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**Citation for published version:**

Behrens, TEJ, Johansen-Berg, H, Drobnyak, I, Brady, JM, Matthews, PM, Smith, SM & Higham, DJ 2004, 'Deliniation of Functional Subunits in the Human Cortex from Diffusion Based Connectivity Matrices.'

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**Document Version:**

Peer reviewed version

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# Delimitation of functional subunits in the human cortex from diffusion based connectivity matrices.

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## Synopsis

We aim to explore whether diffusion tractography can be used to define functionally relevant anatomical subunits in the human visual system. Probabilistic diffusion tractography is used to generate connectivity distributions from every voxel in the visual system. A connectivity matrix of the visual system is derived from these distributions and submitted to a spectral reordering routine such that nearby nodes in the reordered matrix are strongly related in the data. The reordered matrix exhibits a hierarchical form in which clusters of nodes emerge. When mapped back into anatomical space, these clusters appear to correspond well with the ventral and dorsal processing streams in the visual system and primary visual cortex.

## Introduction

The anatomical connectivity pattern of a brain region determines its function [1]. Brain areas with distinct functions have different connectivity patterns. Conversely, regions with similar functions have similar connectivity patterns and are highly interconnected. The visual system in the primate brain exhibits both of these characteristics. In simple terms, visual information is sent from primary visual cortex (V1) along 2 broadly parallel processing streams [2] (Figure 1). The ventral pathway processes object form information and includes projections to inferior temporal lobe. The dorsal pathway processes information on object motion and includes projections to posterior parietal cortex. These two processing streams are densely intra-connected, but sparsely inter-connected [3]. Systems that exhibit these distinctive relationships in their connectivity patterns are known as hierarchically connected. A defining feature of such systems is that their connectivity matrices may be reordered (by simultaneous permutation of rows and columns) such that blocks of high connectivity appear around the leading diagonal [4]. Here we use non-invasive imaging of the human brain to provide pairwise connectivity information between all areas of the human visual system and submit these data to a spectral matrix reordering routine to test the hypothesis that they may be organised into a hierarchical form.

Diffusion Tractography has previously been used to track major white matter pathways e.g. [5,6] and to define boundaries in grey matter based on connectivity to predefined cortical regions [7]. Here, using only connectivity data derived from probabilistic diffusion tractography [8] we are able to divide the human visual system into anatomically discrete subunits that plausibly correspond to known functional units.

## Methods

Diffusion-weighted data were acquired with an optimised method [9] based on echo planar imaging, implemented on a General Electric 1.5 T Signa Horizon scanner with a standard quadrature head-coil and maximum gradient strength of 22 mT/m. 60 diffusion weighted volumes were acquired with diffusion gradients isotropically distributed in angular space, with a maximum b-value of 1150  $\text{mm}^2$ . Cardiac gating was applied to minimize artefacts due to CSF pulsatile flow.

Probabilistic tractography was carried out from each seed voxel in structural space, according to [8]. Connectivity values were stored from each seed voxel to every other voxel in the visual system (seed/target masks were resampled to a coarse resolution of  $10 \times 10 \times 10 \text{mm}^3$ ). Log connectivity information was arranged in a matrix, **A**. Symmetry was imposed on this matrix by computing  $C = (A + A^T) / 2$  (figure 2 (A)). The nodes in this matrix were then permuted using a spectral reordering algorithm [10]. This algorithm looks for the node reordering which minimises the sum of element values multiplied by the squared distance of that element from the diagonal, hence forcing large values to the diagonal. The algorithm does not search for clusters in the matrix. Clusters that emerge are due to organisation in the data.

## Results

Figure 2 shows the connectivity matrix in its original form (**A**) and after spectral reorganisation (**B**). The matrix was divided by eye into 3 dominant clusters (horizontal coloured bars in Fig 2(b)). These clusters were then mapped back onto their anatomical location (Figure 3). The first cluster (blue) included lateral parietal lobe corresponding to putative dorsal visual stream. The second cluster (yellow) included inferior occipital lobe and inferior temporal lobe corresponding to putative ventral visual stream. The third cluster (red) included medial occipital lobe corresponding to putative primary visual cortex (V1). Clusters are consistent across subjects.

Ventral and dorsal streams

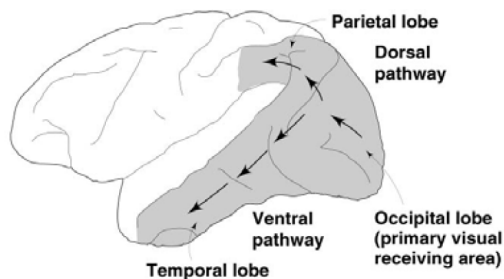


Fig 1

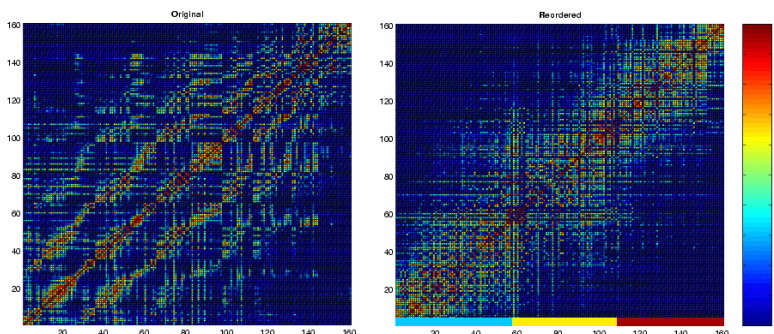


Fig 2

A

B

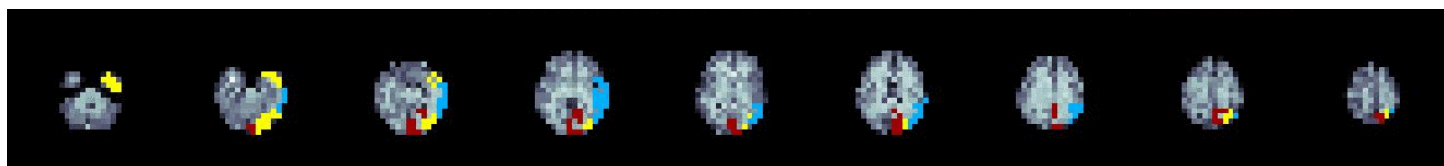


Fig. 3

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