BRAIN TUMOR PATIENT CLUSTERING

Resting state fMRI (rs-fMRI) provides an important glimpse into intrinsic communication patterns in the brain. Clustering techniques for rs-fMRI are useful data driven approaches to explore functional organization of the brain [1]. Temporally synchronous clusters are seen as representing brain networks. For clinical purposes, mapping the language networks (Broca’s and Wernicke’s area) in brain tumor patients using fMRI is crucial for preoperative planning and can reduce surgical time and better predict preoperative deficits [2].

Rs-fMRI scans for N brain tumor patients were concatenated into matrix $X \in \mathcal{R}^{M \times NT}$ where M is the number of voxels and T is number of time points per patient. Tumor voxels are identified and recorded in binary matrix $B \in \mathcal{R}^{M \times NT}$ that has 0’s at tumorous voxels and 1’s elsewhere. The new K-means model takes both X and B as inputs and computes the appropriate cluster weightings $W \in \mathcal{R}^{M \times 1}$ and $V \in \mathcal{R}^{1 \times NT}$ from B , where W corresponds to row weights and V corresponds to centroid weights. The objective function from which the updates are derived is

$$\arg \min_{Z, \mu} \sum_{j=1}^C \sum_{i=1}^M Z_{ij} \|w_i \cdot (X_i \circ B_i) - \mu_j \circ V\|_2^2,$$

where Z_{ij} is an indicator and C is the number of clusters.

2. RESULTS

Rs-fMRI data was preprocessed using the pipeline of [2]. Tumorous voxels were manually recorded into the matrix B .

	Seed with Broca’s	Seed with Wernicke’s	Broca’s with Wernicke’s
AAL	.66±.16	.57±.15	.36±.19
K-Means	.68±.13	.69±.12	.55±.17

Table 1. Mean plus or minus standard deviation of Pearson correlation values in 20 patients.

Our K-means was run with $K = 116$ and 20 iterations. Language seed voxels were identified based on high activation during a language fMRI paradigm, which was acquired just prior to the rs-fMRI data. The language seed is the mean time course of these voxels in the patient’s rs-fMRI data. To identify Broca’s and Wernicke’s area, we first created an anatomical boundary in which we expected to find the cluster of interest. Two different boundaries were drawn, one for Broca’s area and one for Wernicke’s area. Per patient, we then chose the cluster or anatomical parcel within the boundary that had the highest correlation with the patient’s language seed. Table 1 shows mean \pm standard deviation of Pearson correlation values between Broca’s and the language seed (left column), Wernicke’s and the language seed (middle column) and Broca’s and Wernicke’s (right column). Compared to AAL, our algorithm shows higher correlation between the language seed and Wernicke’s area and between Broca’s area and Wernicke’s area in a single patient (yellow).

The higher correlations show that our model captures functional networks in brain tumor patients better than a standard anatomical parcellation. This result is highlighted in our improved performance relating to Wernicke’s area, which is more anatomically variable relative to Broca’s area. These developments could be valuable in preoperative settings.

3. REFERENCES

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