RELIABLE SEGMENTATION OF SUBCORTICAL GRAY MATTER STRUCTURES USING MAGNETIZATION TRANSFER (MT) MAPS

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Introduction:

While much work has been devoted to MRI-based segmentation and voxel-based morphometry (VBM) of cortical anatomy, comparatively few studies have investigated deep grey matter structures. These are of particular interest for study of the structural correlates of neurological and neuropsychiatric disorders associated with basal ganglia dysfunction (1). The relatively small number of segmentation studies is partly due to difficulties delineating these structures using standard methods of structural T1-weighted 3D MRI (for review, see (2)). Automatic segmentation of the basal ganglia and thalamic structures is less reliable, since unlike the cortex, the basal ganglia and thalamus are made up of a large number of neuronal nuclei that are connected by complex and intertwined axonal tracts. Also the high iron content of some midbrain nuclei of the extrapyramidal pathway (e.g., substantia nigra) shortens T1 significantly (3). The partial volume effect and shortened T1 reduce the contrast in T1w images and lead to segmentation problems. We propose the use of parameter maps based on magnetization transfer (MT) contrast to overcome these problems, since MT is a more direct measure of the content of "structural material" such as myelin, which is unlike T1 contrast which chiefly reflects the physical properties of tissue water. We compared the segmentation results derived from MT maps (4) to an established T1w MDEFT method (5) in a cohort of 49 subjects. Considerable improvements were observed in putamen, pallidum, substantia nigra and thalamus.

Methods:

Data acquisition

49 healthy adults (age 18-85; m/f = 24/25) were examined on a 3T whole-body MRI system (Siemens Magnetom TIM Trio) operated with a 12-channel head receive and body transmit RF coil. Written informed consent was obtained as supervised by the local Ethics committee. Three whole-head 3D multi-echo FLASH datasets were acquired with predominantly T1-weighting (TR/α = 18.7 ms/20°), PD-w (23.7 ms/6°) and MT-w (23.7 ms/6°, excitation preceded by an off-resonance MT-pulse) at 1 mm isotropic resolution as described in (4). The signals of 6 equidistant bipolar gradient echoes (at 2.2 to 14.7 ms echo time) were averaged to increase the SNR while maintaining a high readout bandwidth for minimal distortions (425 Hz/Px). T1w structural imaging was performed using a 3D MDEFT sequence with compensation for inhomogeneous flip angle excitation (5). Semi-quantitative MT parameter maps, corresponding to the additional saturation created by a single MT pulse, were calculated as described previously (4, 6).

Data processing

Data processing and analysis were performed with SPM5 (Wellcome Trust Centre for Neuroimaging, http://www.fil.ion.ucl.ac.uk/spm) running under Matlab 7 (Mathworks, USA). The pre-processing involved segmentation and normalisation of the three-dimensional image data. The structural data were partitioned into different tissue classes - gray matter (GM), white matter (WM) and non-brain voxels (CSF, skull) using the unified segmentation approach in SPM5 (7). The resulting segments were registered to the same stereotactic space using DARTEL, which estimates normalisation parameters by simultaneously and iteratively registering the gray and white matter images of all subjects (8). Subsequently, all probability (ß) image intensities were "modulated" by the appropriate Jacobian determinants and then averaged across the group.

Results:

The population-averaged GM maps revealed a greater probability of identification of iron-rich midbrain nuclei on MT maps compared to T1w images, in substantia nigra (Fig. 1a), the posterior putamen (Fig. 1b), and the lateral pallidum. In addition, the segmentation of the pulvinar nuclei of the thalamus improved. However, little or no difference was seen in GM structures containing a large number of axonal connections, like the medial pallidum, the lateral thalamus and the red nucleus. Here, MT was generally higher than in GM being sensitive to myelin and thus axonal content. In regions affected by susceptibility effects, the MT-based GM maps showed better spatial congruence due to the higher bandwidth of the multi-echo FLASH acquisitions (425 Hz/Px).

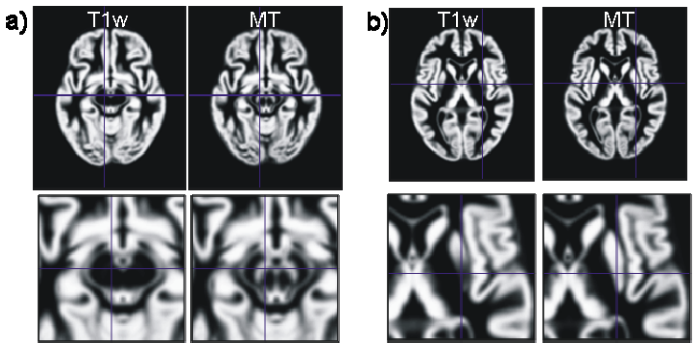

Fig. 1: Population-averaged GM maps based on the T1w MDEFT images or MT maps. a) substantia nigra, b) posterior putamen

Discussion:

We show that the improved contrast in single subject MT maps (4, 6) translates into a significantly improved delineation of subcortical structures in population-averaged GM maps. Via shortening of T1, iron accumulation in normal aging (3) and disease degrades T1 contrast and may systematically interfere with segmentation, which is crucial to T1w-based voxel-based morphometry (VBM). Further, the semi-quantitative MT maps intrinsically correct for any influence of T1 (6). Thus, this method promises to be a powerful novel approach to VBM of subcortical structures. We are currently applying the method to the study of healthy populations and also different neurodegenerative diseases.

References:

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