Diffusion tensor data localises functional boundaries.

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Introduction

Our understanding of functional architecture in the brain relies on our ability to localise neural response with respect to known regions of functional specialisation. The boundaries that describe these regions do not always lie in a consistent location with respect to local landmarks in the gross gyral and sulcal anatomy. A better prediction of the local functional architecture might be expected from the white matter connections emerging from a region: connections to other brain areas directly constrain a region's function. We have previously used diffusion tractography to identify two regions of distinct connectivity within medial frontal cortex, showing with functional MRI that these regions correspond to the supplementary motor area (SMA) and preSMA: cortical regions of distinct function and cytoarchitecture [1]. Here we find a relationship between the functionally defined SMA/preSMA boundary and the *local* diffusion tensor field. The functional boundary lies in a consistent location with respect to features of the diffusion data such as the local fibre orientations, but not with respect to the sulcal and gyral anatomy. We show that if information about local fibre orientation is incorporated in the realignment process, the alignment of the functional boundary across subjects is improved.

Methods

Data Acquisition: We acquired Diffusion tensor, T1-weighted and functional MR data in 9 subjects. During the acquisition of the FMRI data, subjects performed repetitive 30 second blocks of finger tapping ('move'), rest and serial subtraction ('count'). Contrasts of 'move' against 'rest' consistently included activation in the region of medial frontal cortex where we expected to find SMA. Contrasts of 'count' against 'rest' consistently included activation just anterior to this, in the region where we expected to find preSMA.

Data alignment within an individual: Affine transformations were computed between diffusion-weighted, functional and T1-weighted spaces within each subject allowing features in each dataset to be compared directly.

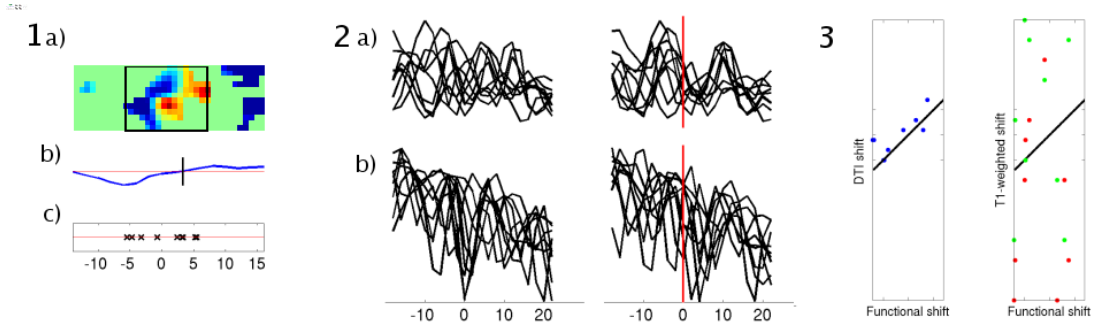
Initial data alignment across individuals: Data were initially aligned across individuals using whole-brain affine registration of the T1-weighted images. The functional and DTI data were transformed according to this affine transformation. Diffusion tensors were reoriented according to [2]. After this stage subjects were considered to be aligned according to their global brain shape. We then tested whether subsequent alignment based on local diffusion tensor or T1-weighted information led to any improvement in functional alignment across subjects.

Results

Functional location of the SMA/preSMA boundary: We computed a contrast between 'count' and 'move' blocks in a region of interest in medial frontal cortex (Fig 1(a): activation within ROI for one subject, posterior to anterior running left to right). The SMA/preSMA boundary lies predominantly in the coronal plane so we formed a profile of this 'count-move' contrast along a line perpendicular to this plane (fig 1(b)) by summing the data along the x and z axes. The SMA/preSMA boundary was taken to be the coronal plane at which this profile crossed zero (i.e., when count>move, black line). Across individuals, the SMA/preSMA boundaries were distributed about the vertical line from the anterior commissure (fig 1c).

Functionally relevant features in diffusion data: In each subject, we formed scalar images of the x, y and z components of the diffusion direction modulated by the fractional anisotropy at each voxel. From each of these images we formed a profile along the anterior-posterior axis similar to the functional profiles described in the previous section. These profiles exhibited little consistency across subjects (Fig 2a left shows the x-profiles across all subjects). We then translated the data from each subject in the anterior/posterior axis such that the functional boundary derived in the previous section occurred at y = 0. After realignment of the subjects on the basis of their functional boundaries, the x and z diffusion profiles exhibited significantly increased consistency across subjects (figure 2(a) right shows the functionally aligned x-profiles). This suggests that local features of the connectional architecture might be used to predict the location of the functional boundary. By contrast, functionally aligning profiles of T1-weighted image intensity in the same way did not improve consistency across subjects (fig 2b –right), suggesting that sulcal and gyral architecture do not predict function.

Functional variability is reduced after local alignment by diffusion tensor data, but not anatomical data: We took data from a small region of interest in two slices of medial frontal cortex after initial alignment according to global brain shape and tested whether subsequent alignment based on either connectional architecture of gross anatomy would affect the alignment of the functional boundary across subjects. First, we searched for the anterior/posterior shift between subjects which maximized the "tensor scalar product" objective function described in [3] after normalisation of the tensors to a constant volume. This will match images according to the orientation of the diffusion tensors at each voxel, reflecting the connectional architecture. We also computed this shift based on the same region of interest in the T1-weighted images and two commonly used objective functions for scalar data, normalised correlation (NC) and mutual information (MI). This will match images according to intensities in the T1 images, reflecting sulcal and gyral anatomy. After applying the optimal shifts computed from each dataset, we tested whether the standard deviation across subjects in the location of the functionally defined boundary had increased or decreased. After realignment on the basis of the DTI data, the standard deviation was reduced by a factor of 1.6 (4.2mm -> 2.6mm). After realignment according the T1-weighted data, the standard deviation was *increased* by factors of 2.2 (NC) and 2.3 (MI). Figure 2 shows a significant correlation between the optimal shifts computed from the DTI data and the shifts required to align the functional boundaries exactly (r=0.78). No such correlation exists for the T1-weighted data (r=-0.018,-0.016).



Discussion

We have shown that incorporating information about local diffusion tensor orientation in the registration process improves functional alignment across subjects. This suggests that there is a consistent relationship between local connectional architecture and functional specialisation. Extending this approach to incorporate diffusion tensor information in non-linear whole brain registration should increase the potential for interrogating functional architecture across individuals.

[1] Johansen-Berg et al. PNAS 2004. [2] Alexander et al. IEEE TMI 2001. [3] Alexander et al, proc. BMVC 1999