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Multivariate functional connectivity between fine-grained cortical activation patterns

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Introduction

Current measures of cortical connectivity generally rely on average activations within cortical areas or use seeds of activation to produce whole brain correlation maps. The distributed pattern of voxel activations in fMRI data contains information that is typically discarded by spatially smoothing or averaging signals. If the detailed neural activation pattern of a cortical region is influenced by the detailed activation pattern in another cortical region, this dependence should be observable in the mutual information between activation patterns in both regions. Here, we address this question by investigating whether the flow of information within cortex can be assessed by looking at relations between patterns of activations in different regions of interest (ROIs).

Methods

We used canonical correlation as a measure to look at the dependence of patterns of activation. More precisely, spatio-temporal activation patterns for a set of ROIs were extracted from an fMRI data set that included slowly paced voluntary finger movements. The dimensionality of the multivariate data was reduced by using principle component analysis (PCA) within ROIs. Finally, canonical correlation analysis (CCA) extracted the linear combinations of the temporal activation of principle components that were best correlated between ROIs. This analysis was repeated for various time delays between the two ROIs yielding a canonical cross-correlation.

Results

The canonical cross-correlation between cortical areas shows that patterns of cortical activation are strongly related with time lag zero, even if average fluctuations within ROIs are discarded. This finding indicates that fine-grained patterns of activation are related between cortical areas. More importantly however, an asymmetry in the canonical cross-correlation function indicates a temporal sequence of the correspondence of cortical activation patterns in different brain regions, which is significant for the group of subjects. The sequence of pattern activations in the data corresponds to the sequence that was inferred from decoding analysis.

Conclusion

The detailed structure of activation patterns within individual brain regions can be exploited to look at functional connections that do not depend on the average fluctuations within ROIs.

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