# Fuzzy Clustering on fMRI Responses Using Autocorrelation Function Features

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## Introduction:

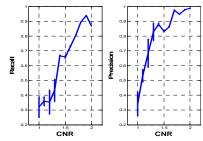
Hypothesis-driven methods (such as general linear model analysis) have been widely adopted for functional magnetic resonance imaging (fMRI) analysis. However, assumptions on hemodynamic response function (HRF) models are always controversial, and a precise relationship between the external stimulus and the brain reaction is essential. On the contrary, data-driven methods (e.g. principle component analysis, independent component analysis, and clustering analysis) are free from these problems, due to their model-free property. The major difference between component analyses and clustering analysis is: original data is decomposed into several components in former methods, while the latter separates data into groups via similarities. The concept of components may be intuitive but questionable because of the strong assumptions on the linearity of components, whereas clustering analysis bears the advantage of the fewest assumptions. Furthermore, in all data-driven methods dimension reduction strategies must be applied to overcome the high computational complexity, and feature extraction preserves key information in spite of dimension reduction. Therefore, we proposed to use signal corresponding features as well as noise features for clustering. Since autocorrelation function (ACF) is a common tool to estimate noise [1] [2], ACF features can thus be used to form the feature space before applying any clustering algorithm.

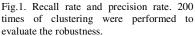
## Simulation:

We took a whole brain EPI (Philips Achieva 3.0T, TE/TR = 35/2000 msec, 20 slices, 64x64 matrix size) and replicated the image set to simulate 100 dynamic scans. Both artificial activation and noise (with well controlled contrast-to-noise ratio from 1.0 to 2.0 in the simulations) were then added. 200 voxels were assigned to be activated, and the activation waveform was simulated as a series of square waves convolved with gamma functions. Furthermore, to simulate the uncertain relationship between the stimulus and the brain reaction, we had the activation onset time vary within  $\pm 1$  scan. Normally distributed random signal was produced as noise, where the variance was scaled according to CNR settings.

### In vivo experiment:

To further explore the ability of clustering, we designed paradigms combining two simultaneous but distinct stimuli: 1) regular finger tapping task (5 scans on and 5 scans off), and 2) irregular visual stimulus (checkerboard, 8Hz flashing rate). The irregular paradigm was designed with random on-off durations (1-3 blocks of scans variation for both "on" and "off" conditions). Scan parameters were the same as in the simulation section, and 140 dynamic scans were collected in one trial. The paradigms were shown in Fig.2 and 3 (bottom, red line). *Method:* 





Data preprocessing included motion estimation, motion correction, and detrend. In order to minimize data manipulation, however, motion correction was neglected whenever possible, depending on the data quality. After preprocessing, features from both time courses and the corresponding ACFs were extracted to build the feature space. Fuzzy *C*-means (FCM) algorithm was applied in our study. We adopted the validity function [3] to evaluate the cluster validity and then determined the proper number of clusters. FCM gave us a set of membership functions, and members of each cluster were then assigned via the maximum membership comparison. The average time course of each cluster was contributed by the belonging members (weighted by the corresponding memberships). Correlation tests between the averaged time courses and the original data set were then performed to create whole brain correlation maps.

#### Result:

The simulations were run 200 times to evaluate clustering robustness. Recall rate (sensitivity) and precision rate (positive predictive value) were used as major robustness indicators (Fig.1). When the CNR value was set to be higher than 1.6, the results from 200 times of clustering came to the close recall and precision rate, implying a satisfactorily robust performance. Meanwhile, roughly 85% of precision rate guaranteed the similarity of the members for the calculation of averaged time courses.

The correlation maps were used to evaluate the clustering result for in vivo experiment data (Fig.2 and 3, top). A high correlation threshold (over 0.8) was selected. Voxels with high correlation values were confined in regions associated with different tasks. Both regular and irregular activations were detected and separated well.

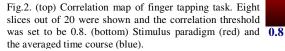
#### Discussion:

Conventionally, fuzzy clustering analysis uses time courses as features, and ACF is used as an estimator to remove potentially inactive voxels [2]. On the contrary, we attempted to use ACF information as our main features. These ACF features implied not only the level of noise, but also the signal characteristics such as periodicity. Thus, even CNR was as low as 1.4, 80% of precision rate was still achieved.

From the correlation maps we can conclude that our features contained sufficient information to differentiate various patterns embedded in one single experiment, form the data itself instead of prior knowledge on the paradigms or presumed hemodynamic models. In addition, the high correlation shown in the results also indicated that the average time courses were closely similar to the actual hemodynamic responses. In other words, the averaged time courses are not contaminated with uninvited members, suggesting the high specificity. Since no paradigm information or model assumption is required, this method is not limited by any assumption. Our proposed method therefore has strong potential in the investigations of complex cognitive functions where the relationship between activation patterns and stimulus paradigm is unclear. **Reference:** 



- 2. Somorjai et al, ISMRM proc, Philadelphia, p. 1718, 1999
- 3. Fadili et al. Med Imag Ana. 5:55-67, 2001



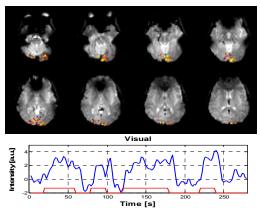


Fig.3. (top) Correlation map of the irregular checkerboard stimulus. Lower slices were shown for better visualization. Same correlation threshold has been chosen.