Parcellation of functional Magnetic Resonance Image (fMRI) Based on Finite Mixture Models via Self-Annealing Expectation Maximization

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Abstract

Purpose

We present a new method for brain parcellation based on a probabilistic model and anatomical and functional features that account for variability of the fMRI response in different brain regions. The goal of this procedure is to segregate the brain into spatially connected and functionally homogeneous components. It helps us achieve a new representation of the fMRI data, useful in region-based analysis of the data, especially in group analysis of the fMRI.

Method

To achieve this goal, the parcellation algorithm relies on the optimization of a compound criterion reflecting both the spatial and functional structures of the individual brains and hence the topology of the dataset. We employ unsupervised learning techniques to analyze fMRI data in an exploratory fashion. We use the most common spatial similarity measure, which favors the closeness in the coordinates system. The functional part of this criterion uses the parameters that characterize the functional properties of the voxels. These parameters are chosen as the βparameters estimated during a first-level GLM analysis of time series data via y=X β+e. Most methods consider raw fMRI time courses and use clustering or Independent Component Analysis (ICA) to estimate a decomposition of the data into a set of distinct time courses. In order to find functionally similar voxels, we use information from the first level analysis of the fMRI data. This effectively projects the original high-dimensional time courses to a low dimensional feature space, and then we perform a clustering in the new space. We have developed an automatic parcellation of the 3D cortex with an adjustable resolution. Our method operates on vectors that represent both the anatomical and functional properties of the voxels. We assume a Finite Mixture Model (FMM) for the distribution of the feature vectors where the voxels of each parcel follow a normal density. The algorithm relies on fitting FMM on the anatomical-functional data by using a self-annealing Expectation Maximization (EM) algorithm. The preference of this approach to Gaussian Mixture Model (with standard EM algorithm) is an initialization strategy, which can be interpreted as a self-annealing algorithm. Moreover, the number of parcels, *K*, is an important issue. We employ Akaike Information Criterion (AIC) to fit the model to the data. The algorithm is run for each *K*, and the criteria evaluated. The K that achieves the minimum value is then selected as the number of parcels. The larger the number of parcels, the higher the degree of

within-parcel homogeneity. However, there exists a trade-off between the within-parcel homogeneity and the signal-to-noise ratio (SNR).

Results

The algorithm is tested on synthetic functional data as well as real fMRI data. We have compared the results of our algorithm with previous parcellation algorithms such as K-means and Gaussian Mixture Model (GMM). We apply all of the above algorithms on synthetic functional data and calculate the confusion matrix and the accuracy (AC) parameter, which is the proportion of the total number of correct detection; it evaluates the performance of each classification. Table 1 shows that our algorithm outperforms the others and has the highest accuracy (AC).

Table 1- The performance of each algorithm demonstrated by calculating the accuracy (AC) parameter

Method	FMM- EM Algorithm self-annealing	K-Means	Gaussian Mixture Model (GMM)
Accuracy (AC)	0.98	0.84	0.63

We also demonstrate the results of our method on a motor fMRI study. Here, we aim to employ our method to discover homogeneous and connected regions, parcels, in the brain in response to a motor task. In order to find the best model, we employ Akaike information criterion (AIC) then the optimal number of parcels $K=10$ is achieved. In Figure 1, we illustrate spatial maps of three parcels in the left and right motor cortices and the cerebellum. Note that these parcels are spatially connected regions, each having a distinct profile of response to the fMRI motor experiment. These regions are reported in prior hypothesis-based studies; however, our exploratory approach is able to define them.

Figure 1. Spatial maps of the three parcels, discovered in the motor cortex and the cerebellum in an fMRI motor experiment, with the corresponding time courses.

Conclusion

In this paper, we presented a probabilistic model for unsupervised parcellation of the brain based on Finite Mixture Models. Applying this method to data from a motor experiment, we were able to find homogeneous and connected regions in the motor cortex and the cerebellum that have been previously found using hypothesis-driven methods. Simulation studies have shown that the parcellation results of our method are more accurate than those of the formerly developed methods.