Using Features of Hemodynamic Response in Fuzzy Cluster Analysis of fMRI

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Synopsis

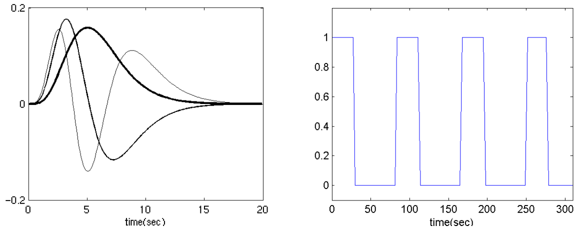
Commonly used hemodynamic response functions (HRF) such as gamma or Gaussian ignore the variability of HRF over different brain areas, subjects and sessions. Using three basis functions that model this variability, we derived three features for each fMRI time series. These features along with conventional correlation coefficient provided a feature space. By applying a Fuzzy C-Means clustering (FCM) on this space, activated areas were detected with an increased sensitivity. This method was applied to a finger tapping fMRI data and revealed activation in sub-cortical areas where FCM on cross correlation feature was unable to detect them.

Introduction

A set of data points, represented by feature vectors x_i, can be partitioned into C fuzzy clusters by fuzzy C-Means (FCM) clustering algorithm. For each point i FCM derives C fuzzy membership numbers u_{ik}, that represent the degree of membership of *i*th point to *k*th cluster. It also finds a centroid v_k for each cluster. FCM has been used in fMRI analysis [1],[2]. The feature vector used for this purpose was either the fMRI time series itself [1], or its cross correlation with a reference signal [2]. In the former case, confounds of the fMRI signal and its noise may mislead the clustering algorithm. In the latter case, the reference signal is usually considered as the stimulation pattern or its convolution with a fixed HRF, implying a fixed HRF over all brain areas or subjects. However, HRF has been shown to vary significantly between different brain areas or subjects [3]. We provide a feature space that covers this variability, and therefore, leads to a more sensitive detection by FCM.

Methods

By systematic analysis of HRF variations, Hossein-Zadeh *et al* [4] showed that various shapes of HRF might be closely approximated by linear combination of three elementary functions (see Fig 1.a). Convolving these functions with the stimulation pattern provides three basis functions ($z_1(t)$, $z_2(t)$, $z_3(t)$) for the signal subspace. Therefore, each fMRI time series may be decomposed as: $y(t) = \alpha_1 z_1(t) + \alpha_2 z_2(t) + \alpha_3 z_3(t) + e(t)$, where $e(t)$ is the residual considered as noise. The unknown coefficients α_1, α_2, and α_3 were estimated for each voxel (through an LS estimation) and were used along with a conventional cross correlation coefficient *cc* (the cross-correlation between $y(t)$ and the stimulation pattern) to provide a feature space for FCM clustering. The number of clusters and fuzziness index were set to $C=6$ and $m=2$ [2]. After FCM algorithm convergence, the cluster with the most similar centroid to the stimulation pattern was selected as active cluster. The membership degree of voxels to this cluster was thresholded by 0.6, and those voxels that had higher membership to this cluster were marked as active. The isolated (single) active voxels were then removed from the activation map, since they may be considered as false alarms.



(a) (b)

Fig. 1. (a) Three elementary functions for modeling the HRF. (b) Stimulation pattern corresponding to right hand finger tapping of the fMRI experiment.

FMRI Experiment and Preprocessing

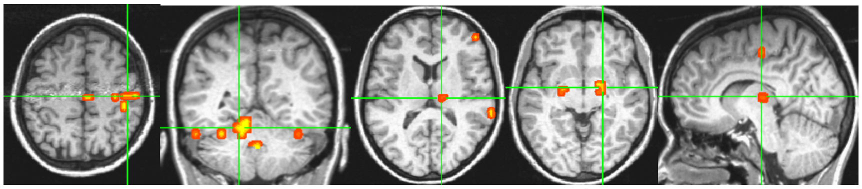
Functional images were acquired from a normal volunteer using a single-shot gradient echo EPI sequence (TR=3,000 ms, TE=50 ms, FOV=250×250×100 mm^3, matrix size=64×64×20) on a 1.5 Tesla MRI scanner. The subject performed a finger to thumb opposition task. The task consisted of 4 periods of 84 seconds, where each period contained 30 seconds of left hand finger opposition, 12 seconds of rest, followed by 30 seconds of right hand finger opposition, and another 12 seconds of rest. A 3D high-resolution anatomical image volume was also acquired from the subject using an MP-RAGE sequence. The EPI data were registered to the MP-RAGE images for anatomical localization. The first four volumes of the functional images were discarded and the remaining volumes were motion corrected using the AFNI software package. Linear drifts and mean components were then removed from each voxel time-series.

Results

One FCM algorithm was applied on a feature space containing four proposed features (α_1, α_2, α_3, and *cc*), and another FCM was applied on a feature space containing only *cc*. The latter detected only motor cortex, cerebellum, and supplementary motor area, where as the former was able to detect not only these areas (Fig 2.a and 2.b) but also some other sub-cortical areas such as thalamus (Fig 2.c and 2.e), temporal gyrus (Fig 2.c), and putamen (Fig 2.d). These sub-cortical areas, which previously reported in [5] using a more transient reference signal, seem to have more transient activation.

Conclusion

A new feature space based on modeling the HRF variability was proposed for FCM clustering of the fMRI data. It was applied to finger tapping fMRI data and revealed additional sensitivity by detecting activation in sub-cortical areas. This superior sensitivity comes from the ability of the elementary functions (and therefore proposed feature space) in modeling different shapes of the HRF.



(a) (b) (c) (d) (e)

Fig 2. Activation areas in a right hand finger opposition task detected using the proposed features.

References

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