Space-time analysis of fMRI by feature space clustering

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Feature-space clustering

The high temporal resolution of fMRI has inspired a host of single-voxel analysis methods. They typically compute some summary statistics characterising the temporal response in each voxel and represent them in the spatial domain by means of a brain map for visual inspection. Identifying regions with similar patterns of activation can however be automated using various clustering techniques. We have previously shown [2] that clustering on the cross-correlation function instead of the raw time series provides increased robustness. As each summary statistics represent part of the information in the fMRI, we extend and generalise this framework by extracting general features from single-voxel time series analysis, then clustering the feature space using the well-known K-means algorithm [1], a non-parametric method that estimates a sub-optimal cluster distribution by iteratively minimising the intra-class inertia of the clustered data.

Data

The dataset was acquired at Hvidovre Hospital on a 1.5 T Magnetom Vision MR scanner, with a 2D gradient echo EPI (T2* weighted) scanning sequence with 66 ms echo time, 50 degrees RF flip angle, and a scan target of 128x128 pixels, FOV of 230 mm, and 10 mm slice thickness. Images were obtained in a para-axial orientation parallel to the calcarine sulcus. Visual paradigm: 20 seconds rest (darkness), 10 seconds of full-field checker board reversing at 8 Hz, and 20 seconds rest. 10 runs of 150 images were acquired in 50 seconds (330 ms/image). Our dataset was built by leaving out the first and last 25 scans in 3 runs, corresponding to a total 300 time samples for each voxel.

Results

Three features are extracted from the cross-correlation of the fMRI activation with the paradigm: delay from stimulus onset to peak activation, strength of the peak activation and energy of the cross-correlated signal. Note that limited data lead to a noisy cross-correlation, hence potentially spurious features. This is countered by smoothing the resulting cross-correlation with an Epanechnikov kernel [3] using a common kernel size ($\sigma = 5$) for the entire volume. The 3-dimensional feature space is clustered with K-means using 9 clusters. Figure 1 displays a 2-dimensional PCA projection of the extracted features. Clusters are indicated by different markers: 98% of the voxels are non activated, and grouped in 5 evenly spread clusters, indicated by dots on the figure. Crosses and stars correspond to voxels with positive activation, located mainly in the visual field. Activation strength and energy are positively correlated with the first principal component, indicating a particularly high activation for the two starred voxels (top right). Circles correspond to voxels with a moderate *negative* activation. The average delay of the voxels with negative activation is $3\frac{1}{2}$ seconds, while the positive activations are delayed of an average 5 seconds. A study of the empirical delay distribution shows that this difference is significant at the 2% level.

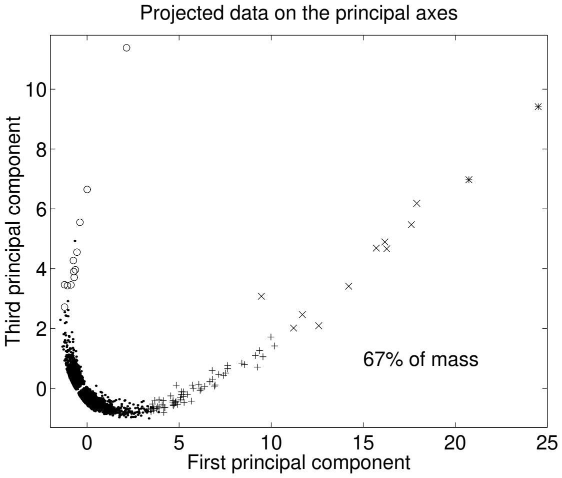

Figure 1: PCA of clustered features

Conclusions

Cluster analysis of feature space provides an original scheme for mapping the spatio-temporal distribution of focal neural activation. Current work addresses the use of a larger number of features, meta-analysis using features from different modelling and statistical methods, and employing more efficient clustering techniques.

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References

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