AUTOMATED SEGMENTATION OF MIDBRAIN STRUCTURES USING QUANTITATIVE SUSCEPTIBILITY MAPPING IMAGES

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TARGET AUDIENCE: Researchers interested in segmentation of midbrain structures and/or quantitative susceptibility mapping.

PURPOSE: Segmentation techniques based on T1w images cannot provide accurate segmentation of the red nucleus, subthalamic nucleus and substantia nigra, owing to their low contrast. These structures are, nevertheless, clearly visible on quantitative susceptibility mapping (QSM) images due to their high iron content. Given the research and clinical interest in these brain structures[1–3], in the present work we propose a fully automated multi-atlas segmentation method based on QSM images.

METHODS: Subjects were imaged on a Discovery MR750 3T scanner (General Electric, Milwaukee, WI, USA) with an 8-channel phased array receiving coil. T1w 3D SPGR images were obtained with 0.9375 × 0.9375 × 1 mm^3 voxel size (TE = 3.06 ms, TR = 7.908 ms, TI = 450 ms, FoV = 24 cm, 176 axial slices, flip angle of 12°). Additionally, a 3D multi-echo gradient-echo sequence was also acquired, with spatial resolution of 0.9375 × 0.9375 × 1 mm^3 (TR = 37.52 ms, FoV = 24 cm, 146 axial slices, flip angle of 20°). The first echo time was equal to 3.74 ms and it was followed by seven additional ones, with a 3.752 ms interval between consecutive echoes. Quantitative susceptibility maps were obtained using the pipeline available in http://weill.cornell.edu/mri/pages/qsm.html. Firstly, the frequency at each voxel was estimated from the complex multi-gradient echo signal via a non-linear least squares fitting [4]. The resulting frequency maps were then spatially unwrapped and the projection on dipole fields algorithm applied to estimate the background field gradients, which were subsequently removed from the data. Morphology enabled dipole inversion was employed to produce the final susceptibility maps[5]. An operator delineated manually the red nucleus (RNl/RNr), substantia nigra (SNl/SNr) and subthalamic nucleus (STNl/STNr) on QSM images visualized with the MRIcron software (http://www.mccauslandcenter.sc.edu/ mricro/mricron/). The manual labels together with the T1w image and the QSM image form an atlas. To produce the segmentation of a target subject, first of all the T1w images were non-linearly registered to the target T1w image (with FNIRT from the FSL library, http://fsl.fmrib.ox.ac.uk). In order to align the midbrain more accurately, a second non-linear registration was computed using QSM image intensities only within this region. The transformations obtained were concatenated and applied to the labels to propagate them to the space of the target subject. This process was repeated for each of the atlases. The propagated labels for all the atlases were combined under a label fusion scheme to produce spatial probability maps for each of the structures. These maps were included as spatial priors in a generative model representing image intensities as a mixture of Gaussians (two for the background class and one for each of the structures of interest), and parameter estimation was done by expectation-maximization. This process was done in a cross-validated fashion to obtain segmentations of each of 16 subjects using N randomly selected atlases, with N varying from 1 to 15.

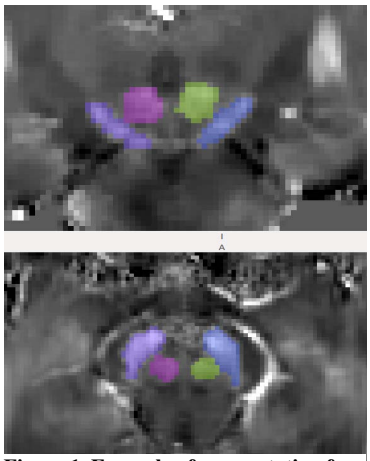

Figure 1. Example of segmentation for one subject (only RN and SN shown).

RESULTS: Figure 1 shows an example of segmentation for one subject. Dice overlap scores comparing the manual and the automated segmentations are shown in figure 2A, ranging from 0.66 (STN) to 0.85 (RN). The dependence between Dice scores and the number of atlases is depicted in figure 2B.

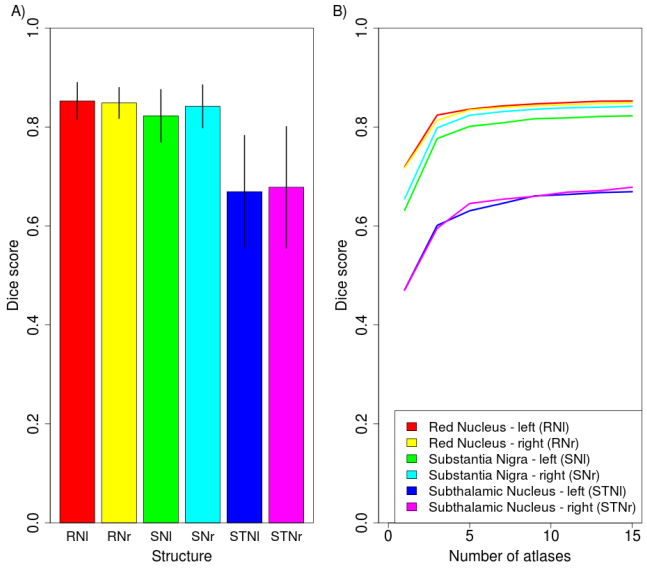

Figure 2 A) Dice scores for the midbrain structures. B) Dependence of the Dice scores on the number of atlases used.

DISCUSSION: The algorithm showed appropriate performance under visual inspection. Overlap scores were high for RN and SN, and moderate for the STN, which is a smaller structure with lower contrast. There was little additional performance gain when using more than ten atlases. Future enhancements of the algorithm will include smoothness constraints, performance optimization and validation on a larger dataset.

CONCLUSION: We present a fully automated algorithm for segmentation of the RN, SN and STN from a pair of T1w and QSM images, aimed at providing accurate, objective and reproducible segmentations of these structures.

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