Principal networks: A new approach to graph-based neural connectivity analysis

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Introduction

There has recently been a considerable amount of interest in network representations of connectivity and other interrelationships between brain regions, and the derivation of such networks from MRI. In this approach, functional or structural connectivity information is represented in terms of a graph, a collection of “vertices”, representing brain regions, connected by “edges”, representing interconnections between regions (Bullmore 2009). The importance or weight of each edge is usually calculated in terms of a connectivity or correlational measure, and edges are selected by thresholding this measure. By contrast, the choice of regions to use as vertices is usually made in advance, despite the dependence of estimated network measures on this choice (Zalesky 2010). Here we use the technique of principal components analysis (PCA) as the basis for decomposing connectivity information into independent subnetworks. We demonstrate this new “principal networks” method with cortical thickness data derived from a volunteer group.

Methods

Two T_1-weighted 3D FLASH images were obtained for each of 8 healthy young adult volunteers (4 male, ages 23–31 yr) on a 1.5 T clinical MRI scanner. Automated cortical parcellation and estimation of cortical thickness was performed for each subject using the Freesurfer package (see Fig. 1), resulting in mean cortical thickness values for 32 gyral regions per hemisphere (Desikan 2006).

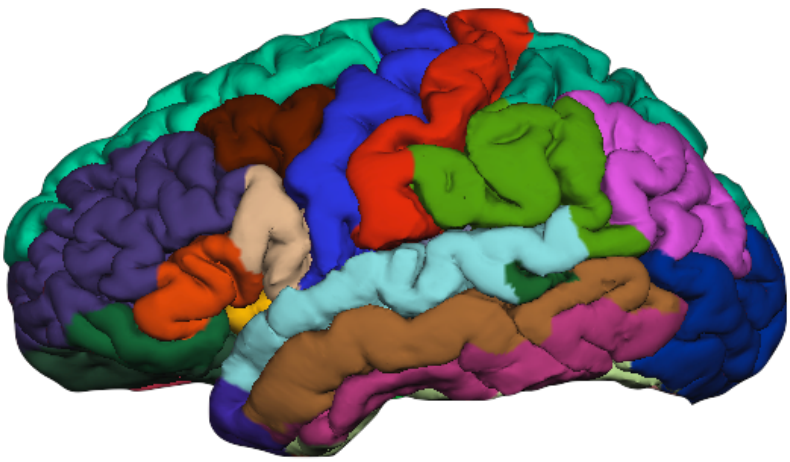

Figure 1

As in previous studies using cortical thickness (e.g. He 2007), we base the network on the correlation between thicknesses of different regions. But rather than consider the full correlation matrix as a single network, we decompose it into several components by applying PCA. This decomposition can be used to obtain a set of matrices which represent interactions between subnetworks of regions which “vary together”. Each component has an associated set of “loadings” which establish the importance of each brain region in that subnetwork.

For each submatrix derived from the PCA, a threshold (0.1 here) was applied to the loadings to determine which vertices to include in the corresponding principal network. Edge weights were calculated by subtracting the submatrices for more major components from the full correlation matrix, and then applying another threshold (0.2 here).

Results

Fig. 2 shows the full correlation matrix derived from our cortical thickness data. On the left is shown the unsorted matrix, whilst on the right appears the same matrix with its row and column order determined from the loadings of each region in the first (most important) principal network (PN).

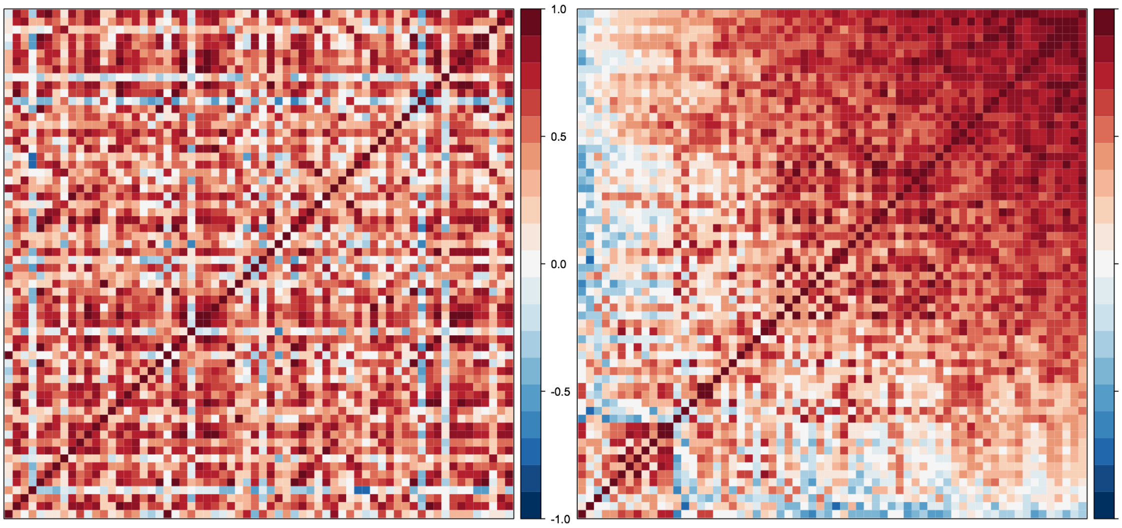

Figure 2

Figs 3 and 4 show the two main PNs as a correlation matrices and graphs respectively. As in Fig. 2, blue colours indicate negative correlations and red colours indicate positive correlations. The first PN—shown on top in each figure—involves 42 of the 64 regions, and is very densely connected (98% of edges were above threshold). It represents the broad links between cortical thickness measurements in the majority of brain regions. By contrast, the second PN involves only 28 of the 64 regions, and is less densely connected (68%). Amongst the most strongly-connected regions in the first PN are the left and right precuneus (vertices 23 and 55 in Fig. 4), an area which has been shown to be important in network studies based on diffusion imaging (e.g. Gong 2009). The two most strongly-connected regions in the second PN are the left and right posterior cingulate (vertices 21 and 53 in Fig. 4), another area which has been highlighted in previous work as representing part of a structural core of the brain (Hagmann 2008).

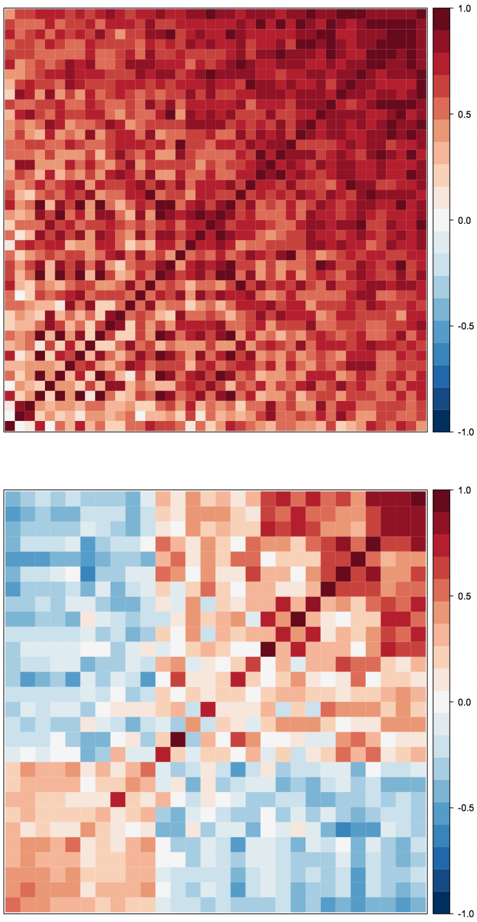

Figure 3

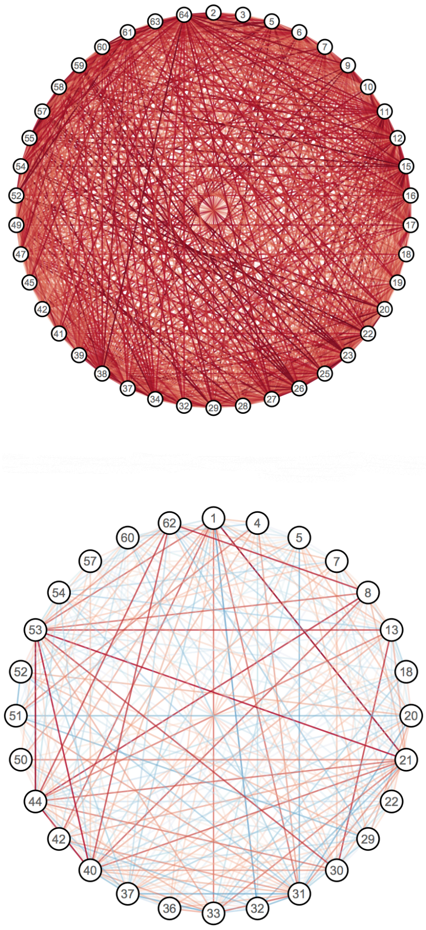

Figure 4

Conclusions

We have presented the concept of principal networks, an approach to decomposing connectivity or correlational information derived from brain imaging into subnetworks which can be analysed separately. We have shown that the most strongly-connected regions in each subnetwork match up to findings in the literature. Future work will expand the scope of the technique.

References

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