fMRI-guided DTI Fiber Tracking: A Verification Study in the Basal Ganglia

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Introduction

Diffusion Tensor Imaging (DTI) [1] is a promising non-invasive method for studying white matter structure of the human brain in vivo. Based on the determined diffusion direction, the fiber network in the brain can be reconstructed by so-called Fiber Tracking (FT) Algorithms [2]. Until now, a variety of different algorithms has been proposed. However, no standard procedure, neither to compare nor to validate the results, has been established. A key obstacle for reconstructing neuronal fibers is the definition of an appropriate seed region. Recently, start regions have been selected in anatomical areas defined by functional MRI (fMRI) activation patterns. With this approach, one attempts to reconstruct the anatomical networks underlying the specific functional systems [3, 4].

In this study, the sensorimotor system has been examined, investigating known cortico-subcortical connections between putamen and primary/sensorimotor cortex (M1/S1). The focus was to combine fMRI with DTI to validate tracking results and to demonstrate the feasibility of fMRI-guided DTI tracking for generating functionally relevant connections. Therefore, the somatotopical organization of the putamen has been derived twice: Firstly, an fMRI based somatotopy was obtained by four motor tasks. Secondly, two tracking algorithms (FACT [2] and advanced Fast Marching (aFM) [5]) were applied to derive somatotopical maps, revealing connection probabilities between fMRI-evoked regions in M1/S1 and putamen. Finally, the somatotopical maps and the fiber connections were compared and analyzed.

Methods

Six healthy, right-handed volunteers (26.5 ± 3.8 years) participated in the study. All acquisitions were performed on a 3 T whole-body system (Philips, Best, the Netherlands), equipped with an 8-element receive head coil array (MRI Devices Corp., Waukesha, USA). Each session consisted of one DTI scan (single-shot spin-echo EPI sequence, acq. matrix = 96 x 96, rec. matrix = 128 x 128, FOV = 200 x 200 mm^2, 60 contiguous slices, thickness = 2.1 mm, TE = 50 ms, NSA = 2, SENSE factor = 2.1, b-factor = 1000 s/mm^2, 15 icosahedral diffusion encoding directions), one high-resolution T1-weighted anatomical scan and four fMRI scans. The anatomical data were obtained using a T1-weighted TFE scan with 180 contiguous slices (slice thickness = 0.7 mm, FOV = 200 x 200 mm^2, matrix = 256x256, TR = 20 ms). The fMRI experiments were carried out using a gradient echo EPI sequence, covering the whole brain with 30 contiguous slices (thickness = 4.2 mm, matrix = 128 x 128, FOV = 200 x 200 mm^2, TR = 3000 ms, TE = 40 ms, SENSE factor = 2.0). The subjects performed four different motor tasks (7 min block paradigm) with closed eyes: (1) Flexion and extension of the right toes, (2) flexion and extension of the right fingers, (3) right cheek movement, (4) horizontal, saccadic eye movement.

The fMRI data were analyzed with SPM2. To compute the fMRI somatotopy, the individual SPM {T} maps were normalized and investigated to find clusters which were commonly activated in several subjects. The DTI-based somatotopical maps were generated as follows: The seed regions for the tracking algorithms were defined in the left PriMC on the basis of the fMRI activations. Therefore the center of gravities (COGs) were calculated for foot, hand and face activation (the eye movement task was excluded from the DTI-analysis because eye movements follow a different mechanism than body movements). In order to launch the tracking algorithms in the adjacent white matter, the COGs were blown up spherically [4]. Tracking was performed thrice for every putamen-voxel, i.e. starting from the foot, face and hand region in the cortex. For the resulting three connections, a connection-probability was calculated and the most probable connection was assigned to the corresponding putamen-voxel. As last step, the individual somatotopical DTI maps were normalized and locations connected most likely to the same cortical region within several subjects were determined.

Results

Fig. 1 illustrates the somatotopical group map obtained by fMRI, revealing areas which were activated in at least 4 out of 6 subjects. The data show a dorso-ventral gradient with foot (red) lying dorsally, face (blue) ventrally and hand (green) and eye (yellow) in between. Furthermore, activity follows an anterio-posterior face-foot gradient with hand and eyes in between. Fig. 2 depicts a somatotopical map derived by DTI, generated with the aFM algorithm. Green voxels represent regions which are most likely connected to the hand area (in at least 5 out of 6 subjects), red voxels to the foot area (in at least 4 out of 6 subjects) and blue voxels to the face area (in at least 4 out of 6 subjects). The hand area is stronger represented than the face or foot area. The DTI somatotopy shows an anterio-posterior gradient, which is consistent with the results of the fMRI somatotopy (Fig. 1). In contrast to the fMRI analysis, the dorso-ventral gradient is not present. This is due to the foot representation, which is located more ventrally compared to the fMRI somatotopy. The FACT algorithm was unable to reconstruct any connections between cortex and putamen. Thus, a somatotopical map could not be compiled. Visual inspection of the fibers reconstructed by the FACT algorithm revealed a deflection of all fibers into major fiber pathways, as e.g. into the system of the Corpus Callosum or into superior longitudinal association tracts.

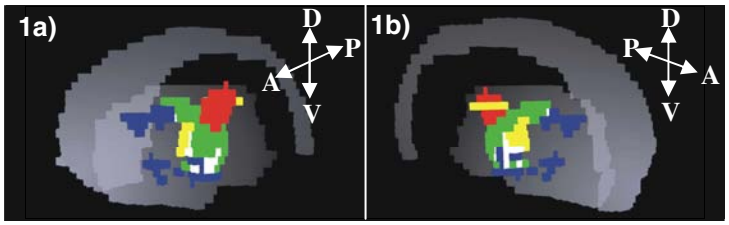

Fig. 1: Lateral (1a) and medial (1b) views of the right basal ganglia. Both figures show the somatotopical group maps, based on the fMRI evoked BOLD activation inside the putamen. Green corresponds to finger, red to toe, yellow to eye and blue to cheek.

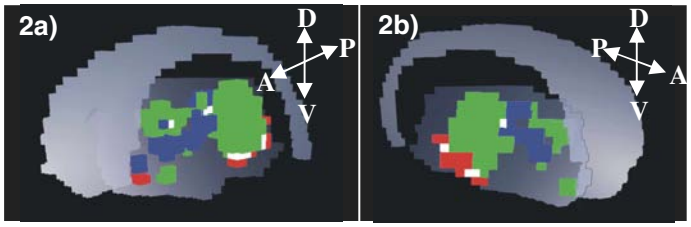

Fig. 2: Lateral (2a) and medial (2b) views of the right basal ganglia, showing the somatotopy based on DTI data. Red voxels correspond to foot, blue voxels to face and green voxels to hand.

Discussion and Conclusion

The fMRI somatotopy is consistent with the findings of a recent fMRI study [6]. The DTI somatotopy generated with the aFM algorithm is also in good agreement with the fMRI outcome. The reconstruction of the connections between cortex and putamen probes the boundaries of DTI fiber tractography. While the aFM algorithm reconstructed a clearly separated somatotopy, the standard FACT algorithm could not find any connection between cortex and putamen. All trajectories were deflected by the gross fiber bundles. Also with the aFM algorithm, which was designed especially for coping well with crossing regions, the effect of major pathways could not be ruled out completely, which reflects in the overrepresentation of the hand area.

The main scope of this work was to evaluate the practicability of fMRI-guided DTI fiber tracking. Based on the fMRI/DTI combination approach, a technique has been developed for in-vivo verification of tracking algorithms. In conclusion, the study demonstrates that DTI highly benefits from the combination with fMRI. FMRI joins in where DTI meets its limits, namely in defining functionally related structures as accurate start regions for fiber tracking. FMRI-guided fiber tracking provides a promising tool for addressing issues of functional connectivity in the human brain. Furthermore, it allows a comparison and validation of tracking results.

References

[1] Basser PJ et al., Biophys J 1994, 66: 259-267. [2] Mori S. et al, NMR in Biomedicine 2002, 15: 468-480. [3] Pamar H et al., J of Computer Assisted Tomography 2004, 28: 551-556. [4] Staempfli P et al. Proc ISMRM 2004, 1287. [5] Staempfli P et al., NeuroImage 2005, In Press. [6] Gerardin E et al., Cereb Cortex 2003, 13: 162-169.